

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 20:27:58 ; Search time 16892 seconds
(without alignments)
11573.266 Million cell updates/sec

Title: US-10-016-496-1
Perfect score: 4134
Sequence: 1 aattccgtgtgtcgggttc.....aagcgcccgacagcaacgg 4134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4134	100.0	4134	6	AR182343 Sequence
2	4134	100.0	4134	6	AR236221 Sequence
3	4134	100.0	4134	6	AR243543 Sequence
4	4134	100.0	4134	6	AR254415 Sequence
5	4134	100.0	4134	6	AR321738 Sequence
6	4134	100.0	4134	6	AR411424 Sequence
7	4134	100.0	4134	6	AR432994 Sequence
8	4134	100.0	4134	6	AX417770 Sequence
9	4134	100.0	4134	6	AX449101 Sequence
10	4134	100.0	4134	6	AX743965 Sequence
11	4116	99.6	4116	5	AF406649 Squalus a
12	1745.2	42.2	3234	6	BD205377 G protein
13	1745.2	42.2	3234	6	AX542191 Sequence
14	1745.2	42.2	3234	6	CO714283 Sequence
15	1745.2	42.2	3783	6	AX548832 Sequence
16	1745.2	42.2	3783	9	HSU20759 Human parat
17	1745.2	42.2	3809	6	AR012624 Sequence
18	1745.2	42.2	3809	6	AR028467 Sequence
19	1745.2	42.2	3809	6	AR078219 Sequence

20	1745.2	42.2	3809	6	AR145170 Sequence
21	1745.2	42.2	3809	6	AR177783 Sequence
22	1745.2	42.2	3809	6	175053 Sequence 3
23	1745.2	42.2	3809	6	AX429806 Sequence
24	1745.2	42.2	3809	6	AX702238 Sequence
25	1743.6	42.2	3234	6	BD240837 Isoforms
26	1743.6	42.2	3234	6	AR270869 Sequence
27	1743.6	42.2	3234	9	HSPCAR1
28	1743.6	42.2	3234	9	S83176 Homo sapien
29	1743.6	42.2	3361	9	HUMCASR
30	1738	42.0	5249	4	S67307
31	1738	42.0	5275	6	AR012622 Sequence
32	1738	42.0	5275	6	AR028465 Sequence
33	1738	42.0	5275	6	AR078217 Sequence
34	1738	42.0	5275	6	AR177781 Sequence
35	1738	42.0	5275	6	175051 Sequence 1
36	1703.6	41.2	5006	6	AR012623 Sequence
37	1703.6	41.2	5006	6	AR028466 Sequence
38	1703.6	41.2	5006	6	AR078218 Sequence
39	1703.6	41.2	5006	6	AR145169 Sequence
40	1703.6	41.2	5006	6	AR177782 Sequence
41	1703.6	41.2	5006	6	175052 Sequence 2
42	1703.6	41.2	5006	6	AX429805 Sequence
43	1703.6	41.2	5006	6	AX702237 Sequence
44	1703.6	41.2	5009	9	HSU20760 Human extra
45	1703.6	41.2	5009	11	G28586 human STS S

ALIGNMENTS

RESULT 1
AR182343
LOCUS AR182343 4134 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6337391.
ACCESSION AR182343
VERSION AR182343.1 GI:20225259
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 4134)
AUTHORS Harris,H.William., Brown,E.M. and Hebert,S.C.
TITLE Polyclonal-sensing receptor in aquatic species and methods of use
JOURNAL Patent: US 6337391-A 1 08-JAN-2002;
FEATURES
Location/Qualifiers
source
1..4134
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN	Query Match	100.0%;	Score 4134;	DB 6;	Length 4134;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 4134;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AATTCGTTGCTGCGTTTCAGTCCAAAGTCTCTCCAGTCCAAATGAGAAATGGTGGTC	60		
Db	1	AATTCGTTGCTGCGTTTCAGTCCAAAGTCTCTCCAGTCCAAATGAGAAATGGTGGTC	60		
Qy	61	GCCATTACAGGAACATGCATCTCTGTTAATGAATATTGTGAGTTATCTGAAGGT	120		
Db	61	GCCATTACAGGAACATGCATCTCTGTTAATGAATATTGTGAGTTATCTGAAGGT	120		
Qy	121	TATTAATAATTTCTGCAAGATGGTTCACGAAATCAATTTGACACCTTTTCCATT	180		
Db	121	TATTAATAATTTCTGCAAGATGGTTCACGAAATCAATTTGACACCTTTTCCATT	180		
Qy	181	GTCAATTCATGAATACTGACCAAGGATGTAACAAATGGAACAAAGCTGAGGACAC	240		
Db	181	GTCAATTCATGAATACTGACCAAGGATGTAACAAATGGAACAAAGCTGAGGACAC	240		
Qy	241	GTTCCACCTTTTCTGGAGCATACGATCAACCTTGAAGGAGATGGAAGACTTGAGGAGAA	300		

Db 241 GTTCACCCCTTTCTTGGAGCATACGATCAACCTCGTAAGGAGATGGAAGACTTTCAGAGGAA 300
Qy 301 ATGGGANTGATCTTCCAGGAGTTCTGTGTAAAGCGATCCCTCAACATTAACAAGATAA 360
Db 301 ATGGGANTGATCTTCCAGGAGTTCTGTGTAAAGCGATCCCTCAACATTAACAAGATAA 360
Qy 361 GCAGAAATCCTCCAGGATCTCTGTGTAAAGCGGCTGGGTAGTGTGGTCTTGTCAAGGAA 420
Db 361 GCAGAAATCCTCCAGGATCTCTGTGTAAAGCGGCTGGGTAGTGTGGTCTTGTCAAGGAA 420
Qy 421 CAGAGACAGGGTGCAATAGGCTCAGCTTCACTGCCAACTCTTATTTCTTGGGATTTACA 480
Db 421 CAGAGACAGGGTGCAATAGGCTCAGCTTCACTGCCAACTCTTATTTCTTGGGATTTACA 480
Qy 481 CTCCTACAGTCGTACAAATCTCTCAGGGTATGCTCCAAACCAAGGCGCCAGAAGAAAGGA 540
Db 481 CTCCTACAGTCGTACAAATCTCTCAGGGTATGCTCCAAACCAAGGCGCCAGAAGAAAGGA 540
Qy 541 GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
Db 541 GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
Qy 601 TTAAATCCAGACCGGAGCGGACAAATGTATTCGGTACAAATTTTCGAGGCTTCGGATGG 660
Db 601 TTAAATCCAGACCGGAGCGGACAAATGTATTCGGTACAAATTTTCGAGGCTTCGGATGG 660
Qy 661 CTCAGGCGATGATATTCGCAATTTGAAGAGATTAACAACAGATGACATTTCTGCCCAAT 720
Db 661 CTCAGGCGATGATATTCGCAATTTGAAGAGATTAACAACAGATGACATTTCTGCCCAAT 720
Qy 721 ATCACCTGGGATATCCGATATTTGACAGGTGTACACCGTGTCCAAAGCGCTAGAGGCA 780
Db 721 ATCACCTGGGATATCCGATATTTGACAGGTGTACACCGTGTCCAAAGCGCTAGAGGCA 780
Qy 781 ACACCTGAGCTTTGGCCAGACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
Db 781 ACACCTGAGCTTTGGCCAGACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
Qy 841 TGCTCTGACCATATCCATCCCAATAGCAGTGGTTCGGGCAACCGGGTCAGGAATCTCC 900
Db 841 TGCTCTGACCATATCCATCCCAATAGCAGTGGTTCGGGCAACCGGGTCAGGAATCTCC 900
Qy 901 ACGGCTGTGGCCATCTATGGGATTTATTTACATTCACAGGTGAGTATGCTCTCCCTCG 960
Db 901 ACGGCTGTGGCCATCTATGGGATTTATTTACATTCACAGGTGAGTATGCTCTCCCTCG 960
Qy 961 AGCAGGCTGTCTAGCAACAAAGATAGTACAAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
Db 961 AGCAGGCTGTCTAGCAACAAAGATAGTACAAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
Qy 1021 GAGCAACAGGCCACCGCCATGCGCCAGATCATCGAGCACTTCAGTGGAATCTGGGTGGGA 1080
Db 1021 GAGCAACAGGCCACCGCCATGCGCCAGATCATCGAGCACTTCAGTGGAATCTGGGTGGGA 1080
Qy 1081 ACCCTGGCAGCCAGCATGACTATGCGCCAGGCAATGACAAGTTCCGGAGAGGCGCC 1140
Db 1081 ACCCTGGCAGCCAGCATGACTATGCGCCAGGCAATGACAAGTTCCGGAGAGGCGCC 1140
Qy 1141 GTTAAGAGGAGACATCTGTATGATCTTCACTGAGATGATCTCTCAGTACTACACCGAAG 1200
Db 1141 GTTAAGAGGAGACATCTGTATGATCTTCACTGAGATGATCTCTCAGTACTACACCGAAG 1200
Qy 1201 CAGTTGGAGTTTATCGCCGAGCTCATCCAGACTCTCTCGCCAGGTCATCTGCTCTTC 1260
Db 1201 CAGTTGGAGTTTATCGCCGAGCTCATCCAGACTCTCTCGCCAGGTCATCTGCTCTTC 1260
Qy 1261 TCCAAATGGCCCGACCTGGAGCGGCTCATCCAGGAGATAGTTTCGGAGAAACATCACCGAT 1320
Db 1261 TCCAAATGGCCCGACCTGGAGCGGCTCATCCAGGAGATAGTTTCGGAGAAACATCACCGAT 1320
Qy 1321 CGGATCTGGCTGGCCAGCGGCTTGGGCGAGCTTCTGCTCATTCGCCAAGCCAGGTAC 1380
Db 1321 CGGATCTGGCTGGCCAGCGGCTTGGGCGAGCTTCTGCTCATTCGCCAAGCCAGGTAC 1380

Qy 1381 TTCCAGTGGTTCGGCGGACCATCGCTTCGTCTCAGGGCGGGCGGTATCCAGGGTTC 1440
Db 1381 TTCCAGTGGTTCGGCGGACCATCGCTTCGTCTCAGGGCGGGCGGTATCCAGGGTTC 1440
Qy 1441 AACAAATTCCTGAAGAGGTTCACCCACGAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG 1500
Db 1441 AACAAATTCCTGAAGAGGTTCACCCACGAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG 1500
Qy 1501 TTCTGGAGGAGACCTTCAACTGCTACTTACCGAGAGACCTCTGACGAGCTGGAAGAT 1560
Db 1501 TTCTGGAGGAGACCTTCAACTGCTACTTACCGAGAGACCTCTGACGAGCTGGAAGAT 1560
Qy 1561 TCCAAGGTGCCCTCGCACGAGCCGGCGGTCAAGGGAGCGGCTCCAAGGCGGGAACTCC 1620
Db 1561 TCCAAGGTGCCCTCGCACGAGCCGGCGGTCAAGGGAGCGGCTCCAAGGCGGGAACTCC 1620
Qy 1621 AGACGACAGCCCTACGCCACCCCTGCACTGGGAGGAGAAACATCACGAGCTGGAGACC 1680
Db 1621 AGACGACAGCCCTACGCCACCCCTGCACTGGGAGGAGAAACATCACGAGCTGGAGACC 1680
Qy 1681 CCCTACCTGATTTATACACACCTGAGGATCTCTCAATGTATACGTGGCGGTCTACTCC 1740
Db 1681 CCCTACCTGATTTATACACACCTGAGGATCTCTCAATGTATACGTGGCGGTCTACTCC 1740
Qy 1741 ATTGCTCAGCCCTCGAAGACATCCATCTTTGCAAAACCGGCGACGGGCTCTTTCGAAAC 1800
Db 1741 ATTGCTCAGCCCTCGAAGACATCCATCTTTGCAAAACCGGCGACGGGCTCTTTCGAAAC 1800
Qy 1801 GGATCTTGTCCAGATATTAATAAGTTGAGGCTGCGAGCTCTCAACATCTGCTGCAAT 1860
Db 1801 GGATCTTGTCCAGATATTAATAAGTTGAGGCTGCGAGCTCTCAACATCTGCTGCAAT 1860
Qy 1861 CTGAAGTTTACCAACAGCATGGGTGAGCGAGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGCGAGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
Qy 1921 GGGAACTACACCATTTCAACTGGCAGCTCTCCGAGAGAGATGAATCGGTGTTGTTCCAT 1980
Db 1921 GGGAACTACACCATTTCAACTGGCAGCTCTCCGAGAGAGATGAATCGGTGTTGTTCCAT 1980
Qy 1981 GAGGTGGGCAACTACAAACGCTTACGCTTAAGCCAGTGAACGACTCAACATCAACGAAAG 2040
Db 1981 GAGGTGGGCAACTACAAACGCTTACGCTTAAGCCAGTGAACGACTCAACATCAACGAAAG 2040
Qy 2041 AAAATCTCTGGAGTGGCTTCTCAAAGTGGTTCCTTTCTCCAACTGCGAGTCCGAGTGT 2100
Db 2041 AAAATCTCTGGAGTGGCTTCTCAAAGTGGTTCCTTTCTCCAACTGCGAGTCCGAGTGT 2100
Qy 2101 GTGCGGGCACCAAGGAGGAGATCATCGAGGGGAGGCCACCTGCTGCTTTGAATGCATG 2160
Db 2101 GTGCGGGCACCAAGGAGGAGATCATCGAGGGGAGGCCACCTGCTGCTTTGAATGCATG 2160
Qy 2161 GCATGTGACAGGGAGAGTTTCAGTGTGAAAACATGCAAGTGGGTGTACAAAGTGGCCG 2220
Db 2161 GCATGTGACAGGGAGAGTTTCAGTGTGAAAACATGCAAGTGGGTGTACAAAGTGGCCG 2220
Qy 2221 AATGATTTCTGCTGATGAGAACCAACGCTGCTGATCGCCAGGAGATCGAGTACCTG 2280
Db 2221 AATGATTTCTGCTGATGAGAACCAACGCTGCTGATCGCCAGGAGATCGAGTACCTG 2280
Qy 2281 TCGTGGAGCGGAGCCCTTCGGGATCGCTCTGACCATCTTCGCCCTACTGGGCACTCTGATC 2340
Db 2281 TCGTGGAGCGGAGCCCTTCGGGATCGCTCTGACCATCTTCGCCCTACTGGGCACTCTGATC 2340
Qy 2341 ACCTCTTGTGCTGGGGTCTTCATCAAGTTTCAGAGACATCCCATCTGAGGAGCCACC 2400
Db 2341 ACCTCTTGTGCTGGGGTCTTCATCAAGTTTCAGAGACATCCCATCTGAGGAGCCACC 2400
Qy 2401 AACCGGAGTTGTCTACTGCTGCTCTTCTCCTCATCTGCTGCTTCTCCAGTCTGCTC 2460
Db 2401 AACCGGAGTTGTCTACTGCTGCTCTTCTCCTCATCTGCTGCTTCTCCAGTCTGCTC 2460

121 TATTAAAAATGTTTCTCAAGATGGCTTCACAGAAATCAATCTGCAGTTTCCCAAT 180
181 GTCAATGTATGAATAA CTGACCAAGAGGATGTAACAAAATGGAACAAAGCTGAGACCAAC 240
181 GTCAATGTATGAATAA CTGACCAAGAGGATGTAACAAAATGGAACAAAGCTGAGACCAAC 240
241 GTTCACCTTTCTTGGAGCATACGATCAACCTGAGAGGATGGAAGCTTGGAGGAA 300
241 GTTCACCTTTCTTGGAGCATACGATCAACCTGAGAGGATGGAAGCTTGGAGGAA 300
301 ATGGGATTTGATCTTCCAGAGTTCTGCTGTAAGCGATCCCTCAACATTAACAAGATAA 360
301 ATGGGATTTGATCTTCCAGAGTTCTGCTGTAAGCGATCCCTCAACATTAACAAGATAA 360
361 GCGAATAATCCTCGAGCATCTCTGTAACGGGCTGGGTAGTGGCTTGGTCAAGGAA 420
361 GCGAATAATCCTCGAGCATCTCTGTAACGGGCTGGGTAGTGGCTTGGTCAAGGAA 420
421 CAGACAGGGCTGCACATGCTCAGCTTCACTGCCAATCTTATCTTGGGATTTACA 480
421 CAGACAGGGCTGCACATGCTCAGCTTCACTGCCAATCTTATCTTGGGATTTACA 480
481 CTCCTACAGTGTACAATCTCTGAGGATGATGTCACAAACCAAGGGCCAGAGAAAGGA 540
481 CTCCTACAGTGTACAATCTCTGAGGATGATGTCACAAACCAAGGGCCAGAGAAAGGA 540
541 GACATCATCTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
541 GACATCATCTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
601 TTAATAATCAGAGCCGAGGCGCAAAAATGTAATTCGGTACAAATTTTCGAGGCTTCGGATGG 660
601 TTAATAATCAGAGCCGAGGCGCAAAAATGTAATTCGGTACAAATTTTCGAGGCTTCGGATGG 660
661 CTCAGGCGATGATATTCGCAATTTGAAGATTAACACAGTATGACTTTCCTGCCCAAT 720
661 CTCAGGCGATGATATTCGCAATTTGAAGATTAACACAGTATGACTTTCCTGCCCAAT 720
721 ATCACCTCGGATATCGCATATTTGACAGTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780
721 ATCACCTCGGATATCGCATATTTGACAGTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780
781 ACACCTAGCTTTGTGGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
781 ACACCTAGCTTTGTGGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
841 TCGCTCGACCATATCCATCCCAATAGCAGTGTGGGGCAACCGGTCAGGATCTCC 900
841 TCGCTCGACCATATCCATCCCAATAGCAGTGTGGGGCAACCGGTCAGGATCTCC 900
901 ACGGCTGTGGCCAAATCTATTGGGATTTTACATTCACAGGTCAGCTATGCCCTCTCCG 960
901 ACGGCTGTGGCCAAATCTATTGGGATTTTACATTCACAGGTCAGCTATGCCCTCTCCG 960
961 ACGAGGCTCTCAGCAACAGATGATGATCAGAGGCTTCTCGAGGACCATCCCAATGAT 1020
961 ACGAGGCTCTCAGCAACAGATGATGATCAGAGGCTTCTCGAGGACCATCCCAATGAT 1020
1021 GAGCAACAGGCGCACCGGCTGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
1021 GAGCAACAGGCGCACCGGCTGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
1081 ACCCTGGAGCGACATGATGATATGGCGCCAGAGGATGACAGTTCCGGGAGAGGCC 1140
1081 ACCCTGGAGCGACATGATGATATGGCGCCAGAGGATGACAGTTCCGGGAGAGGCC 1140
1141 GTTAAGAGGACATCTGATTTGACTTTCAGTGAAGTGTCTCTCAGTACTACACCCAGAG 1200
1141 GTTAAGAGGACATCTGATTTGACTTTCAGTGAAGTGTCTCTCAGTACTACACCCAGAG 1200
1201 CAGTTGGAGTTCATCGCCGACGTCTATCCAGAACTCTCTCGGCCAAGGTCATCGTGGTCTTC 1260

1201 CAGTTGGAGTTCATCGCCGAGCTCATCCAGAACTCTCTCGGCCAAGGTCATCGTGGTCTTC 1260
1261 TCCAAATGGCCCCGACCTGGAGCCGCTCATCCAGAGATAGTTCCGAGAAACATCATCCCGAT 1320
1261 TCCAAATGGCCCCGACCTGGAGCCGCTCATCCAGAGATAGTTCCGAGAAACATCATCCCGAT 1320
1321 CGGATCTGGCTGGCCAGAGAGGCTTGGCCAGCTCTTCGCTCATTTCCCAAGCCAGAGTAC 1380
1321 CGGATCTGGCTGGCCAGAGAGGCTTGGCCAGCTCTTCGCTCATTTCCCAAGCCAGAGTAC 1380
1381 TTCCACGTGTCTGGCGGACCATCGGCTTCTCTCAGGCGGGGGCTATCCCAAGGTTTC 1440
1381 TTCCACGTGTCTGGCGGACCATCGGCTTCTCTCAGGCGGGGGCTATCCCAAGGTTTC 1440
1441 AACAGTTTCTGAAGAGGTCACCCCGAGAGTCTCGGACAAATGGGTTTGTCAAGGAG 1500
1441 AACAGTTTCTGAAGAGGTCACCCCGAGAGTCTCGGACAAATGGGTTTGTCAAGGAG 1500
1501 TTCTGGAGAGAGCTTCAACTGCTACTTTCACCGAGAAGACCCCTGACGAGCTTGAAGAAT 1560
1501 TTCTGGAGAGAGCTTCAACTGCTACTTTCACCGAGAAGACCCCTGACGAGCTTGAAGAAT 1560
1561 TCCAGGTGCCCTTGCACCGAGCCGGGCTCAAGGGACGGCTCCAAAGGGGGGAACTCC 1620
1561 TCCAGGTGCCCTTGCACCGAGCCGGGCTCAAGGGACGGCTCCAAAGGGGGGAACTCC 1620
1621 AGACGAGACGCCCTACGCCACCCCTGACCTGGGGAGGAGAAATACACAGCGTGGAGACC 1680
1621 AGACGAGACGCCCTACGCCACCCCTGACCTGGGGAGGAGAAATACACAGCGTGGAGACC 1680
1681 CCTACCTGATTTATACACACTGAGGATCTCTCAATGTATATCGTGGCGCTTACTCTC 1740
1681 CCTACCTGATTTATACACACTGAGGATCTCTCAATGTATATCGTGGCGCTTACTCTC 1740
1741 ATTGCTCAGCCCTCGAAGACATCACTCTTGCAAAACCGGACCGGCTCTTTGCAAAAC 1800
1741 ATTGCTCAGCCCTCGAAGACATCACTCTTGCAAAACCGGACCGGCTCTTTGCAAAAC 1800
1801 GGATCTTTGTCAGATTTAAAAAAGTTGAGGCTGCGAGGTCCTCAACCATCTGTGCAAT 1860
1801 GGATCTTTGTCAGATTTAAAAAAGTTGAGGCTGCGAGGTCCTCAACCATCTGTGCAAT 1860
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
1921 GGGAACTTACACCATTTCAACTGGCAGCTCTCCGACAGGATGAATCGGTGTTGTTCCAT 1980
1921 GGGAACTTACACCATTTCAACTGGCAGCTCTCCGACAGGATGAATCGGTGTTGTTCCAT 1980
1981 GAGGTGGGCAATTAACAGCCTTACGCTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040
1981 GAGGTGGGCAATTAACAGCCTTACGCTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040
2041 AAAATCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGACAGTGGAGTCTGT 2100
2041 AAAATCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGACAGTGGAGTCTGT 2100
2101 GTCCCGGCAACCAAGGAGGATCATCGAGGGGGAGCCCACTGCTGCTTTTGAATGCAATG 2160
2101 GTCCCGGCAACCAAGGAGGATCATCGAGGGGGAGCCCACTGCTGCTTTTGAATGCAATG 2160
2161 GCATGTGACAGGGAGGATTCAGTGTGAAGATGCAAGTGCCTGTGTAAGTGCCTCG 2220
2161 GCATGTGACAGGGAGGATTCAGTGTGAAGATGCAAGTGCCTGTGTAAGTGCCTCG 2220
2221 AATGATTTCTGTGTCGAATGAGAACCAACAGCTGTCATCGCCAAAGGAGATCGAGTACCTG 2280
2221 AATGATTTCTGTGTCGAATGAGAACCAACAGCTGTCATCGCCAAAGGAGATCGAGTACCTG 2280
2281 TCGTGAACGAGGCCCTTCGGGATCGCTCTGACATCTTCGCGTACTGGGATCCTGATC 2340
2281 TCGTGAACGAGGCCCTTCGGGATCGCTCTGACATCTTCGCGTACTGGGATCCTGATC 2340

QY 1 AATTCGGTTCGTCGGTTTCAGTCCAGTCTCCTCCAGTGCAGAAATGAGAAATGCTGGTC 60
Db |||||
QY 1 AATTCGGTTCGTCGGTTTCAGTCCAGTCTCCTCCAGTGCAGAAATGAGAAATGCTGGTC 60
Db |||||
QY 61 GCATTACAGGAACATGCACTACATCTGTGTTAAATGAAATATGTGAGTTATCTGAAGT 120
Db |||||
QY 61 GCATTACAGGAACATGCACTACATCTGTGTTAAATGAAATATGTGAGTTATCTGAAGT 120
Db |||||
QY 121 TATTAAATGTTTCTCAAGGATGGCTTCACAGAAATCAATCTTGACAGTTTCCCAT 180
Db |||||
QY 121 TATTAAATGTTTCTCAAGGATGGCTTCACAGAAATCAATCTTGACAGTTTCCCAT 180
Db |||||
QY 181 GTCAATGTATGAATACTGACCAAGAGGATGTAAACAAATGAAACAAAGCTGAGGACAC 240
Db |||||
QY 181 GTCAATGTATGAATACTGACCAAGAGGATGTAAACAAATGAAACAAAGCTGAGGACAC 240
Db |||||
QY 241 GTTCAACCTTTCTTGAGCATACGATCAACCTGAGGAGATGGAAGACTTGAGAGGAA 300
Db |||||
QY 241 GTTCAACCTTTCTTGAGCATACGATCAACCTGAGGAGATGGAAGACTTGAGAGGAA 300
Db |||||
QY 301 ATGGGATTTGATCTTCCAGGATTTCTGCTGTAAGCGATCCCTCAACATTAACAAGATAA 360
Db |||||
QY 301 ATGGGATTTGATCTTCCAGGATTTCTGCTGTAAGCGATCCCTCAACATTAACAAGATAA 360
Db |||||
QY 361 GCAGAAATCCTCCAGGATCTCTGTAACCGGCTGGGCTAGTGTGGTTCGTAAGGAA 420
Db |||||
QY 361 GCAGAAATCCTCCAGGATCTCTGTAACCGGCTGGGCTAGTGTGGTTCGTAAGGAA 420
Db |||||
QY 421 CAGAGACAGGCTGCAATGGCTAGCTTCACTGCAACTCTTATCTTGGGATTTTACA 480
Db |||||
QY 421 CAGAGACAGGCTGCAATGGCTAGCTTCACTGCAACTCTTATCTTGGGATTTTACA 480
Db |||||
QY 481 CTCCTACAGTCGTACAAATGCTCAGGATGTGTCACAAAGGCGCCAGAGAAAGGA 540
Db |||||
QY 481 CTCCTACAGTCGTACAAATGCTCAGGATGTGTCACAAAGGCGCCAGAGAAAGGA 540
Db |||||
QY 541 GACATCATCTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCAAGATCAGGAC 600
Db |||||
QY 541 GACATCATCTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCAAGATCAGGAC 600
Db |||||
QY 601 TTAATAATCAGACCGGAGCGCAAAATGTAATTCGTTACAAATTTTCGAGGCTTCGATGG 660
Db |||||
QY 601 TTAATAATCAGACCGGAGCGCAAAATGTAATTCGTTACAAATTTTCGAGGCTTCGATGG 660
Db |||||
QY 661 CTCAGGCGATGATATTCGAATGAGAGATTAACAACAGTATGACTTCTCGGCCAAT 720
Db |||||
QY 721 ATCACCCTGGGATATCGCATATTTGACAGTGTACACCGTGTCCAGGCGCTAGAGCA 780
Db |||||
QY 721 ATCACCCTGGGATATCGCATATTTGACAGTGTACACCGTGTCCAGGCGCTAGAGCA 780
Db |||||
QY 781 ACACTCAGCTTTCTGGCCCAAGAAATCGACTCGCTGAATAGATCAGTTCTGTAAAC 840
Db |||||
QY 781 ACACTCAGCTTTCTGGCCCAAGAAATCGACTCGCTGAATAGATCAGTTCTGTAAAC 840
Db |||||
QY 841 TGTCTTGACCATATCCCATTCACATAGCAGTGTGTCGGGCAACCGGCTCAGGAATCTCC 900
Db |||||
QY 841 TGTCTTGACCATATCCCATTCACATAGCAGTGTGTCGGGCAACCGGCTCAGGAATCTCC 900
Db |||||
QY 901 ACGGCTGTGGCAATCTATTGGGATTTATTTACATTCACAGGTCAGCTATGCTCTCTCG 960
Db |||||
QY 901 ACGGCTGTGGCAATCTATTGGGATTTATTTACATTCACAGGTCAGCTATGCTCTCTCG 960
Db |||||
QY 961 AGCAGGCTCTCAGCAACAAAGATAGTACAGGCTTCTTGAGCAACCATCCCAATGAT 1020
Db |||||
QY 961 AGCAGGCTCTCAGCAACAAAGATAGTACAGGCTTCTTGAGCAACCATCCCAATGAT 1020
Db |||||
QY 1021 GAGCAACGCGCAGGCTATGCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Db |||||
QY 1021 GAGCAACGCGCAGGCTATGCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Db |||||
QY 1081 ACCCTGGACCGCAGATGACTATGSCCCGCCAGGCAATGACAACTTCGGAGAGGCCC 1140
Db |||||

Db 1081 ACCCTGGACCGCAGATGACTATGSCCCGCCAGGCAATGACAACTTCGGAGAGGCCC 1140
QY 1141 GTTAAGAGGACATCTGTATTGACTTCACTGAGTATGAGTATGACAACTTCGGAGAGGCCC 1200
Db |||||
QY 1141 GTTAAGAGGACATCTGTATTGACTTCACTGAGTATGAGTATGACAACTTCGGAGAGGCCC 1200
Db |||||
QY 1201 CAGTTGAGTTCATCCGCGACGTCATCCAGAACTCCTCGGCCAAGGTCATCGTGGTCTTC 1260
Db |||||
QY 1201 CAGTTGAGTTCATCCGCGACGTCATCCAGAACTCCTCGGCCAAGGTCATCGTGGTCTTC 1260
Db |||||
QY 1261 TCCAAATGCCCCGACCTTGAGCGGCTCATCCAGGAGATAGTTCCGAGAAACATCAACGAT 1320
Db |||||
QY 1261 TCCAAATGCCCCGACCTTGAGCGGCTCATCCAGGAGATAGTTCCGAGAAACATCAACGAT 1320
Db |||||
QY 1321 CGATCTGGCTGGCAGCAGGCTTGGCCAGCTCTTCCGCTCAATTCGCAAGCCAGAGTAC 1380
Db |||||
QY 1321 CGATCTGGCTGGCAGCAGGCTTGGCCAGCTCTTCCGCTCAATTCGCAAGCCAGAGTAC 1380
Db |||||
QY 1381 TTCCACGTGTCGGCGCACCATCGGCTTCCAGGCGGGGCTATCCAGGCTTC 1440
Db |||||
QY 1381 TTCCACGTGTCGGCGCACCATCGGCTTCCAGGCGGGGCTATCCAGGCTTC 1440
Db |||||
QY 1441 AACAGTTCTGAGGAGGTCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG 1500
Db |||||
QY 1441 AACAGTTCTGAGGAGGTCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG 1500
Db |||||
QY 1501 TTCTGGGAGGAGACTTCAACTGCTTCAACCGAGAACCTCTGACGAGCTGGAAGAT 1560
Db |||||
QY 1501 TTCTGGGAGGAGACTTCAACTGCTTCAACCGAGAACCTCTGACGAGCTGGAAGAT 1560
Db |||||
QY 1561 TCCAGGTGCTCGCAGCAGCGGCTTCAAGGAGCGGCTTCAAGCGGGAATCTCC 1620
Db |||||
QY 1561 TCCAGGTGCTCGCAGCAGCGGCTTCAAGGAGCGGCTTCAAGCGGGAATCTCC 1620
Db |||||
QY 1621 AGAGGACGCTTACGCCACCTGCACTGGGGAGGAGAACATCACACGCTGGAGACC 1680
Db |||||
QY 1621 AGAGGACGCTTACGCCACCTGCACTGGGGAGGAGAACATCACACGCTGGAGACC 1680
Db |||||
QY 1681 CCTTACCTGATTTATACACACTGAGGATCTCTCAATGTATGATGCTGCTACTCTC 1740
Db |||||
QY 1681 CCTTACCTGATTTATACACACTGAGGATCTCTCAATGTATGATGCTGCTACTCTC 1740
Db |||||
QY 1741 ATTGCTCAGCCCTGCAAGACATCTCTTGCAAAACCGGCAAGGCTTCTTGAAC 1800
Db |||||
QY 1741 ATTGCTCAGCCCTGCAAGACATCTCTTGCAAAACCGGCAAGGCTTCTTGAAC 1800
Db |||||
QY 1801 GGATCTTGTGCAGATTTAAATAAGTTGAGGCTGAGGCTCTCAACCATCTGCTGCAT 1860
Db |||||
QY 1801 GGATCTTGTGCAGATTTAAATAAGTTGAGGCTGAGGCTCTCAACCATCTGCTGCAT 1860
Db |||||
QY 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACCATCAAGGTGACCTCAAG 1920
Db |||||
QY 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACCATCAAGGTGACCTCAAG 1920
Db |||||
QY 1921 GGGAACTTACCAACTTACCTGCGAGCTCTCGCAGAGGATGAATCGGTTGTTCCAT 1980
Db |||||
QY 1921 GGGAACTTACCAACTTACCTGCGAGCTCTCGCAGAGGATGAATCGGTTGTTCCAT 1980
Db |||||
QY 1981 GAGGTGGCAACTACAAACGCTTACGCTAAGCCAGTGACCGACTCAACATCAACGAAAG 2040
Db |||||
QY 1981 GAGGTGGCAACTACAAACGCTTACGCTAAGCCAGTGACCGACTCAACATCAACGAAAG 2040
Db |||||
QY 2041 AAATCTCTGAGTGGCTTCTCAAAGTGGTTCCTTCTTCAACCTGCTGCTTGAATGATG 2100
Db |||||
QY 2041 AAATCTCTGAGTGGCTTCTCAAAGTGGTTCCTTCTTCAACCTGCTGCTTGAATGATG 2100
Db |||||
QY 2101 GTCCGGGCAACAGGAGGATCATCGAGGGGAGCCACCTGCTGCTTGAATGATG 2160
Db |||||
QY 2101 GTCCGGGCAACAGGAGGATCATCGAGGGGAGCCACCTGCTGCTTGAATGATG 2160
Db |||||
QY 2161 GCATGTGAGAGGAGGATTCAGTATGAAACGATGCAAGTGCCTGTCGTAACAGTCCCG 2220
Db |||||

source		i. .4134		/organism="unknown"		/mol_type="genomic DNA"	
ORIGIN		Query Match		Best Local Similarity		Matches 4134; Conservative	
		100.0%; Score 4134; DB 6; Length 4134;		100.0%; Pred. No. 0;		0; Mismatches	
		0; Gaps		0; Indels		0; Gaps	
QY	1	AAATCCGTTGCTGTCGGGTTCAAGTCTCCTCCAGTGCAGAAATGAGAAATGGTGGTC	60				
DB	1	AAATCCGTTGCTGTCGGGTTCAAGTCTCCTCCAGTGCAGAAATGAGAAATGGTGGTC	60				
QY	61	GCATTTACAGGAACATGCACTACATCTGTGTTAAATGAAATATTGTCACTTCTGAAGGT	120				
DB	61	GCATTTACAGGAACATGCACTACATCTGTGTTAAATGAAATATTGTCACTTCTGAAGGT	120				
QY	121	TATTAATAATGTTTCTGCAAGGATGGCTTACGAGAAATCAATTTCTGCAGTTTCCCAT	180				
DB	121	TATTAATAATGTTTCTGCAAGGATGGCTTACGAGAAATCAATTTCTGCAGTTTCCCAT	180				
QY	181	GTCAATGATGAATACTGACCAAGAGGATGTAAACAAATGGAACAAAGCTGAGACACC	240				
DB	181	GTCAATGATGAATACTGACCAAGAGGATGTAAACAAATGGAACAAAGCTGAGACACC	240				
QY	241	GTTCACCTTTCTTGAGGATACGATCAACCTGTAAGGAGATGGAAGACTTGGAGGAA	300				
DB	241	GTTCACCTTTCTTGAGGATACGATCAACCTGTAAGGAGATGGAAGACTTGGAGGAA	300				
QY	301	ATGGGGAATGATCTTCCAGGATTTCTGTGTAAGAGCATCCCTACCAATTAACAAGATA	360				
DB	301	ATGGGGAATGATCTTCCAGGATTTCTGTGTAAGAGCATCCCTACCAATTAACAAGATA	360				
QY	361	GCAGAAATCTCGAGCATCTCTGTAAACGGCTGGGTAGTGGTCTGTAAGAA	420				
DB	361	GCAGAAATCTCGAGCATCTCTGTAAACGGCTGGGTAGTGGTCTGTAAGAA	420				
QY	421	CAGAGACAGGGGTGCACAAATGGCTCAGCTTCACTGCCAACTCTTATTTCTGGGATTTACA	480				
DB	421	CAGAGACAGGGGTGCACAAATGGCTCAGCTTCACTGCCAACTCTTATTTCTGGGATTTACA	480				
QY	481	CTCCTACAGTGTGAATGTCTCAGGATGTGTCACAAACAAAGGCCCGCAGAGAAAGGA	540				
DB	481	CTCCTACAGTGTGAATGTCTCAGGATGTGTCACAAACAAAGGCCCGCAGAGAAAGGA	540				
QY	541	GACATCATCTGGAGGTCTCTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600				
DB	541	GACATCATCTGGAGGTCTCTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600				
QY	601	TTAAATTCGAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTTCGGATGG	660				
DB	601	TTAAATTCGAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTTCGGATGG	660				
QY	661	CTCCAGGCGATGATATTCGCAATGAGAGATTAACACAGTATGACATTTCTGCGCCCAAT	720				
DB	661	CTCCAGGCGATGATATTCGCAATGAGAGATTAACACAGTATGACATTTCTGCGCCCAAT	720				
QY	721	ATCACCTCGGATATCGCATATTTGACAGTGTAAACACCGTGTCCAAAGCGCTAGAGGCA	780				
DB	721	ATCACCTCGGATATCGCATATTTGACAGTGTAAACACCGTGTCCAAAGCGCTAGAGGCA	780				
QY	781	ACACTCAGCTTTGTGGCCAGAACAAATCGACTCGTGAATAGATGAGTTCGTAAAC	840				
DB	781	ACACTCAGCTTTGTGGCCAGAACAAATCGACTCGTGAATAGATGAGTTCGTAAAC	840				
QY	841	TGCTCTGACCATATCCCATCCCAATAGCAGTGGTTCGGGCGCAACCGGGTCAAGAAATCTCC	900				
DB	841	TGCTCTGACCATATCCCATCCCAATAGCAGTGGTTCGGGCGCAACCGGGTCAAGAAATCTCC	900				
QY	901	ACGGCTGTGGCCCAATCTATTTGGATATTTTACATTTCCACAGTACGTATGCTCTCTCG	960				
DB	901	ACGGCTGTGGCCCAATCTATTTGGATATTTTACATTTCCACAGTACGTATGCTCTCTCG	960				

QY	961	AGCAGGCTGCTCAGCAACAGAAATGATCAAGGCTTCTCTGAGGACCATCCCAATGAT	1020
DB	961	AGCAGGCTGCTCAGCAACAGAAATGATCAAGGCTTCTCTGAGGACCATCCCAATGAT	1020
QY	1021	GAGCAACAGGCCACGGCCATGCGAGATCATCGAGCATTTCCAGTGAATCGGTGGGA	1080
DB	1021	GAGCAACAGGCCACGGCCATGCGAGATCATCGAGCATTTCCAGTGAATCGGTGGGA	1080
QY	1081	ACCTGGCAGCCACCATGACTATGCGCCCGCCAGCATTTGACAAGTTCCGGAGGAGGCC	1140
DB	1081	ACCTGGCAGCCACCATGACTATGCGCCCGCCAGCATTTGACAAGTTCCGGAGGAGGCC	1140
QY	1141	GTAAAGAGGACATCTGTATTGACTTTCAGTGAAGATCTCTCAGTACTACACCAAGA	1200
DB	1141	GTAAAGAGGACATCTGTATTGACTTTCAGTGAAGATCTCTCAGTACTACACCAAGA	1200
QY	1201	CAGTTGAGTTTCAATCCGACGTCATCCAGAACTCTCGGCCAAGTCTCGTGGTCTTC	1260
DB	1201	CAGTTGAGTTTCAATCCGACGTCATCCAGAACTCTCGGCCAAGTCTCGTGGTCTTC	1260
QY	1261	TCCAAATGGCCCGACCTGGAGCGCTCATCCAGAGATAGTTCCGAGAAACATCACCGAT	1320
DB	1261	TCCAAATGGCCCGACCTGGAGCGCTCATCCAGAGATAGTTCCGAGAAACATCACCGAT	1320
QY	1321	CGATCTGGTGCCAGCGAGGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380
DB	1321	CGATCTGGTGCCAGCGAGGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380
QY	1381	TTCCAGTGTGTCGGCGCACCATCGGCTTCTCAGGCGGGGGGTATCCAGAGTTTC	1440
DB	1381	TTCCAGTGTGTCGGCGCACCATCGGCTTCTCAGGCGGGGGGTATCCAGAGTTTC	1440
QY	1441	AACAAGTTCTGAAGAGAGTCCACCCAGCAGGTCTCTCGGACAAATCGGTTTGTCAAGGAG	1500
DB	1441	AACAAGTTCTGAAGAGAGTCCACCCAGCAGGTCTCTCGGACAAATCGGTTTGTCAAGGAG	1500
QY	1501	TTCTGGAGAGACATTCACTGCTACTTCCCGAGAACCTGACGAGCTGAAGAT	1560
DB	1501	TTCTGGAGAGACATTCACTGCTACTTCCCGAGAACCTGACGAGCTGAAGAT	1560
QY	1561	TCCAAGTGCCTCGACCGACCGGGGTCCAAAGGGAGCGGTCTCCAAAGCGGGGAACTCC	1620
DB	1561	TCCAAGTGCCTCGACCGACCGGGGTCCAAAGGGAGCGGTCTCCAAAGCGGGGAACTCC	1620
QY	1621	AGACGACAGCCCTACGCGACCCCTGCACTGGGGAGGAGAAATCACACGAGCTGGAGAC	1680
DB	1621	AGACGACAGCCCTACGCGACCCCTGCACTGGGGAGGAGAAATCACACGAGCTGGAGAC	1680
QY	1681	CCCTACTGGAATTTATACACCTGAGATCTCTCAATGTATACGTGCGCTCTACTCC	1740
DB	1681	CCCTACTGGAATTTATACACCTGAGATCTCTCAATGTATACGTGCGCTCTACTCC	1740
QY	1741	ATTGCTCAGCCCTGCAAGACATCCACTTTGCAAAACCGGACCGGCGATCTTTGCAAAAC	1800
DB	1741	ATTGCTCAGCCCTGCAAGACATCCACTTTGCAAAACCGGACCGGCGATCTTTGCAAAAC	1800
QY	1801	GGATCTTGTGAGATTTAAAGAGTTGAGGCTGCGAGCTCTCAACATCTCTGTCAT	1860
DB	1801	GGATCTTGTGAGATTTAAAGAGTTGAGGCTGCGAGCTCTCAACATCTCTGTCAT	1860
QY	1861	CTGAAGTTTACCAACAGCATGGGTGAGAGCTTTGACTTTGACGATCAAGGTGCTCAAG	1920
DB	1861	CTGAAGTTTACCAACAGCATGGGTGAGAGCTTTGACTTTGACGATCAAGGTGCTCAAG	1920
QY	1921	GGGAACTACACCATTTAACTGGAGCTCTCGAGAGGATGAATCGGTGTTGTTCCAT	1980
DB	1921	GGGAACTACACCATTTAACTGGAGCTCTCGAGAGGATGAATCGGTGTTGTTCCAT	1980
QY	1981	GAGGTGGGCAACTACACGCTACGCTAAGCCAGGTGACCGACTCAACATCAACGAAAG	2040
DB	1981	GAGGTGGGCAACTACACGCTACGCTAAGCCAGGTGACCGACTCAACATCAACGAAAG	2040
QY	2041	AAATCTCTGGAGTGGCTTCTCCAAAGTGGTCTCTTCTTCCAACTGCAGTCCAGACTGT	2100

Db	2041	TCCCTCTGGAGTGGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTCGAGTCGAGACTGT	2100
Qy	2101	GTGCCGGGCACAGGAAGGGGATCATCGAGGGGAGCCACCTGCTGCTTTGAATGATG	2160
Db	2101	GTGCCGGGCACAGGAAGGGGATCATCGAGGGGAGCCACCTGCTGCTTTGAATGATG	2160
Qy	2161	GCATGTGAGAGGGAGAGTTTCAGTGTAGAAACGATGCAAGTGCGTGTACAAAGTGC	2220
Db	2161	GCATGTGAGAGGGAGAGTTTCAGTGTAGAAACGATGCAAGTGCGTGTACAAAGTGC	2220
Qy	2221	AATGATTTCTGCTGCAATGAGAACACACGTCGTGCATTCGCCAAGGAGATCGAGTACCTG	2280
Db	2221	AATGATTTCTGCTGCAATGAGAACACACGTCGTGCATTCGCCAAGGAGATCGAGTACCTG	2280
Qy	2281	TCGTGGAACGAGCCCTTCGGGATCGCTCTGTGACCATCTTCGCCGTATCTGGGCATCTG	2340
Db	2281	TCGTGGAACGAGCCCTTCGGGATCGCTCTGTGACCATCTTCGCCGTATCTGGGCATCTG	2340
Qy	2341	ACCTCCTTCGTCTGGGGGCTTTCATCAAGTTCAGGAACACTCCATCGTGAAGGCCACC	2400
Db	2341	ACCTCCTTCGTCTGGGGGCTTTCATCAAGTTCAGGAACACTCCATCGTGAAGGCCACC	2400
Qy	2401	AACCGGAGTTGTCTACCTGCTGCTCTCTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC	2460
Db	2401	AACCGGAGTTGTCTACCTGCTGCTCTCTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC	2460
Qy	2461	ATCTTCATCGGAGCCAGGAGCTGACCTGTTCGGCTTCGGCTCGCCAAACCGGCTTTGGCATC	2520
Db	2461	ATCTTCATCGGAGCCAGGAGCTGACCTGTTCGGCTTCGGCTCGCCAAACCGGCTTTGGCATC	2520
Qy	2521	AGCTTCGTCTCTGTCATCTCTGTCATCTCTGTTGAAGACCAACCGGGTGCTGCTGGTCTTC	2580
Db	2521	AGCTTCGTCTCTGTCATCTCTGTCATCTCTGTTGAAGACCAACCGGGTGCTGCTGGTCTTC	2580
Qy	2581	GAGGCCAAGATCCCAACAGCCTCCACCGAAAGTGGGTGGGCTCAACCTGCAAGTTCCTC	2640
Db	2581	GAGGCCAAGATCCCAACAGCCTCCACCGAAAGTGGGTGGGCTCAACCTGCAAGTTCCTC	2640
Qy	2641	CTGGTCTCTCTGTCATCTCTGTCGCAATCGTCACTGTCATCTGGCTCTACACCGCG	2700
Db	2641	CTGGTCTCTCTGTCATCTCTGTCGCAATCGTCACTGTCATCTGGCTCTACACCGCG	2700
Qy	2701	CCTCCCTCCAGCTACAGAAACCATGAGCTGGAGAACGAGTCTATCTTCATCACCTCGCAC	2760
Db	2701	CCTCCCTCCAGCTACAGAAACCATGAGCTGGAGAACGAGTCTATCTTCATCACCTCGCAC	2760
Qy	2761	GAGGCTCGCTCATGGGCTGGGCTTCTCATCGGCTACACCTGCTCTCCGGCGGCATC	2820
Db	2761	GAGGCTCGCTCATGGGCTGGGCTTCTCATCGGCTACACCTGCTCTCCGGCGGCATC	2820
Qy	2821	TGCTTCTTCTTTCGCTTCAAGTCCGCTAAGCTGCGGAGAACTTCAACGAGGTCAAGTTC	2880
Db	2821	TGCTTCTTCTTTCGCTTCAAGTCCGCTAAGCTGCGGAGAACTTCAACGAGGTCAAGTTC	2880
Qy	2881	ATGACCTTCAGCATGTTGATCTTCTTCATCGTCTGGATCTCTTCATCTCCCGGCTATGTC	2940
Db	2881	ATGACCTTCAGCATGTTGATCTTCTTCATCGTCTGGATCTCTTCATCTCCCGGCTATGTC	2940
Qy	2941	AGCACCTACGCAAGTTTGTCTCGCCCGTGGAGTGATTGCCATCTCTGGGCTCCAGCTTC	3000
Db	2941	AGCACCTACGCAAGTTTGTCTCGCCCGTGGAGTGATTGCCATCTCTGGGCTCCAGCTTC	3000
Qy	3001	GGGCTGCTGGGCTGCATTTACTTCAAAGTGTTCATCATCTGTTTCAAGCGTGC	3060
Db	3001	GGGCTGCTGGGCTGCATTTACTTCAAAGTGTTCATCATCTGTTTCAAGCGTGC	3060
Qy	3061	AACACCATTCGAGGAGTGGCTGCAGCACGGCGCCACGCTTCAAGTGGCGGCGCG	3120
Db	3061	AACACCATTCGAGGAGTGGCTGCAGCACGGCGCCACGCTTCAAGTGGCGGCGCG	3120
Qy	3121	GCCACCTTCGGCGACGCGCGCTCTCCGAAAGCGTCCAGACGCTGTGGGCTCCAC	3180

[illegible]

RESULT 5
AR321738
LOCUS
DEFINITION
ACCESSION
VERSION

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 4134)
AUTHORS	Harris,H.W. Jr., Russell,D.R., Nearing,J. and Betka,M.
TITLE	Methods for raising pre-adult and/or anadromous fish
JOURNAL	Patent: US 6564747-A 17 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..4134
	/organism="unknown"
ORIGIN	/mol_type="genomic DNA"
Query Match	100.0%; Score 4134; DB 6; Length 4134;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 4134; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AATTCCGTTGCTCGGTTCACTCCAGTCTCCTCCAGTGCAAAATGAAATGGTGTGTC 60
DB	1 AATTCCGTTGCTCGGTTCACTCCAGTCTCCTCCAGTGCAAAATGAAATGGTGTGTC 60
QY	61 GCCATTACAGGAACATGCATCTGTGTTAATGAAATATGTCAGTTATCTGAAGGT 120
DB	61 GCCATTACAGGAACATGCATCTGTGTTAATGAAATATGTCAGTTATCTGAAGGT 120
QY	121 TATTAAATGTTTTCAGGATGCTTCACAGAAATCAATCTGCAGGTTTCCCAATT 180
DB	121 TATTAAATGTTTTCAGGATGCTTCACAGAAATCAATCTGCAGGTTTCCCAATT 180
QY	181 GTCAATTGATGAATACTACCAAGAGGATGTAACAAATGGAACAAAGCTGAGACCAAC 240
DB	181 GTCAATTGATGAATACTACCAAGAGGATGTAACAAATGGAACAAAGCTGAGACCAAC 240
QY	241 GTTACACCTTTCTTGAGCATACGATCAACCTGAGAGGATGGAAGCTTGAGAGGAA 300
DB	241 GTTACACCTTTCTTGAGCATACGATCAACCTGAGAGGATGGAAGCTTGAGAGGAA 300
QY	301 ATGGGATGATCTTCCAGGATCTCTGTAAGAGGATCCCTCACCATTACAAAGATAA 360
DB	301 ATGGGATGATCTTCCAGGATCTCTGTAAGAGGATCCCTCACCATTACAAAGATAA 360
QY	361 GCAGAAATCCTCCAGGATCCTCTGTAAGAGGATCCCTCACCATTACAAAGATAA 420
DB	361 GCAGAAATCCTCCAGGATCCTCTGTAAGAGGATCCCTCACCATTACAAAGATAA 420
QY	421 CAGAGACAGGCTGCAATGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 480
DB	421 CAGAGACAGGCTGCAATGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 480
QY	481 CTCTACAGTGTACAAATGCTCAGGATGCTGTCACAAACCAAGGCGCCAGAGAAAGGA 540
DB	481 CTCTACAGTGTACAAATGCTCAGGATGCTGTCACAAACCAAGGCGCCAGAGAAAGGA 540
QY	541 GACATCATCTGGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
DB	541 GACATCATCTGGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
QY	601 TTAATAATCGAGACCGGAGCGCAAAATGTTATTCGGTACAAATTTTCGAGGCTTCCGATGG 660
DB	601 TTAATAATCGAGACCGGAGCGCAAAATGTTATTCGGTACAAATTTTCGAGGCTTCCGATGG 660
QY	661 CTCAGGCGGATGATAATTCGCAATGAGAGATTAACAAGATGAGTCTTCCGCGCAAT 720
DB	661 CTCAGGCGGATGATAATTCGCAATGAGAGATTAACAAGATGAGTCTTCCGCGCAAT 720
QY	721 ATCACCTGGGATATCGCATATTTGACAGTGTAAACCGGTGTCACAGGCGCTAGAGGCA 780
DB	721 ATCACCTGGGATATCGCATATTTGACAGTGTAAACCGGTGTCACAGGCGCTAGAGGCA 780
QY	781 ACACCTCAGCTTTGGGCCAGAAACAAATTCGATCTGCTGAATAGATGAGTCTGTAAAC 840
DB	781 ACACCTCAGCTTTGGGCCAGAAACAAATTCGATCTGCTGAATAGATGAGTCTGTAAAC 840

QY 1921 GGGAACTACACCATATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCAT 1980
Db |||||
1921 GGGAACTACACCATATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCAT 1980
QY |||||
1981 GAGGTGGCACTACAAAGCCCTACCTAAGCCAGTACCGACTCAACATCAACGAAAG 2040
Db |||||
1981 GAGGTGGCACTACAAAGCCCTACCTAAGCCAGTACCGACTCAACATCAACGAAAG 2040
QY |||||
2041 AAAATCCTCTGGAGTGGTCTTCCAAAGTGGTCTCTTCTCAACTGCGAGACTGT 2100
Db |||||
2041 AAAATCCTCTGGAGTGGTCTTCCAAAGTGGTCTCTTCTCAACTGCGAGACTGT 2100
QY |||||
2101 GTGCCGGGACACAGAAAGGATCATCGAGGGGAGCCACCTGCTGTTTGAATGATG 2160
Db |||||
2101 GTGCCGGGACACAGAAAGGATCATCGAGGGGAGCCACCTGCTGTTTGAATGATG 2160
QY |||||
2161 GCATGTGAGAGGAGAGTTCAAGTATGAAGCAAGTGAAGTGGGTGACAAAGTGCCCG 2220
Db |||||
2161 GCATGTGAGAGGAGAGTTCAAGTATGAAGCAAGTGAAGTGGGTGACAAAGTGCCCG 2220
QY |||||
2221 AATGATTTCTGGTGAATGAGAAACACACGTCGTGCATGCGCAAGGAGATCGAGTAC 2280
Db |||||
2221 AATGATTTCTGGTGAATGAGAAACACACGTCGTGCATGCGCAAGGAGATCGAGTAC 2280
QY |||||
2281 TCGTGGAGGAGCCCTTCGGGATCGCTGACCATCTTTCGCGTACTGGGCATCCTGATC 2340
Db |||||
2341 ACCTCCTTCGTGGGGTCTTCAATCAAGTTTCAGAAACACTGCCCATCGTGAAGGCCACC 2400
QY |||||
2401 AACGGGAGTGTCTACTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTCGTCTC 2460
Db |||||
2401 AACGGGAGTGTCTACTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTCGTCTC 2460
QY |||||
2461 ATCTTCATCGGAGCCAGGAGTGAACCTGTGCGCTCCGCAACCGGCTTTGGCATC 2520
Db |||||
2461 ATCTTCATCGGAGCCAGGAGTGAACCTGTGCGCTCCGCAACCGGCTTTGGCATC 2520
QY |||||
2521 AGCTTCGTCTGTGATCTCTGTCATCTGTCGATCGTGAAGACCAACCGGCTCTGCTGCTTC 2580
Db |||||
2581 GAGGCCAAGATCCCAACAGCTCTCACCGCAAGTGGGTGGGCTCAACCTGCAGTCTCTC 2640
Db |||||
2641 CTGGTCTTCTCTGTCATCTGTCGATCTGTCGATCTGTCGATCTGTCGATCTGTCGATCT 2700
QY |||||
2701 CCTCCTTCAGGTACAGGAACATGAGCTGAGGAGGAGTCACTTTCATCACCCTGGAC 2760
Db |||||
2701 CCTCCTTCAGGTACAGGAACATGAGCTGAGGAGGAGTCACTTTCATCACCCTGGAC 2760
QY |||||
2761 GAGGCTCGCTCATGGCGTGGCTTCTCTCATCGCTACCTGCTCTCGCGCCCATC 2820
Db |||||
2761 GAGGCTCGCTCATGGCGTGGCTTCTCTCATCGCTACCTGCTCTCGCGCCCATC 2820
QY |||||
2821 TGCCTTCTTCTGCTCTCAAGTCCGTAAGCTGCGGAGAACTTCAACGAGGCTAAAGTTC 2880
Db |||||
2881 ATCCTCTTCAGATGTGATCTTCTTCATCGTCTGATCTCTCTCATCCCGCTATGTC 2940
Db |||||
2881 ATCCTCTTCAGATGTGATCTTCTTCATCGTCTGATCTCTCTCATCCCGCTATGTC 2940
QY |||||
2941 AGCACTACGGCAAGTTTGTGCGCCGCTGAGGAGTGAATGCGCATCTCGGCTCCAGCTTC 3000
Db |||||
2941 AGCACTACGGCAAGTTTGTGCGCCGCTGAGGAGTGAATGCGCATCTCGGCTCCAGCTTC 3000
QY |||||
3001 GGGCTGCTGGGCTGATTTACTTCAACAAAGTGTATCATCTCTTCAACGCCGTGCCGT 3060

Db |||||
3001 GGGCTGCTGGGCTGATTTACTTCAACAAAGTGTATCATCTCTTCAACGCCGTGCCGT 3060
QY |||||
3061 AACACCATCGAGAGTGGCTGCAGCAGCGGCGCCAGCCCTTCAAGTGGCGGCCCG 3120
Db |||||
3061 AACACCATCGAGAGTGGCTGCAGCAGCGGCGCCAGCCCTTCAAGTGGCGGCCCG 3120
QY |||||
3121 GCCACCTTCGGGCGAGCGCGCTCTCGCAAGCGTCCAGCAGCTGTGCGGCTCCACC 3180
Db |||||
3121 GCCACCTTCGGGCGAGCGCGCTCTCGCAAGCGTCCAGCAGCTGTGCGGCTCCACC 3180
QY |||||
3181 ATCTCTCGCCCGCTCTGTCACCTCGGGCGGGGCTCACCATGAGATGACGCGCTGC 3240
Db |||||
3181 ATCTCTCGCCCGCTCTGTCACCTCGGGCGGGGCTCACCATGAGATGACGCGCTGC 3240
QY |||||
3241 AGCAGCAGAAAGTCAAGTTCGGCAGCGCACCGTCACTGCTGCTCAGCTTCGAGGAG 3300
Db |||||
3241 AGCAGCAGAAAGTCAAGTTCGGCAGCGCACCGTCACTGCTGCTCAGCTTCGAGGAG 3300
QY |||||
3301 ACAGGCGGATACGCCACCTCAGCCGAGCGGCCCGCAGCAGGAATCGCGGATGCGCGC 3360
Db |||||
3301 ACAGGCGGATACGCCACCTCAGCCGAGCGGCCCGCAGCAGGAATCGCGGATGCGCGC 3360
QY |||||
3361 AGCGGCGACGACTGCTCATCTAGACACCGACGCGGCCGCTCAGAAATCGAGGCC 3420
Db |||||
3361 AGCGGCGACGACTGCTCATCTAGACACCGACGCGGCCGCTCAGAAATCGAGGCC 3420
QY |||||
3421 CAGCCGCGCAACGATCCGCGATACAAAGCGCGCCGACCAAGGGCACCTTAGAGTGGCG 3480
Db |||||
3421 CAGCCGCGCAACGATCCGCGATACAAAGCGCGCCGACCAAGGGCACCTTAGAGTGGCG 3480
QY |||||
3481 GCGGCGAGAAAGAGCGGCCCAACTATGAGGAACTTAATCCAACTCCCTCCATCAAC 3540
Db |||||
3481 GCGGCGAGAAAGAGCGGCCCAACTATGAGGAACTTAATCCAACTCCCTCCATCAAC 3540
QY |||||
3541 CCCAAGAAATCTCTCCACGCGACCGCTCGACAACTGACATCAACTCTCTAACCGGTGGC 3600
Db |||||
3541 CCCAAGAAATCTCTCCACGCGACCGCTCGACAACTGACATCAACTCTCTAACCGGTGGC 3600
QY |||||
3601 TGCCCAACCTCTCCCTCGGCACTTTCGCTGAGTGGAGTGGAGCATCTCGAGT 3660
Db |||||
3601 TGCCCAACCTCTCCCTCGGCACTTTCGCTGAGTGGAGTGGAGCATCTCGAGT 3660
QY |||||
3661 TCTTTTATCCCTGATTTTCTGATATTTTACTAGTGTGCGATGAATATCAAC 3720
Db |||||
3661 TCTTTTATCCCTGATTTTCTGATATTTTACTAGTGTGCGATGAATATCAAC 3720
QY |||||
3721 AATAGATGTCACAAATAGGTGAGCAGAGTGTGTCAAAGTATCTGAATCTCTGAAGT 3780
Db |||||
3721 AATAGATGTCACAAATAGGTGAGCAGAGTGTGTCAAAGTATCTGAATCTCTGAAGT 3780
QY |||||
3781 ATCTGACTACTTTATCTCTCGAATTTATACAAACATTTGAAGTATTTTAGTGACA 3840
Db |||||
3781 ATCTGACTACTTTATCTCTCGAATTTATACAAACATTTGAAGTATTTTAGTGACA 3840
QY |||||
3841 TTATGTTTAAACTTGTCAAGATAATTTGTACAAATATAAGGTACCACTGAAGCAGT 3900
Db |||||
3841 TTATGTTTAAACTTGTCAAGATAATTTGTACAAATATAAGGTACCACTGAAGCAGT 3900
QY |||||
3901 GACTGAGATTGCCACTGTGATGACAACTGTTTATACATTTATCATTTGAACCTGGA 3960
Db |||||
3901 GACTGAGATTGCCACTGTGATGACAACTGTTTATACATTTATCATTTGAACCTGGA 3960
QY |||||
3961 TTGCAACAGGAATATTAATGACTGTAAACAAAATTTGTTATCTTAAAATGCAAT 4020
Db |||||
3961 TTGCAACAGGAATATTAATGACTGTAAACAAAATTTGTTATCTTAAAATGCAAT 4020
QY |||||
4021 TGTAAATCAGATGTGAAAATTTGTAATTTACTTCTGTACATTAATGCAATTTCTTTGATA 4080
Db |||||
4021 TGTAAATCAGATGTGAAAATTTGTAATTTACTTCTGTACATTAATGCAATTTCTTTGATA 4080
QY |||||
4081 ARAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA 4134

QY 1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTTGGGAGGTCCTCAACCATCTGCTGCAT 1860
Db 1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTTGGGAGGTCCTCAACCATCTGCTGCAT 1860
QY 1861 CTGAAGTTTACCAACAGCATCGGTGAGCAGGTTGACCTTTGACGATCAAGGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATCGGTGAGCAGGTTGACCTTTGACGATCAAGGTGACCTCAAG 1920
QY 1921 GGGAACTACACCATTAATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTTGTTCCAT 1980
Db 1921 GGGAACTACACCATTAATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTTGTTCCAT 1980
QY 1981 GAGGTGGGCACTACAAAGCCCTACGCTAAGCCAGTGACCGACTCAACATCAAGAAAG 2040
Db 1981 GAGGTGGGCACTACAAAGCCCTACGCTAAGCCAGTGACCGACTCAACATCAAGAAAG 2040
QY 2041 AAAATCCTCTGAGTGGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCGAGACTGT 2100
Db 2041 AAAATCCTCTGAGTGGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCGAGACTGT 2100
QY 2101 GTGCCGGGACACAGAAAGGGATCATGAGGGGAGCCCACTGCTGCTTTGAAATGCAATG 2160
Db 2101 GTGCCGGGACACAGAAAGGGATCATGAGGGGAGCCCACTGCTGCTTTGAAATGCAATG 2160
QY 2161 GCATGTGAGAGGAGAGTTCAAGTGCATGAACAGATGCAAGTGGGTGACAAAGTGCCCG 2220
Db 2161 GCATGTGAGAGGAGAGTTCAAGTGCATGAACAGATGCAAGTGGGTGACAAAGTGCCCG 2220
QY 2221 AATGATTTCTGTCGAAATGAGAACACACGCTGTCATCGCCACAGGAGATCGAGTACCTG 2280
Db 2221 AATGATTTCTGTCGAAATGAGAACACACGCTGTCATCGCCACAGGAGATCGAGTACCTG 2280
QY 2281 TGCTGGAGGAGCCCTTGGGATCGCTGACCATCTTGGCGTACTGGGATCCTGATC 2340
Db 2281 TGCTGGAGGAGCCCTTGGGATCGCTGACCATCTTGGCGTACTGGGATCCTGATC 2340
QY 2341 ACCTCCTTCTGTCGGGCTTCTCAATCAAGTTTCAAGAACTCCCATCGTGAAGGCCACC 2400
Db 2341 ACCTCCTTCTGTCGGGCTTCTCAATCAAGTTTCAAGAACTCCCATCGTGAAGGCCACC 2400
QY 2401 AACGGGAGTTGTCCTACTGCTGCTTCTTCCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
Db 2401 AACGGGAGTTGTCCTACTGCTGCTTCTTCCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
QY 2461 ATCTTTCATCGGAGCCAGGACTGGACCTGTGGCTCGGCAACCGGCTTTGGGATC 2520
Db 2461 ATCTTTCATCGGAGCCAGGACTGGACCTGTGGCTCGGCAACCGGCTTTGGGATC 2520
QY 2521 AGCTTCGTCTGTGATCTCTGCACTCTGTGTAAGACCAACCGGCTGCTGCTGCTTC 2580
Db 2521 AGCTTCGTCTGTGATCTCTGCACTCTGTGTAAGACCAACCGGCTGCTGCTGCTTC 2580
QY 2581 GAGGCAAGATCCCAACGAGCTCCACCGAGTGGTGGGCTCAACCTGAGTTCTC 2640
Db 2581 GAGGCAAGATCCCAACGAGCTCCACCGAGTGGTGGGCTCAACCTGAGTTCTC 2640
QY 2641 CTGGTCTTCTCTGATCTGCTGCAATCGTCACCTGATCATCTGCTCTACACCGCG 2700
Db 2641 CTGGTCTTCTCTGATCTGCTGCAATCGTCACCTGATCATCTGCTCTACACCGCG 2700
QY 2701 CCTCCCTCAGCTACAGAACCATGAGCTGGAGGACGAGTCACTTCTATCACCTGGCAC 2760
Db 2701 CCTCCCTCAGCTACAGAACCATGAGCTGGAGGACGAGTCACTTCTATCACCTGGCAC 2760
QY 2761 GAGGCTCGCTCATGGGCTGGGCTTCTCATCGGCTACACCTGCTCTCGCGCCATC 2820
Db 2761 GAGGCTCGCTCATGGGCTGGGCTTCTCATCGGCTACACCTGCTCTCGCGCCATC 2820
QY 2821 TGCCTTCTTCTTCCCTTCAAGTCCCGTAAGCTGCGGAGAACTTCAAGAGGCTAAGTTC 2880
Db 2821 TGCCTTCTTCTTCCCTTCAAGTCCCGTAAGCTGCGGAGAACTTCAAGAGGCTAAGTTC 2880

QY 2881 ATCACCTTCAGCATGTTGATCTTCTTCATCGCTGATCTCTTTCATCCCGCTATGTC 2940
Db 2881 ATCACCTTCAGCATGTTGATCTTCTTCATCGCTGATCTCTTTCATCCCGCTATGTC 2940
QY 2941 AGCACCTACGGCAAGTTTGTGTCGGCGGTGAGGTGATTGCCATCTGCTCCAGCTTC 3000
Db 2941 AGCACCTACGGCAAGTTTGTGTCGGCGGTGAGGTGATTGCCATCTGCTCCAGCTTC 3000
QY 3001 GGGCTCTGGGCTGCAATTTACTTCAACAAGTGTACATCATCTGTTCAAGCGTCCGT 3060
Db 3001 GGGCTCTGGGCTGCAATTTACTTCAACAAGTGTACATCATCTGTTCAAGCGTCCGT 3060
QY 3061 AACACCATCGAGAGGTGCGTCTGACGACGGCGGCCACGCCCTTCAAGTGGCGGCCGG 3120
Db 3061 AACACCATCGAGAGGTGCGTCTGACGACGGCGGCCACGCCCTTCAAGTGGCGGCCGG 3120
QY 3121 GCACACCTTCGGCGCAGCGCGGTCTGCAAGCGGTTCAGCAGCGCTGTGCGGCTCCACC 3180
Db 3121 GCACACCTTCGGCGCAGCGCGGTCTGCAAGCGGTTCAGCAGCGCTGTGCGGCTCCACC 3180
QY 3181 ATCTCTCGCCCGCTCGTCCACTCGGCGCGGCTCACCATGAGATGAGCGCTGC 3240
Db 3181 ATCTCTCGCCCGCTCGTCCACTCGGCGCGGCTCACCATGAGATGAGCGCTGC 3240
QY 3241 AGCAGCAGAAAGTTCAGCTTCGGCAGCGGCACTGCTCAGCTGCTGCTGCTGAGGAG 3300
Db 3241 AGCAGCAGAAAGTTCAGCTTCGGCAGCGGCACTGCTCAGCTGCTGCTGCTGAGGAG 3300
QY 3301 ACAGGCGGATACCCACCTTCAGCCGACGGCGCGCAGCAGGAACTCGCGGATGCGCG 3360
Db 3301 ACAGGCGGATACCCACCTTCAGCCGACGGCGCGCAGCAGGAACTCGCGGATGCGCG 3360
QY 3361 AGCGGCGACGACCTGCGCATCTAGACACCGACGAGCGGCGGCTCAGAAATCGAGGCC 3420
Db 3361 AGCGGCGACGACCTGCGCATCTAGACACCGACGAGCGGCGGCTCAGAAATCGAGGCC 3420
QY 3421 CAGCGCGCCAAAGATGCGCGATACAGGGCGCGCCGACGAGGGACCTTAGAGTGGCG 3480
Db 3421 CAGCGCGCCAAAGATGCGCGATACAGGGCGCGCCGACGAGGGACCTTAGAGTGGCG 3480
QY 3481 GGGGCGAGAAAGAGAGCGGCCCAACTATGAGAGAACTTATCCAACTCTCCATCAAC 3540
Db 3481 GGGGCGAGAAAGAGAGCGGCCCAACTATGAGAGAACTTATCCAACTCTCCATCAAC 3540
QY 3541 CCAAGAACAATCTCCACGCGCAGCAGCGTGACAACTGACATCAACTCTTAAACCGTGGC 3600
Db 3541 CCAAGAACAATCTCCACGCGCAGCAGCGTGACAACTGACATCAACTCTTAAACCGTGGC 3600
QY 3601 TGCCCAACCTCTCCCTCTCCGCACTTTGCGTTTCTGCTGAAGATTGCGAGCATCTGAGT 3660
Db 3601 TGCCCAACCTCTCCCTCTCCGCACTTTGCGTTTCTGCTGAAGATTGCGAGCATCTGAGT 3660
QY 3661 TCCTTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCAAC 3720
Db 3661 TCCTTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCAAC 3720
QY 3721 ATAATGAGTTGCAATTAGTGTGAGCAGAGTTGTGTCAAAGTATCTGAATCTGAAGT 3780
Db 3721 ATAATGAGTTGCAATTAGTGTGAGCAGAGTTGTGTCAAAGTATCTGAATCTGAAGT 3780
QY 3781 ATCTGAACACTACTTATCTCGAAATTTGATTAACAACATTTTGAAGTATTTTAGTGACA 3840
Db 3781 ATCTGAACACTACTTATCTCGAAATTTGATTAACAACATTTTGAAGTATTTTAGTGACA 3840
QY 3841 TTATGTTCTAACATTTGTAAGATAATTTGTTTACAACATATAAGGTACCACTGAAGCAGT 3900
Db 3841 TTATGTTCTAACATTTGTAAGATAATTTGTTTACAACATATAAGGTACCACTGAAGCAGT 3900
QY 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTTTATCAATTTATCATTTGAACCTTGA 3960
Db 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTTTATCAATTTATCATTTGAACCTTGA 3960
QY 3961 TTGCAACAGGAATATAATGACTGTGTACAAAAAATTTGTTGATTATCTTAAAAATGCAAT 4020

```

Db      3961 TTGCAACGGAATAAATGACTGTACAAAAAATTTGTTATCTTAAAAATGCAAA 4020
Qy      4021 TGTAAATCAGATGTGTAATAATGGTAATACCTCTGTACATTAATGCAATATTTCTTGATA 4080
Db      4021 TGTAAATCAGATGTGTAATAATGGTAATACCTCTGTACATTAATGCAATATTTCTTGATA 4080
Qy      4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGG 4134
Db      4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGG 4134

RESULT 7
AR432994
LOCUS      4134 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION      Sequence 17 from patent US 6655318.
ACCESSION      AR432994
VERSION      AR432994.1 GI:40195659
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 4134)
AUTHORS      Harris,H.W. Jr., Russell,D.R., Nearing,J. and Betka,M.
TITLE      Methods for raising pre-adult anadromous fish
JOURNAL      Patent: US 6655318-A 17-02-DEC-2003;
FEATURES
            Location/Qualifiers
            1..4134
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 4134; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AATTCGGTGTGTCGGTTCAGTCAAGTCTCCTCCAGTCAAAATGAAATGAGTGTGTC 60
Db      1 AATTCGGTGTGTCGGTTCAGTCAAGTCTCCTCCAGTCAAAATGAAATGAGTGTGTC 60

Qy      61 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTTGTCAGTTATCTGAAGGT 120
Db      61 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTTGTCAGTTATCTGAAGGT 120

Qy      121 TATTAATAATGTTTCTGCAAGATGCTTCAAGAAATCAATCTGCAAGTCTTCCCAAT 180
Db      121 TATTAATAATGTTTCTGCAAGATGCTTCAAGAAATCAATCTGCAAGTCTTCCCAAT 180

Qy      181 GTCATTGTATGAATACTGACCAAGGGATGTAACAAATGGAACAAAGCTGAGGACCA 240
Db      181 GTCATTGTATGAATACTGACCAAGGGATGTAACAAATGGAACAAAGCTGAGGACCA 240

Qy      241 GTTCAACCTTTCTTGAGCATACGATCAACCTGAAAGAGATGGAAGACTTGAGAGGAA 300
Db      241 GTTCAACCTTTCTTGAGCATACGATCAACCTGAAAGAGATGGAAGACTTGAGAGGAA 300

Qy      301 ATGGGATTTGATCTTCCAGAGTCTGCTGTAAGCGGATCCCTCAACCAATTAAGAGATA 360
Db      301 ATGGGATTTGATCTTCCAGAGTCTGCTGTAAGCGGATCCCTCAACCAATTAAGAGATA 360

Qy      361 GCAGAAATCCTCCAGCATCTCTGTAAGCGGCTGGCGTAGTGTGGTTCGATCAAGGAA 420
Db      361 GCAGAAATCCTCCAGCATCTCTGTAAGCGGCTGGCGTAGTGTGGTTCGATCAAGGAA 420

Qy      421 CAGAGACGGGTGCACANTGCTCAGCTTCACTGCCAATCTTATCTTGGATTTACA 480
Db      421 CAGAGACGGGTGCACANTGCTCAGCTTCACTGCCAATCTTATCTTGGATTTACA 480

Qy      481 CTCCTACAGTCGTAACATGCTCAGGGTATGTTCCAAACCAAGGGCCGAGAGAGGAA 540
Db      481 CTCCTACAGTCGTAACATGCTCAGGGTATGTTCCAAACCAAGGGCCGAGAGAGGAA 540

Qy      541 GACATCATCTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCCAAGATCAGGAC 600

```

```

Db      541 GACATCATCTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGATCAGGAC 600
Qy      601 TTAATTCGAGACCGGAGCGGACAAAATGATTCGGTACAAATTTTCGAGGCTTCGATCG 660
Db      601 TTAATTCGAGACCGGAGCGGACAAAATGATTCGGTACAAATTTTCGAGGCTTCGATCG 660
Qy      661 CTCAGGCGATGATATTCGCAATTTGAAGAGATTAAACAACAGTATGACTTTCTTCCCAAT 720
Db      661 CTCAGGCGATGATATTCGCAATTTGAAGAGATTAAACAACAGTATGACTTTCTTCCCAAT 720
Qy      721 ATCACCTGGGATATCGCATATTTGACAGCTGTAACACCGTGTCCAGGCGCTAGAGGCA 780
Db      721 ATCACCTGGGATATCGCATATTTGACAGCTGTAACACCGTGTCCAGGCGCTAGAGGCA 780
Qy      781 ACACCTAGCTTTGTCGCCCAAGAAACAAATCGACTCGCTGAACTTAGATGAGTTCTCTAAC 840
Db      781 ACACCTAGCTTTGTCGCCCAAGAAACAAATCGACTCGCTGAACTTAGATGAGTTCTCTAAC 840
Qy      841 TGCTCTGACCATATCCCATCCCAATAGCAGTGGTCCGGGCAACCGGGTCAGGAATCTCC 900
Db      841 TGCTCTGACCATATCCCATCCCAATAGCAGTGGTCCGGGCAACCGGGTCAGGAATCTCC 900
Qy      901 ACGGCTGTGCCAATCTATTGGGATTTATTTACATTCACAGGTGAGTATGCTCTCCG 960
Db      901 ACGGCTGTGCCAATCTATTGGGATTTATTTACATTCACAGGTGAGTATGCTCTCCG 960
Qy      961 AGCAGGCTGCTCAGCAACAAAGATGAGTACAAGGCTTCTCAGGACCAATCCCAATGAT 1020
Db      961 AGCAGGCTGCTCAGCAACAAAGATGAGTACAAGGCTTCTCAGGACCAATCCCAATGAT 1020
Qy      1021 GAGCAACAGCCACCGCCATGCGGAGATCATCGACATTCAGTGGAACTGGGTGGGA 1080
Db      1021 GAGCAACAGCCACCGCCATGCGGAGATCATCGACATTCAGTGGAACTGGGTGGGA 1080
Qy      1081 ACCTGGCAGCCAGCATGACTATGCGCCGCCAGGCAATTCACAAAGTTCGGGAGGAGGCC 1140
Db      1081 ACCTGGCAGCCAGCATGACTATGCGCCGCCAGGCAATTCACAAAGTTCGGGAGGAGGCC 1140
Qy      1141 GTTAAAGGAGACATCTGTATTTGACTTCAGTGGAGATGATCTCTCAGTACTACACCCAGA 1200
Db      1141 GTTAAAGGAGACATCTGTATTTGACTTCAGTGGAGATGATCTCTCAGTACTACACCCAGA 1200
Qy      1201 CAGTTGAGTTCATCGCCGAGCTCATCCAGAACTCTCGGCCAAAGTCACTCGTGTCTTC 1260
Db      1201 CAGTTGAGTTCATCGCCGAGCTCATCCAGAACTCTCGGCCAAAGTCACTCGTGTCTTC 1260
Qy      1261 TCCAAATGGCCCCGACCTGGAGCGCTCATCCAGGAGATAGTTCCGGAGAAACATCAACGAT 1320
Db      1261 TCCAAATGGCCCCGACCTGGAGCGCTCATCCAGGAGATAGTTCCGGAGAAACATCAACGAT 1320
Qy      1321 CGGATCTGGTGCACGAGGCTTCGGCCAGCTCTTCCTCATTCGCCAAGCAGAGTAC 1380
Db      1321 CGGATCTGGTGCACGAGGCTTCGGCCAGCTCTTCCTCATTCGCCAAGCAGAGTAC 1380
Qy      1381 TTCCAGTGTGTGCGCGCACCATTCGGCTTCCTCAGGGCGGGCGGTATCCCAAGGTTTC 1440
Db      1381 TTCCAGTGTGTGCGCGCACCATTCGGCTTCCTCAGGGCGGGCGGTATCCCAAGGTTTC 1440
Qy      1441 AACAGTTCTGTAAGAGGTTCACCCAGAGGTCTCCGACAAATGGGTTTGTCAAGGAG 1500
Db      1441 AACAGTTCTGTAAGAGGTTCACCCAGAGGTCTCCGACAAATGGGTTTGTCAAGGAG 1500
Qy      1501 TTCTGGAGGAGACCTTCAACTCTACTTCAACCGAAGACCTTCAGCAGCTGAGAGAT 1560
Db      1501 TTCTGGAGGAGACCTTCAACTCTACTTCAACCGAAGACCTTCAGCAGCTGAGAGAT 1560
Qy      1561 TCCAGAGTGTCTGCAAGGAGCGGCTCAAGGGGAGCGGTCCAAAGCGGGGAACTCC 1620
Db      1561 TCCAGAGTGTCTGCAAGGAGCGGCTCAAGGGGAGCGGTCCAAAGCGGGGAACTCC 1620
Qy      1621 AGACGACAGCCCTCAGCCACCCCTCACTGGGAGAGAAACATCACAGGCTGGAGACC 1680

```

1621 AGACGGACAGCCCTACGCCACCCCTGCACTGGGAGGAGAAACATCACAGCGTGGAGACC 1680
1681 CCCTACCTGGATATATACACACTGAGGATCTCTCAATATGATAGTGGCGCTCTACTCC 1740
1681 CCCTACCTGGATATATACACACTGAGGATCTCTCAATATGATAGTGGCGCTCTACTCC 1740
1741 ATTGCTCAGCGCTCAGAGACATCACTCTTGGAAACCCGGCAGCGGCATCTTTGCAAAAC 1800
1741 ATTGCTCAGCGCTCAGAGACATCACTCTTGGAAACCCGGCAGCGGCATCTTTGCAAAAC 1800
1801 GGATCTTGTGAGATATTTAAATAAGTTGAGCGCTGGCAGGTCCTCAACCATCTCTGTCAT 1860
1801 GGATCTTGTGAGATATTTAAATAAGTTGAGCGCTGGCAGGTCCTCAACCATCTCTGTCAT 1860
1861 CTGAAGTTTACCAACAGCATGGTGAGCAGAGTTGACTTTTGACGATCAAGGTGACTCAAG 1920
1861 CTGAAGTTTACCAACAGCATGGTGAGCAGAGTTGACTTTTGACGATCAAGGTGACTCAAG 1920
1921 GGGAACTACACCATATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTTTCCAT 1980
1921 GGGAACTACACCATATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTTTCCAT 1980
1981 GAGTGGGCACTACAAAGCCCTACGCTAAGCCAGTGAACGACTCAACATCAAGAAAG 2040
1981 GAGTGGGCACTACAAAGCCCTACGCTAAGCCAGTGAACGACTCAACATCAAGAAAG 2040
2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTCTCCAACTGAGTGGAGACTGT 2100
2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTCTCCAACTGAGTGGAGACTGT 2100
2101 GTGCGGGACACAGAAAGGGATCATCGAGGGGAGGCCACCTGTCTTTGAATGCATG 2160
2101 GTGCGGGACACAGAAAGGGATCATCGAGGGGAGGCCACCTGTCTTTGAATGCATG 2160
2161 GCATGTGAGAGGGAGTTGATGATGAATAACGATGAAGTGGCTGACAAAGTGCCCG 2220
2161 GCATGTGAGAGGGAGTTGATGATGAATAACGATGAAGTGGCTGACAAAGTGCCCG 2220
2221 AATGATTTCTGTCGAATGAGAACACACGCTGTGTCATCGCCAGGAGATCGAGTACCTG 2280
2221 AATGATTTCTGTCGAATGAGAACACACGCTGTGTCATCGCCAGGAGATCGAGTACCTG 2280
2281 TCGTGAAGGAGCCCTTGGGATCGCTGACCATCTTCCGGTACTGGGATCTCTGATC 2340
2281 TCGTGAAGGAGCCCTTGGGATCGCTGACCATCTTCCGGTACTGGGATCTCTGATC 2340
2341 ACCTCTCTGCTGGGGTCTTTCATCAAGTTTCAAGAACACTCCCATCGTGAAGGCCACC 2400
2341 ACCTCTCTGCTGGGGTCTTTCATCAAGTTTCAAGAACACTCCCATCGTGAAGGCCACC 2400
2401 AACCGGAGTTGCTTACCTGCTGCTTCTCCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
2401 AACCGGAGTTGCTTACCTGCTGCTTCTCCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
2461 ATCTTCATCGGAGCCAGGACTGGACCTGTCGGCTCCGCCAACCCGGCTTTGGCATC 2520
2461 ATCTTCATCGGAGCCAGGACTGGACCTGTCGGCTCCGCCAACCCGGCTTTGGCATC 2520
2521 AGCTTCGCTGCTGCTATCTCTGATCTCTGTTGAGAACCAACCGGCTGCTGCTCTTC 2580
2521 AGCTTCGCTGCTGCTATCTCTGATCTCTGTTGAGAACCAACCGGCTGCTGCTCTTC 2580
2581 GAGGCCAAGATCCCAACAGCTCCACCGCAAGTGGTGGGCTCAACCTGCAAGTCTC 2640
2581 GAGGCCAAGATCCCAACAGCTCCACCGCAAGTGGTGGGCTCAACCTGCAAGTCTC 2640
2641 CTGGTCTTCTCTGCTATCTCTGTCGAAATCGTCACTGATCATCTGGCTCTTACACCGG 2700
2641 CTGGTCTTCTCTGCTATCTCTGTCGAAATCGTCACTGATCATCTGGCTCTTACACCGG 2700
2701 CTTCCCTCAGCTACAGGAACCAATGAGCTGGAGGAGGCTCATCTTCACTGAGTGGAC 2760
2701 CTTCCCTCAGCTACAGGAACCAATGAGCTGGAGGAGGCTCATCTTCACTGAGTGGAC 2760

2761 GAGGGCTCGCTCATGCGCTGGGCTTCTCTCATCGCTACACCTGCTCTCTCGCGGCATC 2820
2761 GAGGGCTCGCTCATGCGCTGGGCTTCTCTCATCGCTACACCTGCTCTCTCGCGGCATC 2820
2821 TGCTTCTTCTTCCCTTCAAGTCCCTAAGTCCCGGAGAACTTCAACAGAGCTAAGTTC 2880
2821 TGCTTCTTCTTCCCTTCAAGTCCCGGAGAACTTCAACAGAGCTAAGTTC 2880
2881 ATCACCTTCAGCATGTTGATCTTCTCATCGCTGATCTCTTCACTCCCGCTATGTC 2940
2881 ATCACCTTCAGCATGTTGATCTTCTCATCGCTGATCTCTTCACTCCCGCTATGTC 2940
2941 AGCACCTTACGGCAAGTTTGTGTGCGCGCTGGAGGTGATTGCCATCTGCGCTCCAGCTTC 3000
2941 AGCACCTTACGGCAAGTTTGTGTGCGCGCTGGAGGTGATTGCCATCTGCGCTCCAGCTTC 3000
3001 GGCTGTGGCTGCAATTTACTTCAACAAGTGTATCATCTCTGTTCAGCGCTGCCGT 3060
3001 GGCTGTGGCTGCAATTTACTTCAACAAGTGTATCATCTCTGTTCAGCGCTGCCGT 3060
3061 AACACCATTCAGGAGGTGCGCTGCAGCAGCGCGGCCACCGCTTCAAGGTGGCGGCCGG 3120
3061 AACACCATTCAGGAGGTGCGCTGCAGCAGCGCGGCCACCGCTTCAAGGTGGCGGCCGG 3120
3121 GCCACCTTCCGGCGAGCGCGCTCTCGAAGCGCTTCCAGCAGCTGTGCGCTCCACC 3180
3121 GCCACCTTCCGGCGAGCGCGCTCTCGAAGCGCTTCCAGCAGCTGTGCGCTCCACC 3180
3181 ATCTCTCGCGCTCTCTCCACTTGGCGCGGGCTCACCATGAGATGCGAGCGTGC 3240
3181 ATCTCTCGCGCTCTCTCCACTTGGCGCGGGCTCACCATGAGATGCGAGCGTGC 3240
3241 AGCACGAGAGGTTCAGCTTTCGGCAGCGCACCGCTCACCTGTCTGCTTTCAGAGGAG 3300
3241 AGCACGAGAGGTTCAGCTTTCGGCAGCGCACCGCTCACCTGTCTGCTTTCAGAGGAG 3300
3301 ACAGCGCGATACGCCACCTCAGCGCACCGCGCGGAGGAACTCGCGGATGCGCGC 3360
3301 ACAGCGCGATACGCCACCTCAGCGCACCGCGCGGAGGAACTCGCGGATGCGCGC 3360
3361 AGCGCGACGACCTGCTCATCTAGACACACGACGAGCGCGCGCTCAGAAATCGAGGCC 3420
3361 AGCGCGACGACCTGCTCATCTAGACACACGACGAGCGCGCGCTCAGAAATCGAGGCC 3420
3421 CAGCGCGCAACGATGCCGATACAGGCGCGCGCGCACCAAGGGCACCTTAGAGTGGCG 3480
3421 CAGCGCGCAACGATGCCGATACAGGCGCGCGCGCACCAAGGGCACCTTAGAGTGGCG 3480
3481 GCGGCGACGAGGAGCGCCCAACTATGAGGAGAACTTAATCCAACTCTCTCAATCAAC 3540
3481 GCGGCGACGAGGAGCGCCCAACTATGAGGAGAACTTAATCCAACTCTCTCAATCAAC 3540
3541 CCCAAGAACATCTCTCCACGCGCAGCAGCGCTGACACTGACACTCTTAAACCGGTGGC 3600
3541 CCCAAGAACATCTCTCCACGCGCAGCAGCGCTGACACTGACACTCTTAAACCGGTGGC 3600
3601 TGCCCAACCTCTCCCTCTCGGCACTTTGGGTTTCTGAAATTCAGCATCTGAGTGGAGT 3660
3601 TGCCCAACCTCTCCCTCTCGGCACTTTGGGTTTCTGAAATTCAGCATCTGAGTGGAGT 3660
3661 TCTTTTATCCCTGATTTTCTGACTTGGATTTTCTAGTGTGCGATGGAATATCAAC 3720
3661 TCTTTTATCCCTGATTTTCTGACTTGGATTTTCTAGTGTGCGATGGAATATCAAC 3720
3721 ATATGAGTTCACAATTAGGTGAGGAGTGTGTGCAAAAGTATCTGAACTATCTGAGT 3780
3721 ATATGAGTTCACAATTAGGTGAGGAGTGTGTGCAAAAGTATCTGAACTATCTGAGT 3780
3781 ATCTGAACTACTTTTCTCTCGAATTTGATTAACAACTTTGAAATTTTGTAGTGACA 3840
3781 ATCTGAACTACTTTTCTCTCGAATTTGATTAACAACTTTGAAATTTTGTAGTGACA 3840

```
QY 3841 TTATGTTCTAATCTGTCAGATAATTTGTTACACATATAAGGTACCACCTGAGCAGT 3900
Db 3841 TTATGTTCTAATCTGTCAGATAATTTGTTACACATATAAGGTACCACCTGAGCAGT 3900
QY 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATACATTTATCAATTTGAAACCTGGA 3960
Db 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATACATTTATCAATTTGAAACCTGGA 3960
QY 3961 TTGCAACAGGATATTAATGACTGTACAAAAAATTTGTTGATATCTTAAAAATGCAAT 4020
Db 3961 TTGCAACAGGATATTAATGACTGTACAAAAAATTTGTTGATATCTTAAAAATGCAAT 4020
QY 4021 TGTAAATCAGATGTGTAATAATTTGTTGATATCTTGTACATTAATGCAATTTCTTTGATA 4080
Db 4021 TGTAAATCAGATGTGTAATAATTTGTTGATATCTTGTACATTAATGCAATTTCTTTGATA 4080
QY 4081 AAAAAAATTTGTTGATATCTTGTACATTAATGCAATTTCTTTGATA 4134
Db 4081 AAAAAAATTTGTTGATATCTTGTACATTAATGCAATTTCTTTGATA 4134

RESULT 8
AX417770 4134 bp DNA linear PAT 18-JUN-2002
LOCUS AX417770
DEFINITION Sequence 17 from Patent WO230182.
ACCESSION AX417770
VERSION AX417770.1 GI:215222908
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
            unclassified.
REFERENCE
1
AUTHORS Hartz Jr, W. H., Betka, M., Russel, D. R. and Nearing, J.
TITLE Methods for raising pre-adult anadromous fish
JOURNAL Patent: WO 0230182-A 17 18-APR-2002;
AQUABIO PRODUCTS SCIENCES L L (US)
FEATURES
    source
        Location/Qualifiers
            1..4134
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
                /note="Dogfish Shark"

ORIGIN

Query Match 100.0%; Score 4134; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGGTTGCTGCGTTTCAGTCCAAAGTCTCCTCCAGTGCAGAAATGAGAAATGTTGTC 60
Db 1 AATTCGGTTGCTGCGTTTCAGTCCAAAGTCTCCTCCAGTGCAGAAATGAGAAATGTTGTC 60
QY 61 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTTGTCAGTTATCTGAAGT 120
Db 61 GCCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATTTGTCAGTTATCTGAAGT 120
QY 121 TATTAATAATGTTTTCAGAGGATGCTTCAGAGAAATCAATTTCTGACGTTTCCCAAT 180
Db 121 TATTAATAATGTTTTCAGAGGATGCTTCAGAGAAATCAATTTCTGACGTTTCCCAAT 180
QY 181 GTCAATTTGATGAATACTGACCAAAAGGATGTAACAAATGGAACAAAGCTGAGACCAAC 240
Db 181 GTCAATTTGATGAATACTGACCAAAAGGATGTAACAAATGGAACAAAGCTGAGACCAAC 240
QY 241 GTTACACCTTTCTTGAGGATACAGTCAACCTGAGGAGATGGAAGCTTGGAGAGAA 300
Db 241 GTTACACCTTTCTTGAGGATACAGTCAACCTGAGGAGATGGAAGCTTGGAGAGAA 300
QY 301 ATGGGGATTGATCTTCCAGAGGTTCTGCTGTAAGAGCATCCTCACCATTACAAAGATAA 360
Db 301 ATGGGGATTGATCTTCCAGAGGTTCTGCTGTAAGAGCATCCTCACCATTACAAAGATAA 360
QY 361 GCAGAAATCCTCCAGGATCTCTGTAAACGGGCTGGCGGTAGTGTGGTTCAGAGGAA 420
```

```
Db 361 GCAGAAATCCTCCAGGATCTCTGTAAACGGGCTGGCGGTAGTGTGGTTCAGAGGAA 420
QY 421 CAGAGACAGGGCTGCACAATGGCTCAGGTTCACTGCCAACTCTTATTTCTTGGGATTTACA 480
Db 421 CAGAGACAGGGCTGCACAATGGCTCAGGTTCACTGCCAACTCTTATTTCTTGGGATTTACA 480
QY 481 CTCCTCAGTCGTACAAATGCTCAGGGTATGTCCTCAAAACCAAGGGCCCAAGAGAAAGGA 540
Db 481 CTCCTCAGTCGTACAAATGCTCAGGGTATGTCCTCAAAACCAAGGGCCCAAGAGAAAGGA 540
QY 541 GACATCATCTGGAGGCTCTCTTTCCCAATACATTTTGGAGTAGCCGCCAAGGATCAGGAC 600
Db 541 GACATCATCTGGAGGCTCTCTTTCCCAATACATTTTGGAGTAGCCGCCAAGGATCAGGAC 600
QY 601 TTAATAATCGAGACCGGAGCGGACAAAATGTTTCGGTACAAATTTTCGAGGCTTCCGATGG 660
Db 601 TTAATAATCGAGACCGGAGCGGACAAAATGTTTCGGTACAAATTTTCGAGGCTTCCGATGG 660
QY 661 CTCAGGCGGATGATATTTGCAATTTGAAGAGATTAAACAAGATGATGACTTTCTGCCCCAAT 720
Db 661 CTCAGGCGGATGATATTTGCAATTTGAAGAGATTAAACAAGATGATGACTTTCTGCCCCAAT 720
QY 721 ATCAACCTGGGATATCGCATATTTTGACAGTGTAAACACCGTGTCCAAAGGCGGTAGAGGCA 780
Db 721 ATCAACCTGGGATATCGCATATTTTGACAGTGTAAACACCGTGTCCAAAGGCGGTAGAGGCA 780
QY 781 ACACCTCAGCTTTGTCGCCAGAAACAAATCGACTCGCTGAACTTTAGATGAGTCTCTAAC 840
Db 781 ACACCTCAGCTTTGTCGCCAGAAACAAATCGACTCGCTGAACTTTAGATGAGTCTCTAAC 840
QY 841 TGCTCTGACCATATCCCATCCACAATAGCAGTGGTTCGGGCAACCCGGGTACAGAAATCTCC 900
Db 841 TGCTCTGACCATATCCCATCCACAATAGCAGTGGTTCGGGCAACCCGGGTACAGAAATCTCC 900
QY 901 ACGGCTGTGCGCAATCTATTTGGGATTTATTTTCAATTTCCACAGTCACTATGCTCTCTCG 960
Db 901 ACGGCTGTGCGCAATCTATTTGGGATTTATTTTCAATTTCCACAGTCACTATGCTCTCTCG 960
QY 961 AGCAGGCTGTCTCAGCAACAAAGAAATGAGTACAAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
Db 961 AGCAGGCTGTCTCAGCAACAAAGAAATGAGTACAAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
QY 1021 GAGCAACAGGCCACGGCCATGCGCGAGATCATCGACACTTCCAGTGGAACTGGGTGGGA 1080
Db 1021 GAGCAACAGGCCACGGCCATGCGCGAGATCATCGACACTTCCAGTGGAACTGGGTGGGA 1080
QY 1081 ACCCTGGCAGCCAGCATGACTATGCGCCGCCAGGCAATGCAAAAGTTCGGGAGGAGGCC 1140
Db 1081 ACCCTGGCAGCCAGCATGACTATGCGCCGCCAGGCAATGCAAAAGTTCGGGAGGAGGCC 1140
QY 1141 GTTAAAGGAGACATCTGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1200
Db 1141 GTTAAAGGAGACATCTGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1200
QY 1201 CAGTTGAGTTTCAATCGGACGCTCATCCAGAACTCTCGGCCAAAGTTCATCGTGTCTTC 1260
Db 1201 CAGTTGAGTTTCAATCGGACGCTCATCCAGAACTCTCGGCCAAAGTTCATCGTGTCTTC 1260
QY 1261 TCCAAATGGCCCCGACCTGGAGCGCTCATCCAGAGATAGTTTCGGAGAAACATCACCGAT 1320
Db 1261 TCCAAATGGCCCCGACCTGGAGCGCTCATCCAGAGATAGTTTCGGAGAAACATCACCGAT 1320
QY 1321 CGGATCTGGCTGCGCAGCGAGGCTTGGCGCAGCTCTTCGCTCATTTGCCAGGACAGGTAC 1380
Db 1321 CGGATCTGGCTGCGCAGCGAGGCTTGGCGCAGCTCTTCGCTCATTTGCCAGGACAGGTAC 1380
QY 1381 TTCCAGTGTGTGGCGGCGACCATCGCTTCTCAGGCGGGGGCTATCCACAGGTTTC 1440
Db 1381 TTCCAGTGTGTGGCGGCGACCATCGCTTCTCAGGCGGGGGCTATCCACAGGTTTC 1440
QY 1441 AACAGTTCTCTGAAGAGGAGTCCACCCAGGAGTCTCTCGCAAAATGGGTTTGTCAAGGAG 1500
```

Db	1441	AA	CAAGTTCTG	AAGAGGTCTCACCCGACGAGGTCTCGGACAAATGGGTTTGTCAAGGAG	1500
Qy	1501	TT	CTGGAGAGAC	CTTTCAACTGCTACTTCAACCGAGAAGACCTTGACGAGCTGAAGAA	1560
Db	1501	TT	CTGGAGAGAC	CTTTCAACTGCTACTTCAACCGAGAAGACCTTGACGAGCTGAAGAA	1560
Qy	1561	T	CAAGTGCCTTC	GCACGACCGGCGGCTCAAGGGGACGGCTCAAGCGGGGAACTCC	1620
Db	1561	T	CAAGTGCCTTC	GCACGACCGGCGGCTCAAGGGGACGGCTCAAGCGGGGAACTCC	1620
Qy	1621	AG	ACGACACCCCT	TAGCCACCCCTGCATCTGGGGGAGGAGAAATCAACACGCTGGAGACC	1680
Db	1621	AG	ACGACACCCCT	TAGCCACCCCTGCATCTGGGGGAGGAGAAATCAACACGCTGGAGACC	1680
Qy	1681	CC	CTACTGGAATTA	CACACCTTGAGGATCTCTCAATGTATACGTGCGGCTCTACTCC	1740
Db	1681	CC	CTACTGGAATTA	CACACCTTGAGGATCTCTCAATGTATACGTGCGGCTCTACTCC	1740
Qy	1741	AT	TGCTCAGCCCT	CGAAGACATCCACTCTTGAAACCCGGGACCGGGCATCTTTGCAAA	1800
Db	1741	AT	TGCTCAGCCCT	CGAAGACATCCACTCTTGAAACCCGGGACCGGGCATCTTTGCAAA	1800
Qy	1801	GG	ATCTTTGT	CAGATATATAAAAAAGTTGAGGCTGGCAGGTCTCTCAACATCTGTGCA	1860
Db	1801	GG	ATCTTTGT	CAGATATATAAAAAAGTTGAGGCTGGCAGGTCTCTCAACATCTGTGCA	1860
Qy	1861	CT	GAAGTTTAC	CAACAGCATGGGTGACGAGTTGACTTTGACCATCAAGTGACCTCAAG	1920
Db	1861	CT	GAAGTTTAC	CAACAGCATGGGTGACGAGTTGACTTTGACCATCAAGTGACCTCAAG	1920
Qy	1921	GG	AACTACACCA	TATTAACATGGCAGCTCTCGCAGAGGATGAATCGGTGTGTTTCCAT	1980
Db	1921	GG	AACTACACCA	TATTAACATGGCAGCTCTCGCAGAGGATGAATCGGTGTGTTTCCAT	1980
Qy	1981	G	AGTGGGCA	ACTCAACGGCTAGCTTAAGCCAGTGACCGACTCAACATCAACGAAAG	2040
Db	1981	G	AGTGGGCA	ACTCAACGGCTAGCTTAAGCCAGTGACCGACTCAACATCAACGAAAG	2040
Qy	2041	A	AATCTCTG	GAGTGCTCTCCAAAGTGGTTCCTTTCTCCAACCTGCAGTCCGAGACTGT	2100
Db	2041	A	AATCTCTG	GAGTGCTCTCCAAAGTGGTTCCTTTCTCCAACCTGCAGTCCGAGACTGT	2100
Qy	2101	GT	CGCGGCAC	AGGAATCATCGAGGGGAGCCACTCTGCTGCTTTGAATGCATG	2160
Db	2101	GT	CGCGGCAC	AGGAATCATCGAGGGGAGCCACTCTGCTGCTTTGAATGCATG	2160
Qy	2161	GC	ATGTCAGAGG	GAGATTCAGTGAAGATCGATCAAGTGGTGTACAAAGTGCCCG	2220
Db	2161	GC	ATGTCAGAGG	GAGATTCAGTGAAGATCGATCAAGTGGTGTACAAAGTGCCCG	2220
Qy	2221	A	ATGATTTCT	GGTCCGAATGAAACCAACGCTCGCATCGCCAGGAGATCGAGTACCTG	2280
Db	2221	A	ATGATTTCT	GGTCCGAATGAAACCAACGCTCGCATCGCCAGGAGATCGAGTACCTG	2280
Qy	2281	TC	GTGACGAG	CCCTTCGGGATCGCTTGACCATCTTCGCGTACTGGGCACTCTGATC	2340
Db	2281	TC	GTGACGAG	CCCTTCGGGATCGCTTGACCATCTTCGCGTACTGGGCACTCTGATC	2340
Qy	2341	AC	CTCTCTG	TGCTGGGGTCTTTCATCAAGTTACAGAACACTCCCATCGTGAAGGCCACC	2400
Db	2341	AC	CTCTCTG	TGCTGGGGTCTTTCATCAAGTTACAGAACACTCCCATCGTGAAGGCCACC	2400
Qy	2401	A	ACGGGAGT	TGCTACTCGTGTCTTCTCCCTCATCTGTGCTCTCTCCAGTCTGCTC	2460
Db	2401	A	ACGGGAGT	TGCTACTCGTGTCTTCTCCCTCATCTGTGCTCTCTCCAGTCTGCTC	2460
Qy	2461	AT	CTTCAT	CGGAGCCACGAGCTGTCGGTTCGCCAACCGGCTTTTGGCATC	2520
Db	2461	AT	CTTCAT	CGGAGCCACGAGCTGTCGGTTCGCCAACCGGCTTTTGGCATC	2520
Qy	2521	AG	CTTCGCTG	TCATCTCTGATCTCTGATGAAGACCAACCGGCTGCTGCTGCTTTC	2580
Db	2521	AG	CTTCGCTG	TCATCTCTGATCTCTGATGAAGACCAACCGGCTGCTGCTGCTTTC	2580

Qy	2581	GAGGCCAAGATCCCAACAGCCTCCACCAGAGTGGGTGGGCTCAACTGTGAGTTCTCTC	2640
Db	2581	GAGGCCAAGATCCCAACAGCCTCCACCAGAGTGGGTGGGCTCAACTGTGAGTTCTCTC	2640
Qy	2641	CTGGTCTTCTCTGCACTCTGTGTGAAATCGTCACCTGTCATCATCTGGCTCTACACCGCG	2700
Db	2641	CTGGTCTTCTCTGCACTCTGTGTGAAATCGTCACCTGTCATCATCTGGCTCTACACCGCG	2700
Qy	2701	CCTCCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCACTTTCAATCACTTGCGAC	2760
Db	2701	CCTCCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCACTTTCAATCACTTGCGAC	2760
Qy	2761	GAGGGTCGCTCATGGGCTGGGCTTCCTCATCGGCTACACCTGCTCTCTCGCGCGCATC	2820
Db	2761	GAGGGTCGCTCATGGGCTGGGCTTCCTCATCGGCTACACCTGCTCTCTCGCGCGCATC	2820
Qy	2821	TGCTTCTTCTTCGCCCTTCAAGTCCCCTAAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC	2880
Db	2821	TGCTTCTTCTTCGCCCTTCAAGTCCCCTAAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC	2880
Qy	2881	ATCACCTTCAGCATGTGTATCTTCTTCATCTGCTTGATCTCTTATCTCCGCGCTATGTC	2940
Db	2881	ATCACCTTCAGCATGTGTATCTTCTTCATCTGCTTGATCTCTTATCTCCGCGCTATGTC	2940
Qy	2941	AGCACCTACGGCAAGTTGTGTCGGCGCTGGAGGTGATTGCCCATCTCTGGCTCCAGCTTC	3000
Db	2941	AGCACCTACGGCAAGTTGTGTCGGCGCTGGAGGTGATTGCCCATCTCTGGCTCCAGCTTC	3000
Qy	3001	GGGCTGCTGGGCTGCAATTACTTCAACAAGTGTATACATCATCTGTTCAAGCGTGCCTG	3060
Db	3001	GGGCTGCTGGGCTGCAATTACTTCAACAAGTGTATACATCATCTGTTCAAGCGTGCCTG	3060
Qy	3061	AACACCATCAGAGAGTGCCTCAGCACGGCGGCCACGCCTTCAAGTGGCGGCGCCCG	3120
Db	3061	AACACCATCAGAGAGTGCCTCAGCACGGCGGCCACGCCTTCAAGTGGCGGCGCCCG	3120
Qy	3121	GCACCTCTCGGCGCAGCGCGGCTCTGCAAGCGTTCAGACGACCTGTGCGGCTCCACC	3180
Db	3121	GCACCTCTCGGCGCAGCGCGGCTCTGCAAGCGTTCAGACGACCTGTGCGGCTCCACC	3180
Qy	3181	ATCTCTCGCGGCTCGTCCAACCTGGCGCGCGGCTTACCATGAGATGACAGCGCTGC	3240
Db	3181	ATCTCTCGCGGCTCGTCCAACCTGGCGCGCGGCTTACCATGAGATGACAGCGCTGC	3240
Qy	3241	AGCAGCAGAGGTCAGCTTTCGGCAGCGGCACCGTCAACCTGTGCTCAGCTTCGAGGAG	3300
Db	3241	AGCAGCAGAGGTCAGCTTTCGGCAGCGGCACCGTCAACCTGTGCTCAGCTTCGAGGAG	3300
Qy	3301	ACAGCGCGATACGCCACCTCAGCCGCAACCGCGCAGCAGGAACTCTGGCGGATGGCCGC	3360
Db	3301	ACAGCGCGATACGCCACCTCAGCCGCAACCGCGCAGCAGGAACTCTGGCGGATGGCCGC	3360
Qy	3361	AGCGGACAGCATGCGCATCTAGACACCAAGCAGGCGCCGCTCAGAAATCGAGCCCC	3420
Db	3361	AGCGGACAGCATGCGCATCTAGACACCAAGCAGGCGCCGCTCAGAAATCGAGCCCC	3420
Qy	3421	CAGCGCGCAACGATGCGCGATCAAGCGCGCGCGCCACCAAGGCGCACCTTAGAGTGC	3480
Db	3421	CAGCGCGCAACGATGCGCGATCAAGCGCGCGCGCCACCAAGGCGCACCTTAGAGTGC	3480
Qy	3481	GGCGGACAGAGGAGCGGCCCAACATATGAGGAAACCTTAATCCAACCTCTCCATCAAC	3540
Db	3481	GGCGGACAGAGGAGCGGCCCAACATATGAGGAAACCTTAATCCAACCTCTCCATCAAC	3540
Qy	3541	CCCAGAACATCTCTCCAGCGCAGCACCGTTCGACAACTGACATCAACTCTCTAAACCGGTGGC	3600
Db	3541	CCCAGAACATCTCTCCAGCGCAGCACCGTTCGACAACTGACATCAACTCTCTAAACCGGTGGC	3600
Qy	3601	TGCCCAACCTCTCCCTCTCCGCACTTTCGGTTTCTGAAAGTTCGACATCTGCAGT	3660
Db	3601	TGCCCAACCTCTCCCTCTCCGCACTTTCGGTTTCTGAAAGTTCGACATCTGCAGT	3660

```

QY 3661 TCCTTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATACAAAC 3720
Db 3661 TCCTTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATACAAAC 3720
QY 3721 ATATGAGTTGCAATATAGGTAGAGAGAGTGTGTGTCCTCAAGTATCTGAACTATCTGAAGT 3780
Db 3721 ATATGAGTTGCAATATAGGTAGAGAGAGTGTGTGTCCTCAAGTATCTGAACTATCTGAAGT 3780
QY 3781 ATCTGAACACTTTATTTCTCTGAAATGTTATTAACAAACATTTTGAAGTATTTTGTAGTACA 3840
Db 3781 ATCTGAACACTTTATTTCTCTGAAATGTTATTAACAAACATTTTGAAGTATTTTGTAGTACA 3840
QY 3841 TTATGTTTAAACATTTCTCAAGATAATTTCTTAAACATATAAGGTACCACTTGAAGCAGT 3900
Db 3841 TTATGTTTAAACATTTCTCAAGATAATTTCTTAAACATATAAGGTACCACTTGAAGCAGT 3900
QY 3901 GACTGAGATTGCCACTGTGATGACAGACTGTTTATTAACATTTATTAACATTTTGAAGTATTT 3960
Db 3901 GACTGAGATTGCCACTGTGATGACAGACTGTTTATTAACATTTATTAACATTTTGAAGTATTT 3960
QY 3961 TTGCAACAGGAATATTAATGACTGTACAAACAAATTTGTTGATTTATTTTAAATGCAAT 4020
Db 3961 TTGCAACAGGAATATTAATGACTGTACAAACAAATTTGTTGATTTATTTTAAATGCAAT 4020
QY 4021 TGTAAACAGATGTTAAATTTGGTAAATTTACTTCTGTACATTTAAATGCAATTTCTTGATA 4080
Db 4021 TGTAAATCAGATGTTAAATTTGGTAAATTTACTTCTGTACATTTAAATGCAATTTCTTGATA 4080
QY 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCGACAGCAAGG 4134
Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCGACAGCAAGG 4134

RESULT 9
AX449101
LOCUS AX449101 4134 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 23 from Patent WO0230215.
ACCESSION AX449101
VERSION AX449101.1 GI:21697918
KEYWORDS
SOURCE Mustelus canis (smooth dogfish)
ORGANISM Mustelus canis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
Triakidae; Mustelus.
REFERENCE 1
AUTHORS Harris,H.W., Russell,D.R., Nearing,J. and Betka,M.
TITILE Growing marine fish in freshwater
JOURNAL Patent: WO 0230215-A 23 18-APR-2002;
Aquadio Products Sciences, L.L.C. (US)
FEATURES
    source
        1..4134
            /organism="Mustelus canis"
            /mol_type="unassigned DNA"
            /db_xref="taxon:7812"

ORIGIN
    Query Match 100.0%; Score 4134; DB 6; Length 4134;
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGGTTGTCGTTTCAAGTCTCTCCAGTGCAGAAATGAGAAATGGTGTG 60
Db 1 AATTCGGTTGTCGTTTCAAGTCTCTCCAGTGCAGAAATGAGAAATGGTGTG 60
QY 61 GCATTACAGGAACATGCATCATCTGTGTTAATGAATATTTGCTTATCTGAAGT 120
Db 61 GCATTACAGGAACATGCATCATCTGTGTTAATGAATATTTGCTTATCTGAAGT 120
QY 121 TATTAATATGTTTCTGCAAGATGGCTTACAGAAATCAATTTCTGACAGTTTCCCAT 180
Db 121 TATTAATATGTTTCTGCAAGATGGCTTACAGAAATCAATTTCTGACAGTTTCCCAT 180

```

```

QY 181 GTCAATTGTATGAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGACCAC 240
Db 181 GTCAATTGTATGAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGACCAC 240
QY 241 GTTCACCCCTTTCTTGGAGCATACGATCAACCCCTGAGGAGATGGAAGATTGAGGAGGA 300
Db 241 GTTCACCCCTTTCTTGGAGCATACGATCAACCCCTGAGGAGATGGAAGATTGAGGAGGA 300
QY 301 ATGGGGATTTGATCTTCCAGGAGTTCTGCTGTAAGGAGATCCCTCACCATTTACAAAGATA 360
Db 301 ATGGGGATTTGATCTTCCAGGAGTTCTGCTGTAAGGAGATCCCTCACCATTTACAAAGATA 360
QY 361 GCAGAAATCTCTCCAGGATCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
Db 361 GCAGAAATCTCTCCAGGATCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
QY 421 CAGAGACAGGCTGCACAAATGGCTCAGCTTCAGTCCCACTCTTATCTTGGGATTTTACA 480
Db 421 CAGAGACAGGCTGCACAAATGGCTCAGCTTCAGTCCCACTCTTATCTTGGGATTTTACA 480
QY 481 CTCCTACAGTCGTACAAATGTTCTCAGGATATGTTTCCAAACCAAGGGCCCAAGAGAAAG 540
Db 481 CTCCTACAGTCGTACAAATGTTCTCAGGATATGTTTCCAAACCAAGGGCCCAAGAGAAAG 540
QY 541 GACATCATCTGGGAGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
Db 541 GACATCATCTGGGAGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
QY 601 TTAATAATCGAGACCGGAGGCGACAAATGTTATTCGGTACAAATTTTCGAGGCTTCCCATG 660
Db 601 TTAATAATCGAGACCGGAGGCGACAAATGTTATTCGGTACAAATTTTCGAGGCTTCCCATG 660
QY 661 CTCAGGCGATGATATTCGCAATTTGAAGATTAACAAACAGATATGACTTTTCTTCCGCAAT 720
Db 661 CTCAGGCGATGATATTCGCAATTTGAAGATTAACAAACAGATATGACTTTTCTTCCGCAAT 720
QY 721 ATCACTCAGTCTTGTGCGCCAGAAACAAATCGACTCGCTGAACCTTAGATGAGTCTGTAAC 840
Db 721 ATCACTCAGTCTTGTGCGCCAGAAACAAATCGACTCGCTGAACCTTAGATGAGTCTGTAAC 840
QY 841 TGCTCTGACCATATCCATCCACAAATAGCAGTGGTGGGGCAACCGGGTCAGGATCTCC 900
Db 841 TGCTCTGACCATATCCATCCACAAATAGCAGTGGTGGGGCAACCGGGTCAGGATCTCC 900
QY 901 ACGGCTGTGGCCAAATCTATTTGGGATTTATTTTACATTTCCACAGTCTAGCTATGCTCTCG 960
Db 901 ACGGCTGTGGCCAAATCTATTTGGGATTTATTTTACATTTCCACAGTCTAGCTATGCTCTCG 960
QY 961 AGCAGGCTGCTCAGCAACAAAGATGATGATCAAGGCTTCTCTGAGGACCATTTCCCAATGAT 1020
Db 961 AGCAGGCTGCTCAGCAACAAAGATGATGATCAAGGCTTCTCTGAGGACCATTTCCCAATGAT 1020
QY 1021 GAGCAACAGGCGCACGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Db 1021 GAGCAACAGGCGCACGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
QY 1081 ACCCTGGAGCGACGATGATATGCGCCCGCAGGCAATTTGCAAGTTCCGGGAGGAGGCC 1140
Db 1081 ACCCTGGAGCGACGATGATATGCGCCCGCAGGCAATTTGCAAGTTCCGGGAGGAGGCC 1140
QY 1141 GTTAAGAGGAGACATCTGATTTGACTTTTCACTGAGATGATCTCTCAGTACTACACCCAGAG 1200
Db 1141 GTTAAGAGGAGACATCTGATTTGACTTTTCACTGAGATGATCTCTCAGTACTACACCCAGAG 1200
QY 1201 CAGTTGAGTTTATCGCCGACGTCATCTCCAGAACTCTCGGCCAAGTCTATCTGTGCTTTC 1260
Db 1201 CAGTTGAGTTTATCGCCGACGTCATCTCCAGAACTCTCGGCCAAGTCTATCTGTGCTTTC 1260
QY 1261 TCCAAATGGCCCCACCTGGAGCGGCTCATCCAGGAGATAGTTTCGGAGAAACATCACCGAT 1320

```


Db 1261 TCCAAATGCGCGACCTGAGCGCTCATCAGGAGATAGTTCGGAGAAACATCACCGAT 1320
 Qy 1321 CGGATCTGGCTGGCCAGCAGAGCTTGGCGAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
 Db 1321 CGGATCTGGCTGGCCAGCAGAGCTTGGCGAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
 Qy 1381 TTCACAGTGGTGGCGGCAACATCGGCTTCGCTCTCAGGGCGGGCGGATCCAGGGTTC 1440
 Db 1381 TTCACAGTGGTGGCGGCAACATCGGCTTCGCTCTCAGGGCGGGCGGATCCAGGGTTC 1440
 Qy 1441 AACAGTTTCCTGAAGAGGTCCACCCAGCAGGCTCCTCGGCAATAGGTTTGTCAAGGAG 1500
 Db 1441 AACAGTTTCCTGAAGAGGTCCACCCAGCAGGCTCCTCGGCAATAGGTTTGTCAAGGAG 1500
 Qy 1501 TTCGGGAGGAGACCTTCAACTGTCTTCACTCCGAGAGAGCCCTGACCGACTGAAGAT 1560
 Db 1501 TTCGGGAGGAGACCTTCAACTGTCTTCACTCCGAGAGAGCCCTGACCGACTGAAGAT 1560
 Qy 1561 TCCAGGTTCCTCCAGCGGACCGCGGCTCAAGGGAGCGGCTCAAGCGGGGAACTCC 1620
 Db 1561 TCCAGGTTCCTCCAGCGGACCGCGGCTCAAGGGAGCGGCTCAAGCGGGGAACTCC 1620
 Qy 1621 AGACGGACAGCCCTACGCCACCCCTGCACTGGGAGGAGAAACATCACCGAGCTGGAGACC 1680
 Db 1621 AGACGGACAGCCCTACGCCACCCCTGCACTGGGAGGAGAAACATCACCGAGCTGGAGACC 1680
 Qy 1681 CCTACCTGGATATACACACTGAGGATCTCTCAATGTATACGTGGCGGCTCTACTCC 1740
 Db 1681 CCTACCTGGATATACACACTGAGGATCTCTCAATGTATACGTGGCGGCTCTACTCC 1740
 Qy 1741 ATTGTCTCAGCCCTCAGAGACATCACCTCTGCAACCCCGGACCGGCTCTTTGCAAC 1800
 Db 1741 ATTGTCTCAGCCCTCAGAGACATCACCTCTGCAACCCCGGACCGGCTCTTTGCAAC 1800
 Qy 1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTCGGAGGTCTCTCAACCATCTGCTGCAT 1860
 Db 1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTCGGAGGTCTCTCAACCATCTGCTGCAT 1860
 Qy 1861 CTGAGTTTACCAACAGATGGTGAGCAGGTTGACTTTGACGATCAAGGTGACTCAAG 1920
 Db 1861 CTGAGTTTACCAACAGATGGTGAGCAGGTTGACTTTGACGATCAAGGTGACTCAAG 1920
 Qy 1921 GGGAACTACACCATTAACCTGGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCCAT 1980
 Db 1921 GGGAACTACACCATTAACCTGGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCCAT 1980
 Qy 1981 GAGGTGGGCACTACAAAGCTTACGTAAGCCAGTGAACGAGTCAACATCAACGAAAG 2040
 Db 1981 GAGGTGGGCACTACAAAGCTTACGTAAGCCAGTGAACGAGTCAACATCAACGAAAG 2040
 Qy 2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGTCTTCTCCAACTGCACTGAGACTGT 2100
 Db 2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGTCTTCTCCAACTGCACTGAGACTGT 2100
 Qy 2101 GTCCGGGCAACAGGAAGGGATCATCGAGGGGAGCCCACTGCTGTTTGAATGCAATG 2160
 Db 2101 GTCCGGGCAACAGGAAGGGATCATCGAGGGGAGCCCACTGCTGTTTGAATGCAATG 2160
 Qy 2161 GCATGTGAGAGGAGATTGATGATGAAGATGCAAGTGCAGTGTGATCAAGTGCAG 2220
 Db 2161 GCATGTGAGAGGAGATTGATGATGAAGATGCAAGTGCAGTGTGATCAAGTGCAG 2220
 Qy 2221 AATGATTTCTGCTGGAATGAGAAACCAACAGCTGCTGATCGCCCAAGGAGATCGAGTAC 2280
 Db 2221 AATGATTTCTGCTGGAATGAGAAACCAACAGCTGCTGATCGCCCAAGGAGATCGAGTAC 2280
 Qy 2281 TCGTGAACGAGGACCTTCGGGATCGCTCTGACATCTTCGCGGTAATCGGATCTGATC 2340
 Db 2281 TCGTGAACGAGGACCTTCGGGATCGCTCTGACATCTTCGCGGTAATCGGATCTGATC 2340
 Qy 2341 ACCTCCTCTGCTGGGGTCTTCACTCAAGTTTCAGGAACACTCCCATCGTGAAGGCCACC 2400

Db 2341 ACCTCCTCTGCTGGGGTCTTCACTCAAGTTTCAGGAACACTCCCATCGTGAAGGCCACC 2400
 Qy 2401 AACCGGAGGTGTCTTACCTGTGCTCTTCTCCCTCATCTGTGCTTCTCCAGCTCGCTC 2460
 Db 2401 AACCGGAGGTGTCTTACCTGTGCTCTTCTCCCTCATCTGTGCTTCTCCAGCTCGCTC 2460
 Qy 2461 ATCTTCATCGGCGAGCCAGGACTCGGACTCGGCTCGGCTCGGCAACCGGCTTTTGCATC 2520
 Db 2461 ATCTTCATCGGCGAGCCAGGACTCGGACTCGGCTCGGCTCGGCAACCGGCTTTTGCATC 2520
 Qy 2521 AGCTTCGTCTGTGCACTCTCTGCTCATCTCTGGTGAAGAACCAACCGGCTGTGCTGCTTC 2580
 Db 2521 AGCTTCGTCTGTGCACTCTCTGCTCATCTCTGGTGAAGAACCAACCGGCTGTGCTGCTTC 2580
 Qy 2581 GAGGCGAAGATCCCAACAGCTTCCACCGAAGTGGTGGGCTCAACCTGAGTTCCTC 2640
 Db 2581 GAGGCGAAGATCCCAACAGCTTCCACCGAAGTGGTGGGCTCAACCTGAGTTCCTC 2640
 Qy 2641 CTGCTCTCTCTGCTCATCTCTGGTGAAGTCTCACTGCTCATCTCTGGCTCTACACCGG 2700
 Db 2641 CTGCTCTCTCTGCTCATCTCTGGTGAAGTCTCACTGCTCATCTCTGGCTCTACACCGG 2700
 Qy 2701 CTTCTCTCTCAGCTACAGGAACCATGAGTGGAGGACGAGTCACTCTTCACTACCTGGAC 2760
 Db 2701 CTTCTCTCTCAGCTACAGGAACCATGAGTGGAGGACGAGTCACTCTTCACTACCTGGAC 2760
 Qy 2761 GAGGCTCTGCTCATGGGCTGGGCTTCTCATCGGCTACACCTGCTCTCTCGCGGCATC 2820
 Db 2761 GAGGCTCTGCTCATGGGCTGGGCTTCTCATCGGCTACACCTGCTCTCTCGCGGCATC 2820
 Qy 2821 TGCTCTTCTTCTGCTTCAAGTCCCGTAAAGTCTCGGAGGAACTTCAACGAGGTAAGTTC 2880
 Db 2821 TGCTCTTCTTCTGCTTCAAGTCCCGTAAAGTCTCGGAGGAACTTCAACGAGGTAAGTTC 2880
 Qy 2881 ATCACTTCAAGATGTGATCTTCTCATGCTGTGATCTCTTCTCATCCCGCTATGTC 2940
 Db 2881 ATCACTTCAAGATGTGATCTTCTCATGCTGTGATCTCTTCTCATCCCGCTATGTC 2940
 Qy 2941 AGCACTTACCGCAAGTTTGTGCTGGCGGTGAGGTGATTCCTCTGAGGCTTCAAGGCTTC 3000
 Db 2941 AGCACTTACCGCAAGTTTGTGCTGGCGGTGAGGTGATTCCTCTGAGGCTTCAAGGCTTC 3000
 Qy 3001 GGGTGTGCTGGCTGCACTTACTTCAACAGTGTATCATCATCTCTTCAAGCGGTGCGGT 3060
 Db 3001 GGGTGTGCTGGCTGCACTTACTTCAACAGTGTATCATCATCTCTTCAAGCGGTGCGGT 3060
 Qy 3061 AACACCATCGAGAGGTGCGCTGACGACGCGGCGCCAGCCCTTCAAGGTGGCGGCCGG 3120
 Db 3061 AACACCATCGAGAGGTGCGCTGACGACGCGGCGCCAGCCCTTCAAGGTGGCGGCCGG 3120
 Qy 3121 GCCACCTCGCGGCGAGCGCGGTCTCGCAAGCTTCCAGCAGCTGTGCGGCTCCACC 3180
 Db 3121 GCCACCTCGCGGCGAGCGCGGTCTCGCAAGCTTCCAGCAGCTGTGCGGCTCCACC 3180
 Qy 3181 ATCTCTCGCGGCTGCTCATCTGCGGCGCGGCTCTACCATGGAGATGAGCGCTGC 3240
 Db 3181 ATCTCTCGCGGCTGCTCATCTGCGGCGCGGCTCTACCATGGAGATGAGCGCTGC 3240
 Qy 3241 AGCAGCAGAGGTTCAGCTTGGCAGCGGCAACCTTCACTGCTGCTCAGCTTCGAGGAG 3300
 Db 3241 AGCAGCAGAGGTTCAGCTTGGCAGCGGCAACCTTCACTGCTGCTCAGCTTCGAGGAG 3300
 Qy 3301 ACAGCGCGATFACGCAACCTCAGCGGCAACCGGCGGAGAGAACTCGGCGGATGCGCG 3360
 Db 3301 ACAGCGCGATFACGCAACCTCAGCGGCAACCGGCGGAGAGAACTCGGCGGATGCGCG 3360
 Qy 3361 AGCGGCGACGACTTGGCTATAGACACACGAGCGGCGGCTCAGAAATCGAGGCC 3420
 Db 3361 AGCGGCGACGACTTGGCTATAGACACACGAGCGGCGGCTCAGAAATCGAGGCC 3420
 Qy 3421 CAGCCGCCAACGATGCCCGATACAGGCGGCGCGGCAAGGGCACCTTAGAGTGCCTCG 3480
 Db 3421 CAGCCGCCAACGATGCCCGATACAGGCGGCGCGGCAAGGGCACCTTAGAGTGCCTCG 3480

```
QY 3481 GGCGGAGCAAGGAGGCGCCCAACAACTATGGAGGAAACCTAATCAAACTCTCCATCAAC 3540
Db 3481 GGCGGAGCAAGGAGGCGCCCAACAACTATGGAGGAAACCTAATCAAACTCTCCATCAAC 3540
QY 3541 CCCAAGAAATCTCCACGGCAGCAGCGTCGCAACTGACATCAACTCTTAACCGGTGGC 3600
Db 3541 CCCAAGAAATCTCCACGGCAGCAGCGTCGCAACTGACATCAACTCTTAACCGGTGGC 3600
QY 3601 TGCCCAACCTCTCCCTCTCCGCACTTTGCGTTTGTGAAGATTGACGATCTGCACT 3660
Db 3601 TGCCCAACCTCTCCCTCTCCGCACTTTGCGTTTGTGAAGATTGACGATCTGCACT 3660
QY 3661 TCCTTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCAAC 3720
Db 3661 TCCTTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCAAC 3720
QY 3721 ATAATCAGTTGCAAAATAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACATCTGAAGT 3780
Db 3721 ATAATCAGTTGCAAAATAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACATCTGAAGT 3780
QY 3781 ATCTGAACCTATTTCTCTCGAATTTATTAACAAATTTGAAGTATTTTAGTGACA 3840
Db 3781 ATCTGAACCTATTTCTCTCGAATTTATTAACAAATTTGAAGTATTTTAGTGACA 3840
QY 3841 TTATGTTCTAACTGTCAGATATTTGTTACACATATAGGTACCACTGAGGAGT 3900
Db 3841 TTATGTTCTAACTGTCAGATATTTGTTACACATATAGGTACCACTGAGGAGT 3900
QY 3901 GACTGAGATTGCCACTGTGATCAGCAACTGTTTATTAACATTTATCAATTTGAACCTGGA 3960
Db 3901 GACTGAGATTGCCACTGTGATCAGCAACTGTTTATTAACATTTATCAATTTGAACCTGGA 3960
QY 3961 TTGCAACAGGATATTAATGACTGTAAACAAAAATTTGTTGATTTCTTAATAATGCAAT 4020
Db 3961 TTGCAACAGGATATTAATGACTGTAAACAAAAATTTGTTGATTTCTTAATAATGCAAT 4020
QY 4021 TGTAAATCAGATGTGTAATTTGTTAACTTCTGTACATTAATTAATTTCTTGATA 4080
Db 4021 TGTAAATCAGATGTGTAATTTGTTAACTTCTGTACATTAATTAATTTCTTGATA 4080
QY 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCGACAGCAACGG 4134
Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCGACAGCAACGG 4134

RESULT 10
AX743965 4134 bp DNA linear PAT 14-MAY-2003
LOCUS Sequence 7 from Patent WO03030639.
DEFINITION AX743965
ACCESSION AX743965
VERSION AX743965.1 GI:30722659
KEYWORDS Squalus acanthias (spiny dogfish)
SOURCE Squalus acanthias
ORGANISM Squalus acanthias
REFERENCE 1
AUTHORS Harris,J.H., Jury,S., Russel,D.R., Nearing,J., Betka,M., Linley,T.
and Brown,E.M.
TITLE Methods for growing and imprinting fish using an odorant
JOURNAL Patent: WO 03030639-A 7 17-APR-2003;
Marical, Inc. (US)
FEATURES
    Location/Qualifiers
        1..4134
            /organism="Squalus acanthias"
            /mol_type="genomic DNA"
            /db_xref="taxon:7797"

Query Match 100.0%; Score 4134; DB 6; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
ORIGIN
```

```
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATTCCTTCTGTCGGTTTCTGTCAGTCCAGTCTCTCCAGTGCAGAAATGAGAAATGTTGGTC 60
Db 1 AATTCCTTCTGTCGGTTTCTGTCAGTCCAGTCTCTCCAGTGCAGAAATGAGAAATGTTGGTC 60
QY 61 GCCATTACAGGAATGCACTACATCTGTTTAAATGAATATTTGTCAGTATCTGAGGT 120
Db 61 GCCATTACAGGAATGCACTACATCTGTTTAAATGAATATTTGTCAGTATCTGAGGT 120
QY 121 TATTAAATATGTTCTGCAAGGATGGTTTACAGAGAAATCAATTTCTGCAAGTTTCCCAT 180
Db 121 TATTAAATATGTTCTGCAAGGATGGTTTACAGAGAAATCAATTTCTGCAAGTTTCCCAT 180
QY 181 GTCAATTGTATGAATACTGACCAAGGGATGTAAACAAATGGAACAAAGCTGAGGACCAAC 240
Db 181 GTCAATTGTATGAATACTGACCAAGGGATGTAAACAAATGGAACAAAGCTGAGGACCAAC 240
QY 241 GTTCACCCCTTTCTTGAGGATACGATCAACCTGAAGGAGATGGAAGCTTGAAGGAGAA 300
Db 241 GTTCACCCCTTTCTTGAGGATACGATCAACCTGAAGGAGATGGAAGCTTGAAGGAGAA 300
QY 301 ATGGGATTCATCTTCCAGGATTTCTGCTGAAGCGATCCCTCACCATTTACAAAGATAA 360
Db 301 ATGGGATTCATCTTCCAGGATTTCTGCTGAAGCGATCCCTCACCATTTACAAAGATAA 360
QY 361 GCAGAAATCTCCAGGATCTCTGTAAGCGGCTGGCTAGTGTGGCTTGGTTCAGGAA 420
Db 361 GCAGAAATCTCCAGGATCTCTGTAAGCGGCTGGCTAGTGTGGCTTGGTTCAGGAA 420
QY 421 CAGAGACAGGCTGCAATGCTCAGCTTCACTGCAAACTCTTATTTCTGGGATTTACA 480
Db 421 CAGAGACAGGCTGCAATGCTCAGCTTCACTGCAAACTCTTATTTCTGGGATTTACA 480
QY 481 CTCCTCAGTCGTACAAATGTCAGGATGTGTCMAAACAAAGGSCCAGAGAAAGAA 540
Db 481 CTCCTCAGTCGTACAAATGTCAGGATGTGTCMAAACAAAGGSCCAGAGAAAGAA 540
QY 541 GACATCATCTGGGAGTCTCTTCCCAATACACTTTGGAGTAGCCGCCCAAGGATCAGGAC 600
Db 541 GACATCATCTGGGAGTCTCTTCCCAATACACTTTGGAGTAGCCGCCCAAGGATCAGGAC 600
QY 601 TTAATTCGAGACCGGAGGCGACAAATGATTTGCTGTAACAAATTTTCAGGCTTCCGATGG 660
Db 601 TTAATTCGAGACCGGAGGCGACAAATGATTTGCTGTAACAAATTTTCAGGCTTCCGATGG 660
QY 661 CTCAGCGGATGATATTCGCAATTTGAAGGATTAACACAGATATGACTTTCTGCCCCAAT 720
Db 661 CTCAGCGGATGATATTCGCAATTTGAAGGATTAACACAGATATGACTTTCTGCCCCAAT 720
QY 721 ATCACCCTGGGATATCGCATATTTGACGCTGTAACACCGTGTCCAAGCGCTAGAGGCA 780
Db 721 ATCACCCTGGGATATCGCATATTTGACGCTGTAACACCGTGTCCAAGCGCTAGAGGCA 780
QY 781 ACATCAGCTTTGTCGCCAGAAACAAATCGACTCGCTGAACTTAGATGAGTCTCTTAC 840
Db 781 ACATCAGCTTTGTCGCCAGAAACAAATCGACTCGCTGAACTTAGATGAGTCTCTTAC 840
QY 841 TGCTCTGACCATATCCATCCCAATAGTAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900
Db 841 TGCTCTGACCATATCCATCCCAATAGTAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900
QY 901 ACGGCTGTGCCAATCTATTGGGATTTATTACATTCACAGTACAGTATGCTCTCTCG 960
Db 901 ACGGCTGTGCCAATCTATTGGGATTTATTACATTCACAGTACAGTATGCTCTCTCG 960
QY 961 AGCAGGCTGTCAGCAACAAAGATGATGAGTCAAGGCTTCTGAGGACCAATCCCCATGAT 1020
Db 961 AGCAGGCTGTCAGCAACAAAGATGATGAGTCAAGGCTTCTGAGGACCAATCCCCATGAT 1020
QY 1021 GAGCAACAGGCCACCGCCATGCGGAGATCATCGAGCACTTCAGTGGAACTCGGTGGGA 1080
Db 1021 GAGCAACAGGCCACCGCCATGCGGAGATCATCGAGCACTTCAGTGGAACTCGGTGGGA 1080
```

1081 ACCCTGGCAGCGACGATGACATATGGCCGCCCCAGGCAATGCAAGTTCCGGGAGGAGGCC 1140
1081 ACCCTGGCAGCGACGATGACATATGGCCGCCCCAGGCAATGCAAGTTCCGGGAGGAGGCC 1140
1141 GTTAAAGAGGACATCTGTATTGACTTCACTGATGATGATCTCTCAGTACTACACCCAGAAG 1200
1141 GTTAAAGAGGACATCTGTATTGACTTCACTGATGATGATCTCTCAGTACTACACCCAGAAG 1200
1201 CAGTTGGAGTTCAATCGCGAGCTCATCCAGAACTCCTCGGCCAAGGTTCATCGTGGTCTTC 1260
1201 CAGTTGGAGTTCAATCGCGAGCTCATCCAGAACTCCTCGGCCAAGGTTCATCGTGGTCTTC 1260
1261 TCCAAATGSCCGGACCTGGAGCGGCTCATCCAGGAGATAGTTCGAGAGAAATCAACCGAT 1320
1261 TCCAAATGSCCGGACCTGGAGCGGCTCATCCAGGAGATAGTTCGAGAGAAATCAACCGAT 1320
1321 CGGATCTGGCTGGCCAGCAGGCTTGGGCCAGCTCTTGCTCATTTGCCAAGCCAGAGTAC 1380
1321 CGGATCTGGCTGGCCAGCAGGCTTGGGCCAGCTCTTGCTCATTTGCCAAGCCAGAGTAC 1380
1381 TTCCAGTGGTGGGGGACCAATCGGCTTCGGCTCTCAGGGCGGGCGGTATCCAGGGTTC 1440
1381 TTCCAGTGGTGGGGGACCAATCGGCTTCGGCTCTCAGGGCGGGCGGTATCCAGGGTTC 1440
1441 AACAAAGTTCCGAAGAGGTCCACCCAGCAGGTCTCGGCAATGGGTTTGTCAAGGAG 1500
1441 AACAAAGTTCCGAAGAGGTCCACCCAGCAGGTCTCGGCAATGGGTTTGTCAAGGAG 1500
1501 TTCTGGGAGGACCTTCAATGTCTTACCGAGAGACCTTCAACCGAGCTGAGGAAT 1560
1501 TTCTGGGAGGACCTTCAATGTCTTACCGAGAGACCTTCAACCGAGCTGAGGAAT 1560
1561 TCCAAAGTGCCTCCGACGGAGCGGCTCAAGGGAGCGCTCAAGGGCGGGGACTCC 1620
1561 TCCAAAGTGCCTCCGACGGAGCGGCTCAAGGGAGCGCTCAAGGGCGGGGACTCC 1620
1621 AGACGGAAGCCCTACGCCACCCCTGCACTGGGGAGGAGAACATCAACAGAGGTGGAGACC 1680
1621 AGACGGAAGCCCTACGCCACCCCTGCACTGGGGAGGAGAACATCAACAGAGGTGGAGACC 1680
1681 CCCTACCTGGATATACACCTGAGGATCTCTCAATGATATAGTGGCGGTCTACTCC 1740
1681 CCCTACCTGGATATACACCTGAGGATCTCTCAATGATATAGTGGCGGTCTACTCC 1740
1741 ATTGTCTACGCCCTCGAGACATCACTCTTCAAAACCGGACGGGCACTTTTGCAGAAC 1800
1741 ATTGTCTACGCCCTCGAGACATCACTCTTGCAGAACCGGACGGGCACTTTTGCAGAAC 1800
1801 GGATCTTGGAGATATTAATAAAGTTGAGGCTTGGAGGCTTCCCAACCACTCTGCTGCAT 1860
1801 GGATCTTGGAGATATTAATAAAGTTGAGGCTTGGAGGCTTCCCAACCACTCTGCTGCAT 1860
1861 CTGAGTTTACCAACAGCATGGTGAGCAGGTTGACTTTGACATCAAGGTGACCTCAAG 1920
1861 CTGAGTTTACCAACAGCATGGTGAGCAGGTTGACTTTGACATCAAGGTGACCTCAAG 1920
1921 GGGAACTACACCAATTAACCTGGAGCTCTCCGAGAGGATGAATCGGTGTGTTTCCAT 1980
1921 GGGAACTACACCAATTAACCTGGAGCTCTCCGAGAGGATGAATCGGTGTGTTTCCAT 1980
1981 GAGGTGGGCACTACAAAGCTTACCTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040
1981 GAGGTGGGCACTACAAAGCTTACCTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040
2041 AAAATCCTGTGAGTGGCTTCCAAAGTGGTTCCTTCTCAACTCGAGTCGAGACTGT 2100
2041 AAAATCCTGTGAGTGGCTTCCAAAGTGGTTCCTTCTCAACTCGAGTCGAGACTGT 2100
2101 GTGCCGGGACCAAGGAGGATCATCGAGGGGAGCCCACTGCTGTTTGAATGCATG 2160
2101 GTGCCGGGACCAAGGAGGATCATCGAGGGGAGCCCACTGCTGTTTGAATGCATG 2160

2161 GCATGTGCAGAGGAGAGTTCAAGTATGATGAAAAAGATGCAAGTGGTGTGTAACAAGTGGCCG 2220
2161 GCATGTGCAGAGGAGAGTTCAAGTATGATGAAAAAGATGCAAGTGGTGTGTAACAAGTGGCCG 2220
2221 AATGATTTCTTGCTGGAATGAGAACCAACGCTCGTGCATCGCCAAAGAGATCGAGTACTCG 2280
2221 AATGATTTCTTGCTGGAATGAGAACCAACGCTCGTGCATCGCCAAAGAGATCGAGTACTCG 2280
2281 TCGTGGACGAGAGCCCTTGGGATCGGTCTGACCATCTTGGCCCTACTGGGCATCTGTATC 2340
2281 TCGTGGACGAGAGCCCTTGGGATCGGTCTGACCATCTTGGCCCTACTGGGCATCTGTATC 2340
2341 ACCTCTCTTCTGCTGGGGCTTTCATCAAGTTGAGAACTCCCATCTGTAAGAGCCACC 2400
2341 ACCTCTCTTCTGCTGGGGCTTTCATCAAGTTGAGAACTCCCATCTGTAAGAGCCACC 2400
2401 AACCGGAGTTGTCTTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTGCTC 2460
2401 AACCGGAGTTGTCTTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTGCTC 2460
2461 ATCTTCACTCGGAGCCAGGAGCTGACCTGTGCGCTCGCCCAACCGGCTTTGGCATC 2520
2461 ATCTTCACTCGGAGCCAGGAGCTGACCTGTGCGCTCGCCCAACCGGCTTTGGCATC 2520
2521 AGCTTCTGCTGTGCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
2521 AGCTTCTGCTGTGCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
2581 GAGGCCAAGATCCCAACAGCTTCCACCGCAAGTGGGTGGGCTTCAACCTGGAAGTCTCTC 2640
2581 GAGGCCAAGATCCCAACAGCTTCCACCGCAAGTGGGTGGGCTTCAACCTGGAAGTCTCTC 2640
2641 CTGGTCTCTCTGCACTCTGCTGGTGGCAATCGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
2641 CTGGTCTCTCTGCACTCTGCTGGTGGCAATCGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGAGGAGAGAGGTCTCTTCTCATCAGCTGCGAC 2760
2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGAGGAGAGAGGTCTCTTCTCATCAGCTGCGAC 2760
2761 GAGGGCTCGCTCATGCGGCTGGGCTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
2761 GAGGGCTCGCTCATGCGGCTGGGCTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
2821 TGCTTCTTCTTCCGCTTCAAGTCCCGTAAAGCTCCGAGAACTTCAACAGAGGTAAAGTTC 2880
2821 TGCTTCTTCTTCCGCTTCAAGTCCCGTAAAGCTCCGAGAACTTCAACAGAGGTAAAGTTC 2880
2881 ATCACTTTCAGATGTTGATCTTCTTCACTGCTGATCTCTTCACTCCCGGCTATGTC 2940
2881 ATCACTTTCAGATGTTGATCTTCTTCACTGCTGATCTCTTCACTCCCGGCTATGTC 2940
2941 AGCACCTACGGCAAGTTTGTGCGCGGTGAGGTGATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
2941 AGCACCTACGGCAAGTTTGTGCGCGGTGAGGTGATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
3001 GGGCTGCTGGGCTGCACTTACTTCAACAAGTGTATACATCATCTGTTCAAGCGCTCCCGT 3060
3001 GGGCTGCTGGGCTGCACTTACTTCAACAAGTGTATACATCATCTGTTCAAGCGCTCCCGT 3060
3061 AACACATCGAGAGGTGGCTGCGAGCGGCGCCCAAGCTTCAAGGTGGGCGGCGG 3120
3061 AACACATCGAGAGGTGGCTGCGAGCGGCGCCCAAGCTTCAAGGTGGGCGGCGG 3120
3121 GCCACCTCCGGCGGAGCGCGGCTCTCGCAAGCGCTCCAGCAGCTGTGGGCTCCACC 3180
3121 GCCACCTCCGGCGGAGCGCGGCTCTCGCAAGCGCTCCAGCAGCTGTGGGCTCCACC 3180
3181 ATCTCTCGCCCGCTGCTCCACTGCGGCGCGGCTCTCACATGAGATGAGAGCTGTC 3240
3181 ATCTCTCGCCCGCTGCTCCACTGCGGCGCGGCTCTCACATGAGATGAGAGCTGTC 3240
3241 AGCACGAGAGGTTCAGCTTCGGCAGCGGCAACCGTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300

[illegible]

RESULT 11
AF406649
LOCUS
DEFINITION
AP406649 4116 bp mRNA linear VRT 21-MAR-2003
Squalus acanthias calcium polyvalent cation receptor/salinity
sensing protein mRNA, complete cds.
ACCESSION
AF406649
VERSION
AF406649.1 GI:21842084
KEYWORDS
SOURCE
ORGANISM
Squalus acanthias (spiny dogfish)
Squalus acanthias
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalae; Hypnosqualea; Squaliformes; Squaloidei;
Squalidae; Squalus.

QY 361 GCAGAAATCCTCCAGGATCCCTCTGTAAACGGGCTGGGTAAGTGTGGTTCGTAAGGAA 420
Db 361 GCAGAAATCCTCCAGGATCCCTCTGTAAACGGGCTGGGTAAGTGTGGTTCGTAAGGAA 420
QY 421 CAGAGACAGGGGTGCACAAATGCTCAGCTTCACTGCCAACTTATTCTTGGGATTTACA 480
Db 421 CAGAGACAGGGGTGCACAAATGCTCAGCTTCACTGCCAACTTATTCTTGGGATTTACA 480
QY 481 CTCCTACAGTCGTACAAATGTCTCAGGGTATGGTCCAAACCAAGGGCCCAAGAAAGGA 540
Db 481 CTCCTACAGTCGTACAAATGTCTCAGGGTATGGTCCAAACCAAGGGCCCAAGAAAGGA 540
QY 541 GACATCATCTGGAGGTCTCTCCCAATACATTTGGAGTAGCGCCCAAGGATCAGGAC 600
Db 541 GACATCATCTGGAGGTCTCTCCCAATACATTTGGAGTAGCGCCCAAGGATCAGGAC 600
QY 601 TTAAATCGAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTTCGATGG 660
Db 601 TTAAATCGAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTTCGATGG 660
QY 661 CTCGAGGGATGATATTCGAAATGAAGATTAACAAGATGACTTTCTGCCCCAAT 720
Db 661 CTCGAGGGATGATATTCGAAATGAAGATTAACAAGATGACTTTCTGCCCCAAT 720
QY 721 ATCACCTGGGATATCGCATATTTGACAGCTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780
Db 721 ATCACCTGGGATATCGCATATTTGACAGCTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780
QY 781 ACACCTCAGCTTTGTGGCCAGAACAAAATCGACTCGCTGAATAGATGAGTTCTGTAAAC 840
Db 781 ACACCTCAGCTTTGTGGCCAGAACAAAATCGACTCGCTGAATAGATGAGTTCTGTAAAC 840
QY 841 TGCTGTGACCATATCCCATCCACATAGCAGTGTGGGGCAACCGGTCAGGATCTCC 900
Db 841 TGCTGTGACCATATCCCATCCACATAGCAGTGTGGGGCAACCGGTCAGGATCTCC 900
QY 901 ACGGCTGTGGCCAACTATTTGGGATTTTACATTCACAGGTCAGCTATGCTCTCTCG 960
Db 901 ACGGCTGTGGCCAACTATTTGGGATTTTACATTCACAGGTCAGCTATGCTCTCTCG 960
QY 961 ACGGCTGTCTCAGCAACAGATGAGTACAAAGGCTTCCTGAGGACCATCCCCAATGAT 1020
Db 961 ACGGCTGTCTCAGCAACAGATGAGTACAAAGGCTTCCTGAGGACCATCCCCAATGAT 1020
QY 1021 GAGCAACAGGCAACGCGCATGCGCGAGATCATCGAGCATCTCCAGTGGAACTGGGTGGGA 1080
Db 1021 GAGCAACAGGCAACGCGCATGCGCGAGATCATCGAGCATCTCCAGTGGAACTGGGTGGGA 1080
QY 1081 ACCCTGGCAGCGGACGATGACTATGGCCGCCAGGCAATTGACAAAGTTCCGGGAGGAGGCC 1140
Db 1081 ACCCTGGCAGCGGACGATGACTATGGCCGCCAGGCAATTGACAAAGTTCCGGGAGGAGGCC 1140
QY 1141 GTTAGAGGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAG 1200
Db 1141 GTTAGAGGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAG 1200
QY 1201 CAGTTTGGAGTTTCATCGCCGAGCTCATCCAGAACTCCTCGGCAAGGTTCATCGTGTCTTC 1260
Db 1201 CAGTTTGGAGTTTCATCGCCGAGCTCATCCAGAACTCCTCGGCAAGGTTCATCGTGTCTTC 1260
QY 1261 TCCAAATGGCCCGACCTGAGCCGCTCATCGAGGATAGTTCGAGAGAAACATCACCGAT 1320
Db 1261 TCCAAATGGCCCGACCTGAGCCGCTCATCGAGGATAGTTCGAGAGAAACATCACCGAT 1320
QY 1321 CGGATCTGGCTGGCCAGGAGGCTTTGGGCGAGCTCTCGCTCATTTGCCAAGCCAGAGTAC 1380
Db 1321 CGGATCTGGCTGGCCAGGAGGCTTTGGGCGAGCTCTCGCTCATTTGCCAAGCCAGAGTAC 1380
QY 1381 TTCCAGTGGTTCGGCGGCAACCATCGGCTTCGCTTCAGGGGGGCGGATCCCAAGGTTTC 1440
Db 1381 TTCCAGTGGTTCGGCGGCAACCATCGGCTTCGCTTCAGGGGGGCGGATCCCAAGGTTTC 1440

QY 1441 AACAAAGTTCTGTAAGAGGTCCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG 1500
Db 1441 AACAAAGTTCTGTAAGAGGTCCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG 1500
QY 1501 TTCTGGAGAGAGACCTTTCAACTGCTACTTCAACGAGAAACCTTGACGACAGCTGAAGAAT 1560
Db 1501 TTCTGGAGAGAGACCTTTCAACTGCTACTTCAACGAGAAACCTTGACGACAGCTGAAGAAT 1560
QY 1561 TCCAAAGTGCCTTCGCAACGAGCCGGGGCTCAAGGGAGCGGCTCCAAAGGCGGGAACTCC 1620
Db 1561 TCCAAAGTGCCTTCGCAACGAGCCGGGGCTCAAGGGAGCGGCTCCAAAGGCGGGAACTCC 1620
QY 1621 AGAGGACAGCCCTAGCCACCCCTGCATCTGGGAGGAGAAACATCACGAGCTGGAGACC 1680
Db 1621 AGAGGACAGCCCTAGCCACCCCTGCATCTGGGAGGAGAAACATCACGAGCTGGAGACC 1680
QY 1681 CCTACTCGATTTATACACCTGAGGATCTCTACAATGTATATACGTGGCGCTTACTCC 1740
Db 1681 CCTACTCGATTTATACACCTGAGGATCTCTACAATGTATATACGTGGCGCTTACTCC 1740
QY 1741 ATTGCTCAGCCCTGCAGACATCCACTTTTGAACCCCGGACGCGCATCTTTGCAAAAC 1800
Db 1741 ATTGCTCAGCCCTGCAGACATCCACTTTTGAACCCCGGACGCGCATCTTTGCAAAAC 1800
QY 1801 GGATCTTGTGAGATTTAAAAAGTTGAGGCTGCGAGGTCTCAACCATCTGCTGCAT 1860
Db 1801 GGATCTTGTGAGATTTAAAAAGTTGAGGCTGCGAGGTCTCAACCATCTGCTGCAT 1860
QY 1861 CTGAAGTTTACCAACAGCATGGGTGAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
QY 1921 GGGAACTACACCATTTCAACTGCGAGCTCTCCGAGAGGATGAATCGGTTGTTTCCAT 1980
Db 1921 GGGAACTACACCATTTCAACTGCGAGCTCTCCGAGAGGATGAATCGGTTGTTTCCAT 1980
QY 1981 GAGTGGGCAACTCAACGCTACGCTAAGCCAGTACCGACTCAACATCAACGAAAG 2040
Db 1981 GAGTGGGCAACTCAACGCTACGCTAAGCCAGTACCGACTCAACATCAACGAAAG 2040
QY 2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTCTCCAACTGCACTGATG 2100
Db 2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTCTCCAACTGCACTGATG 2100
QY 2101 GTGCGGGCACACGAGGAGGATCATCGAGGGGAGGCCACCTGCTTGAATGCATG 2160
Db 2101 GTGCGGGCACACGAGGAGGATCATCGAGGGGAGGCCACCTGCTTGAATGCATG 2160
QY 2161 GCATGTGCAGAGGAGGTTCACTGATGAAAAAGTGAAGTGGTGTACAAAGTGGCCG 2220
Db 2161 GCATGTGCAGAGGAGGTTCACTGATGAAAAAGTGAAGTGGTGTACAAAGTGGCCG 2220
QY 2221 AATGATTTCTGGTTCGATGAGAACACACGCTCGTGCATCGCCAAAGAGATCGAGTACCTG 2280
Db 2221 AATGATTTCTGGTTCGATGAGAACACACGCTCGTGCATCGCCAAAGAGATCGAGTACCTG 2280
QY 2281 TCGTGAAGGAGCCCTTCGGGATCGCTTGAACCATCTTCGCGTACTGGGCACTCTGATC 2340
Db 2281 TCGTGAAGGAGCCCTTCGGGATCGCTTGAACCATCTTCGCGTACTGGGCACTCTGATC 2340
QY 2341 ACCTCCTCTGCTGGGGTCTTCATCAAGTTCAGAAACACTCCCATCTGTAAGGCCACC 2400
Db 2341 ACCTCCTCTGCTGGGGTCTTCATCAAGTTCAGAAACACTCCCATCTGTAAGGCCACC 2400
QY 2401 AACCGGAGTTGTCTTACCTGCTCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460
Db 2401 AACCGGAGTTGTCTTACCTGCTCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460
QY 2461 ATCTTCAATCGGCGAGCCAGGAGTCACTGCTCGGCTCGGCCAACCGGCTTTGGCATC 2520
Db 2461 ATCTTCAATCGGCGAGCCAGGAGTCACTGCTCGGCTCGGCCAACCGGCTTTGGCATC 2520
QY 2521 AGCTTCGCTGCTGATCTCTCTGATCCCTGATGAGAACAAACCGGCTGCTGCTGCTTC 2580

Db	2521	AGCTTCGTCGTGTGCATCTCTCGTCACTCTGGTGAAGACCAACCGGCTGCTGTGGTCTTC	2580
Qy	2581	GAGGCCAAGATCCCAACAGCTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCCTC	2640
Db	2581	GAGGCCAAGATCCCAACAGCTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCCTC	2640
Qy	2641	CTGGTCTTCCTCTGTCATCTCTGGTGCMAATCGTCACCTGCATCATCTGGCTCTACACCGCG	2700
Db	2641	CTGGTCTTCCTCTGTCATCTCTGGTGCMAATCGTCACCTGCATCATCTGGCTCTACACCGCG	2700
Qy	2701	CCTCCCTCAGCTTACAGGAACCATGAGCTGGAGGACGAGTCACTTCATCAGCTCGGAC	2760
Db	2701	CCTCCCTCAGCTTACAGGAACCATGAGCTGGAGGACGAGTCACTTCATCAGCTCGGAC	2760
Qy	2761	GAGGGCTCGCTCATGGCGCTGGGCTTCCTCATCGGCTACACCTGCCTCTCGCGCGCATC	2820
Db	2761	GAGGGCTCGCTCATGGCGCTGGGCTTCCTCATCGGCTACACCTGCCTCTCGCGCGCATC	2820
Qy	2821	TGCTTCTTTCGGCTTCAAGTCCGTAAGCTGCGGAGAACCTTCAACGAGGCTAAGTTC	2880
Db	2821	TGCTTCTTTCGGCTTCAAGTCCGTAAGCTGCGGAGAACCTTCAACGAGGCTAAGTTC	2880
Qy	2881	ATCACCTTCAGCATGTTGATCTTCTTCATCGTCTGGATCTCTTCATCCCGGCTATGTC	2940
Db	2881	ATCACCTTCAGCATGTTGATCTTCTTCATCGTCTGGATCTCTTCATCCCGGCTATGTC	2940
Qy	2941	AGCACCTACGGCAAGTTTGTGTGGCGCTGGAGGTGANTGCCATCTGGCTCCAGCTTC	3000
Db	2941	AGCACCTACGGCAAGTTTGTGTGGCGCTGGAGGTGANTGCCATCTGGCTCCAGCTTC	3000
Qy	3001	GGCTGCTGGCTGCATTACTTCAACAGTGTACATCATCTGTTCAAGCGCTGCCGT	3060
Db	3001	GGCTGCTGGCTGCATTACTTCAACAGTGTACATCATCTGTTCAAGCGCTGCCGT	3060
Qy	3061	AACACCATCAGGAGGTGCGCTGCAGACACGGCGGCCACGCCCTCAAGTGGCGGCCCGG	3120
Db	3061	AACACCATCAGGAGGTGCGCTGCAGACACGGCGGCCACGCCCTCAAGTGGCGGCCCGG	3120
Qy	3121	GCCACCTTCGGCGCAGCGGCGGTCTCGCAAGGCTCCAGAGCTGTGCGGCTCCACC	3180
Db	3121	GCCACCTTCGGCGCAGCGGCGGTCTCGCAAGGCTCCAGAGCTGTGCGGCTCCACC	3180
Qy	3181	ATCTCTCGCGCCGCTCGTCCACCTGCGGCGCGGCGCTCACCATGGAGATGCAGCGCTGC	3240
Db	3181	ATCTCTCGCGCCGCTCGTCCACCTGCGGCGCGGCGCTCACCATGGAGATGCAGCGCTGC	3240
Qy	3241	AGACGAGGAAGTTCAGCTTCGGCAGCGGCGACCGTCACTCTGCTCAGCTTCGAGGAG	3300
Db	3241	AGACGAGGAAGTTCAGCTTCGGCAGCGGCGACCGTCACTCTGCTCAGCTTCGAGGAG	3300
Qy	3301	ACAGCCGATACGCCACCTTCAGCCGACCGCGCGCAGCAGGAACTCGGCGGATGCGCGC	3360
Db	3301	ACAGCCGATACGCCACCTTCAGCCGACCGCGCGCAGCAGGAACTCGGCGGATGCGCGC	3360
Qy	3361	AGCGGCGACGACTGTCATCTAGACACGACGAGGGCGCGCTCAGAAATCGGAGCCC	3420
Db	3361	AGCGGCGACGACTGTCATCTAGACACGAGGGCGCGCGCTCAGAAATCGGAGCCC	3420
Qy	3421	CAGCCGCCAACGATGCCGATACAAGCGCGCGCAGCAAGGGCACCTTAGAGTGC CGG	3480
Db	3421	CAGCCGCCAACGATGCCGATACAAGCGCGCGCAGCAAGGGCACCTTAGAGTGC CGG	3480
Qy	3481	GGCGGCGACGAGCGCCCCAACATATGGAGGAAACCTTAATCCAACTCCTCCATCAAC	3540
Db	3481	GGCGGCGACGAGCGCCCCAACATATGGAGGAAACCTTAATCCAACTCCTCCATCAAC	3540
Qy	3541	CCCAAGAACATCTTCACGCGCAGCACCGTGCAGAACTGACATCAACTCCCTAACCGGTGC	3600
Db	3541	CCCAAGAACATCTTCACGCGCAGCACCGTGCAGAACTGACATCAACTCCCTAACCGGTGC	3600
Qy	3601	TGCCCAAACTCTCCCTCTCTCGGCACCTTTCGTTTTGCTGAAGATTGCAGCATCTGCAGT	3660

Db	3601	TGCCCAACCTCTCCCTCTCCGGCAGCTTTGCGTTTGTGCTGAAGATTGCACCATCTGCAGT	3660
Qy	3661	TCCTTTTATCCCTGATTTCTTCGACTCTGGATATTTACTAGTGTCCGATGGGAATATCAAC	3720
Db	3661	TCCTTTTATCCCTGATTTCTTCGACTCTGGATATTTACTAGTGTCCGATGGGAATATCAAC	3720
Qy	3721	ATAATGAGTTGCACAAATAGGTGAGCAGAGTTGTGTCMAAGTATCTGAACATATCTGAAGT	3780
Db	3721	ATAATGAGTTGCACAAATAGGTGAGCAGAGTTGTGTCMAAGTATCTGAACATATCTGAAGT	3780
Qy	3781	ATCTGAACCTACTTTATCTCTCGAATTTGTTATACAAACATTTTGAAGATTTTTTAGTGACA	3840
Db	3781	ATCTGAACCTACTTTATCTCTCGAATTTGTTATACAAACATTTTGAAGATTTTTTAGTGACA	3840
Qy	3841	TTATGTTCTTAACATTTGTCAAGATAAATTTGTTCACAACTATTAAGTACCACCTGAAGCAGT	3900
Db	3841	TTATGTTCTTAACATTTGTCAAGATAAATTTGTTCACAACTATTAAGTACCACCTGAAGCAGT	3900
Qy	3901	GACTGAGATTGCCACTGTGTATGACAGAACTGTTTTTATAACATTTATCAATTGAAACCTTGGG	3960
Db	3901	GACTGAGATTGCCACTGTGTATGACAGAACTGTTTTTATAACATTTATCAATTGAAACCTTGGG	3960
Qy	3961	TTGCAACAGAGAAATATATGACTGTACACAAAAAATTTGTTGATTATCTTAAAAATGCAAT	4020
Db	3961	TTGCAACAGAGAAATATATGACTGTACACAAAAAATTTGTTGATTATCTTAAAAATGCAAT	4020
Qy	4021	TGTTAATCAGATGTGTAAAAATTTGTTAAATCTCTGTACATTTAAATGCATATTTCTTGATA	4080
Db	4021	TGTTAATCAGATGTGTAAAAATTTGTTAAATCTCTGTACATTTAAATGCATATTTCTTGATA	4080
Qy	4081	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4116	
Db	4081	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4116	
RESULT 12			
BD205377		3234 bp	DNA
LOCUS	BD205377		linear
DEFINITION	G protein-fused receptor and chimeric GABAB receptor.		PAT 17-JUL-2003
ACCESSION	BD205377		
VERSION	BD205377.1	GI:33015147	
KEYWORDS	JP 2002510480-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Storjohann, T.M., Hammerland, L.G., Storjohann, L.L., Busby, J.G., Garrett, J.E. and Seim, R.T.		
AUTHORS	Storjohann, T.M., Hammerland, L.G., Storjohann, L.L., Busby, J.G., Garrett, J.E. and Seim, R.T.		
TITLE	G protein-fused receptor and chimeric GABAB receptor		
JOURNAL	Patent: JP 2002510480-A 1 09-APR-2002;		
COMMENT	NPS PHARMACEUTICALS INC		
	OS Homo sapiens (human)		
	PN JP 2002510480-A/1		
	PD 09-APR-2002		
	PF 02-APR-1999 JP 2000542362		
	PR 03-APR-1998 US 60/080671		
	PI THOMAS M STORJHANN, LANCE G HAMMERLAND, LAURA L STORJOHANN, JAMES G BUSBY,		
	PI JAMES E GARRETT, RACHEL T SEMIN		
	PC C12N15/00, A61K38/00, C07K14/705, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,		
PC	C12N15/00, A61K37/02, C12N5/00		
CC	G protein-fused receptor and chimeric GABAB receptor. FH		Key
FT	Location/Qualifiers		
FT	1. .3234		
	/organism="Homo sapiens (human)"/		
FEATURES	Location/Qualifiers		
source	1. .3234		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
ORIGIN	/db_xref="taxon:9606"		

Query Match		42.2%;	Score 1745.2;	DB 6;	Length 3234;
Best Local Similarity		76.4%;	Pred. No. 7.6e-273;		
Matches 2187;		Conservative	0;	Mismatches 658;	Indels 17; Gaps 3;
Qy	501	CTCAGGATGTGTCACAAACCAAGAGGCGCCAGAGGAGAGACATCATCTACCTGGAGGTCT	560		
Db	51	CTCTCGCTACGGCCAGACGACGAGCCCAAGAGAGGGGACATTAATCTTGGGGGCT	110		
Qy	561	CTTCCCAATACACTTTGGAGTAGCCGCAAGGATCAGGACTTAAATCGAACCGAGGC	620		
Db	111	CTTTCTTATTCATTTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGGCCGGAGTC	170		
Qy	621	GACAAATGTATTCGGTACAAATTTTCGAGGCTTCGATGGTCCAGGGGATGATATTCG	680		
Db	171	TGTGAATGTATCAGGTATATTTCCGTGGGTTTCGCTGGTTACAGGCTATGATATTCG	230		
Qy	681	AATGAAGAGATTAACAACAGTATGACTTTCTGCCCCAATATCAACCTGGGATATCGCAT	740		
Db	231	CATAGAGAGATAAACAAGCAGCCAGCCCTCTTCCCAACTTGACGCTGGGATACAGGAT	290		
Qy	741	ATTTGACAGCTGTACACCGTGTCCAGGCGCTAGAGCAACACTCAGCTTTGTGGCCA	800		
Db	291	ATTTGACACTTGCAACACCGTTTCTAAGCCCTTGAAGCCACCCCTGAGTTTGTGTCA	350		
Qy	801	GAACAAATTCGACTCGCTGAATAGATGAGTTCTGTAACTGCTCTGACCATATCCCATC	860		
Db	351	AAACAAATTTGATCTTTGAACTTGTATGAGTTCTGCAACTGCTCAGAGCACATTCCTC	410		
Qy	861	CACATACAGTGTGCGGGCCACCGGTTCAGGAATCTCCAGGCTTGGGCCATCTATT	920		
Db	411	TACGATTCTGTGTGGGAGCAACTGGCTCAGGCGTCTCCAGGAGTGGCAAAATCTGCT	470		
Qy	921	GGGATTTATTTACATTCACAGGTGAGTATGCTCTCTCGAGCAGGCTGCTCAGCAACA	980		
Db	471	GGGGCTCTTACATTCGCCAGGTGAGTTATGCTTCTCCAGCAGACTCTCTCAGCAACA	530		
Qy	981	GAATGAGTAAAGGCTTCTGAGGACCATCCCCAATGATGAGCAACAGGCCACGGCAT	1040		
Db	531	GAATCAATTCAGTCTTCTCCGAAACCATCCCCAATGATGAGCAACAGGCCACTGGCAT	590		
Qy	1041	GGCCGAGATCATGAGCACTTCCAGTGAACTGGTGGGAACTTGGGAGGAGGAGTGA	1100		
Db	591	GGCAGACATCATGAGTATTTCCGCTGGAATGGGTGGGCAATTTGAGCTGATGAGCA	650		
Qy	1101	CTATGGCCGCCAGGCAATGCAAGTCTCGGGAGAGGCCGTTAAGAGGGACATCTGTAT	1160		
Db	651	CTATGGCGCGCGGATTTGAGAAATTCGAGAGGAGACTGAGGAAAGGGATATCTGCAT	710		
Qy	1161	TGACTTCAGTGAATCTCTCAGTACTACCCAGAGCAGTTGGAGTTCTACGCGCA	1220		
Db	711	CGACTTCAGTGAATCATCTCCAGTACTCTGATGAGGAGAGATCCAGCATGTGGTAGA	770		
Qy	1221	CGTCAATCAGAACTCTCGGCCAAGGTCTATCGTGTCTTCTCCAAATGGCCCGACCTGGA	1280		
Db	771	GGTGATTCAAATTCACGGCCAAAGTCTATCGTGGTTTCTCCAGTGGCCAGATCTTGA	830		
Qy	1281	GCCGCTCATTCAGGAGATGTTCGGAGAAACATACCGATCGGATCTGGCTGGCCAGCA	1340		
Db	831	GCCCCATCATCAAGGAGATTTCCGCGCAATATCACGGGCAAGATCTGGCTGGCCAGCA	890		
Qy	1341	GGCTTGGCCAGCTCTCGCTCATTTGCCAGCCAGGACTTCCACGTGGTCTGGGGCAC	1400		
Db	891	GGCCTGGCCAGCTCTCTCCCTGATCGCCATGCTCAGTACTTCCACGTGGTGGGGCAC	950		
Qy	1401	CATCGGCTTCGCTCAGGGCGGGCGTATCCCCAGGGTTCAACAGTTCTCTGAAGAGGT	1460		
Db	951	CATTGGATTCGCTCTGAAGGCTGGCCAGATCCCCAGGCTTCCGGAAATTCCTGAAGAGT	1010		
Qy	1461	CCACCCAGCAGGTCTCGCAATAGGTTTGTCAAGAGTCTGGAGGAGACCTTCAA	1520		
Db	1011	CCATCCCGAGAGTCTGTCCAAATGSGTTTGGCCAAAGGAGTTTGGGAAGAAACATTTAA	1070		

Qy	1521	CTGCTACTTCCCGAGAGACCTGACGAGCTGAAGATTCACAGGTGCTCGACGG	1580		
Db	1071	CTGCCACTCTCAAGA-----AGGTGCAAAAGGACCTTTACTGTGGACACTTTCTG	1122		
Qy	1581	ACCGGCGGCTCAAGGGGAGCGCTCCAAAGCGGGGAACTCCAGACGGACGCCCTACGCCA	1640		
Db	1123	AGAGG----TCAAGAAAGTGGCGACAGTTTAGCAACAGCTCGACAGCTTCGGACC	1178		
Qy	1641	CCCTGCACTGGGAGGAGNACATCACCAGCTGGAGAGCCCCCTACTCGATTTATACACA	1700		
Db	1179	CTCTGTACAGGGGATGAGAAACATCAGAGTGTGAGAGCCCCCTTACATAGATTTACAGCA	1238		
Qy	1701	CTTGAGGATCTCTACAATGTATACGTGGCGCTACTACTCATTTGCTCAGCCCTGCAAGA	1760		
Db	1239	TTTACGGATATCTACAATGTGTACTTAGCAGTCTACTCCATTTGCCACGCTTGAAGA	1298		
Qy	1761	CATCCACTCTTGGAAACCCGGGACGGGCACTTTTGGAAACGGATCTTGTGAGATATTAA	1820		
Db	1299	TATATATACCTGTACTCTGGGAGAGGGCTCTTCAACAATGGCTCTGTGAGACATCAA	1358		
Qy	1821	AAAAGTTGAGCGCTGCGCAGGTCTCAACCATCTGCTGCATCTCAAGTTTACCAACAGCAT	1880		
Db	1359	GAAAGTTGAGCGCTGCGCAGGTCTCTGAAGCACCTACGGCATCTTAACTTTACAAACAATAT	1418		
Qy	1881	GGGTGAGAGTTGACTTTTGAACATCAAGGTGACCTCAAGGGGAACTACACCAATTATCAA	1940		
Db	1419	GGGGGAGCAGGTGACCTTTGATGAGTGTGCTGACCTGGTGGGAACTATTCCATCATCAA	1478		
Qy	1941	CTGCGAGCTCTCGCGAGAGATGAATCGGTGTGTTTCCATGAGGTGGGCACTACAAAGC	2000		
Db	1479	CTGCGACCTCTCCCCAGAGATGGCTCCATCGTGTTTAAGGAAAGTCGGGTATTACAACT	1538		
Qy	2001	CTACGCTTAAGCCAGTGACCGACTCAACATCAACGAAAGAAATACTCTGAGAGTGGCTT	2060		
Db	1539	CTATGCCAAGAGGAGAAAGACTCTTTCATCAACAGGAGGAAATACTCTGTGAGTGGGT	1598		
Qy	2061	CTCAAGAGTGGTCTTTCTTCCAACTGCGAGTCGAGACTGTGTGCCGGGCAACGAGAGGG	2120		
Db	1599	CTCCAGGAGTGGCTTCTTCCAACTGCGAGCCGAGACTGCTCTGCGAGGACCCAGGAAG	1658		
Qy	2121	GATCTGAGGGGAGCCACCTGCTGCTTTGAAATGCTGCGCATGTGCGAGAGGAGAGTT	2180		
Db	1659	GATCATTGAGGGGAGCCACCTGCTGCTTTGAGTGTGGAGTGTCTGTATGGGAGTA	1718		
Qy	2181	CAGTGATGAAACGATGCAAGTGCCTGTATCAAAGTCCCGAATGATTTCTGTCGAATGA	2240		
Db	1719	TAGTGATGAGACAGATGCCAGTGCCTGTAAAGTCCCAGATGACTTCTGTGCCAATGA	1778		
Qy	2241	GAACCAACGCTGCTGATCGCAAGAGATCGAGTACCTGTGTCGACAGCCCTTCGG	2300		
Db	1779	GAACCAACCTCTGCTGCTTGGCAAGGAGATCGAGTTTCTGTGAGGAGCCCTTGG	1838		
Qy	2301	GATCGCTCTGACCATCTTGGCCGTACTGGGCACTCCTGATCACCTCTTCTGTGGGGT	2360		
Db	1839	GATCGCACTCACCTCTTTGGCGTGTGGGCACTTTTCTTGACAGCCCTTGTGCTGGGT	1898		
Qy	2361	CTTTCATCAGTTTCAAGAACACTCCCATCGTGAAGGCAACACCGGAGTGTTCCTACCT	2420		
Db	1899	GTTTATCAAGTTCCGAAACACACCCATTTGTAAGGGCCACCAACCGAGAGCTCTCTACCT	1958		
Qy	2421	GCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTCATCTTCTCATCGGAGGCCAG	2480		
Db	1959	CTTCTCTTCTCCCTGCTCTGCTGCTTCTCCAGTCCCTGTCTTCTCATCGGAGGCCCA	2018		
Qy	2481	GGACTGGAAGTGTGGCTCGGCAACCGGCTTTTGGCATCAGCTTCGTCTGTGCAATCTC	2540		
Db	2019	GGACTGGAAGTGTGGCTCGGCAACCGGCTTTTGGCATCAGCTTCGTCTGTGCAATCTC	2078		
Qy	2541	CTGCATCTGTTGAAGACCAACCGGCTGTGCTGCTTTCGAGGCCAAGATCCCACACAG	2600		
Db	2079	ATGCATCTGTTGAAGACCAACCGGCTGTGCTGCTTTCGAGGCCAAGATCCCACACAG	2138		
Qy	2601	CTTCCACCGCAAGTGGGTGGGCCCTCAACCTGCGAGTTTCTCTGCTGCTCTCTCTGCT	2660		


```

Db 2139 CTTCCACCGCAAGTGGTGGGGCTCAACTGAGTCTCTGGTTTCTCTGCACCTT 2198
Qy 2661 GGTGAAATCGTCACTGATCATCTGGCTTACACCGGGCTCCTCCAGCTACAGAA 2720
Db 2199 CATGAGATTGTCTGTGTGATCTGGCTTACACCGGGCTCCTCAAGCTACCGAA 2258
Qy 2721 CCATGAGTGGAGGAGGAGTCACTTTCATCACTGCGACGAGGGCTCGCTCATGGGCT 2780
Db 2259 CCAGAGCTGGAGGATGAGATCATCTTTCATCACTGCGACGAGGGCTCCTCATGGGCT 2318
Qy 2781 GGGCTTCTCTATCGGTACACCTGCTCTCTCGCGCCATCTGCTTCTTTCGCTTCAA 2840
Db 2319 GGGCTTCTCTATCGGTACACCTGCTCTCTCGCGCCATCTGCTTCTTTCGCTTCAA 2378
Qy 2841 GTCCGTAAGCTGCGGAGAACTTCAACGAGCTTAAGTTCATCACTTCAGCATGTTGAT 2900
Db 2379 GTCCGGAAGCTGCGGAGAACTTCAATGAAGCCAAAGTTCATCACTTCAGCATGTTGAT 2438
Qy 2901 CTTCTTCACTGCTGATCTCTCTTCACTCCCGCTTATGTACAGCACTACGGCAAGTTGT 2960
Db 2439 CTTCTTCACTGCTGATCTCTCTTCACTCCAGCTTATGCCAGCACTATGCCAAGTTGT 2498
Qy 2961 GTCCGCTGGAGGATGATGGCATCTGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCT 3020
Db 2499 CTTCTGCTGAGGATGATGGCATCTGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCT 2558
Qy 3021 CTTCAACAGTGTATCATCATCTGTTCAAGCGTGGCGTAAACACATCGAGGAGTGGC 3080
Db 2559 CTTCAACAGTGTATCATCATCTGTTCAAGCGTGGCGTAAACACATCGAGGAGTGGC 2618
Qy 3081 CTTCAACAGTGTATCATCATCTGTTCAAGCGTGGCGTAAACACATCGAGGAGTGGC 3140
Db 2619 TTGCAAGCCGAGCTACGCTTCAAGGTGGCTGCGCGGCGCAGCTGCGCGGAGCA 2678
Qy 3141 CGGCTCTCAAGCGTCCAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3200
Db 2679 CGTCTCCCGCAAGCGTCCAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2738
Qy 3201 CACCTGCGGCGCGGCTCACCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3260
Db 2739 CATCAGCAAGAGCAACA-----GCGAAGACCCATTCCTCCAGCGGAGGAGAG 2793
Qy 3261 CGGAGCGGCAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3320
Db 2794 CAGCAGCAGCGCTGCGCTTACCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2853
Qy 3321 CAGCGCGCGCGCGCGAGCAAGTCTGCGCGATGCGCGAG 3362
Db 2854 CAGCAGCAAGATCTCAGCAGCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

```

```

RESULT 13
AX542191
LOCUS 3234 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 18 from Patent WO0229033.
ACCESSION AX542191
VERSION AX542191.1 GI:25276404
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Stormann,T., Hammerland,L.G., Storjohann,L.L., Busby,J.G.,
Garrett,J.E. and Simin,R.T.
TITLE G-protein fusion receptors and chimera gaba b? receptors
JOURNAL Patent: WO 0229033-A 18 11-APR-2002;
NPS PHARMACEUTICALS, INC. (US)
FEATURES
source
1..3234
/organism="Homo sapiens"
/mol_type="unassigned DNA"

```

```

ORIGIN
Query Match 42.2%; Score 1745.2; DB 6; Length 3234;
Best Local Similarity 76.4%; Pred. No. 7.6e-273;
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;
/db_xref="taxon:9606"
Qy 501 CTCAGGATATGGTCCCAAAACCAAGGCGCCAGAGAGAGAGAGATCATATCTGGAGGCT 560
Db 51 CTCTGCTTACGGCCAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 110
Qy 561 CTTCCCAATATACCTTTGGAGTAGCCGCCAAGATCAGGACTTAAATTCAGAGCCGAGGC 520
Db 111 CTTTCTTATTCATTTTGGAGTAGCAGTAAAGATCAAGATCTCAATCAAGCCGAGGTC 170
Qy 621 GACAAATGATTCGGTACAAATTTTCAGGCTTCCGATGCTCCAGGCGATATATTCG 680
Db 171 TGTGGATGATCAGGATTAATTTCCGTGGTTTCCGTGGTACAGGCTATGATATTCG 230
Qy 681 AATTGAAGAGATTAACAAACAGTATGACTTTCCTGCCAATATACCCCTGGGATATCGAT 740
Db 231 CATAGAGAGATTAACAAACAGGAGCCAGCCCTTCTCCCAACTTGAAGCTGGGATACAG 290
Qy 741 AATTGACAGTGTAAACACCGTGTCCAAGCGCTAGAGGCAACACTCAGCTTTGTGGCCA 800
Db 291 AATTGACACTTGAACACCGTGTCTAAGGCTTGGAGGCAACCTGAGTTTGTGCTCA 350
Qy 801 GAACAAATATCGACTCGCTGAACCTTAGATGATGTTCTGTAACTCTGACATATCCATC 860
Db 351 AAACAAATATGATTTCTTGAACCTTGTGATGTTCTGCAACTGCTCAGAGCAGATTCCT 410
Qy 861 CACATAGCAGTGTGGGCAACCGGTCAGAAATCTCCAGGCTGTCGCAACTATTT 920
Db 411 TACGATTTGCTGTGGGAGCAACTGGCTCAGGCTGCTCCAGGAGTGGCAATCTGCT 470
Qy 921 GGGATTTATTTACATTTCCAGGTCAGTATGCTCTCTCCAGCAGGCTGCTCAGCAACA 980
Db 471 GGGCTCTTCTACATTTCCAGGTCAGTATGCTCTCTCCAGCAGACTCTCTCAGCAACA 530
Qy 981 GAATGAGTCAAGGCTTCTTGAGGACCATCCCAATGATGAGCAACAGGCAACGCGCAT 1040
Db 531 GAATCAATCAAGCTTCTTCCGAAACCATCCCAATGATGAGCAACAGGCAACGCGCAT 590
Qy 1041 GCGGAGATCATCAGCACTTCCAGTGGAACTGGGTGGAAACCTCGGAGCGGAGCATGA 1100
Db 591 GGCAGACATCATCGATATTTCCGCTGGAACTGGGTGGGCAACAATGCGAGCTGATGAC 650
Qy 1101 CTATGGCGCCAGGCAATTGACAAAGTTCGGGAGGAGGCGGTTAAGAGGAGCATCTGTAT 1160
Db 651 CTATGGCGCGCGGAGTTGAGAAATTCGAGAGGAGGCTGAGGAAAGGAGATCTGTGAT 710
Qy 1161 TGACTTCAGTGAATGATCTCTCAGTACTACACCCAGAGCAGTGGAGTTCAATCCCGCA 1220
Db 711 CGACTTCAGTGAATCATCTCCAGGACTCTGATGAGGAGAGATCCAGCATGTGTAGA 770
Qy 1221 CGTCAATCCAGAACTCTCGGCAAGGTCATCGTGGTCTTCTCCAAATGGCCCGGAGCTGA 1280
Db 771 GGTGATTCAAATTCAGGSCAAAGTCATCGTGGTCTTCTCCAGTGGCCAGATCTTGA 830
Qy 1281 GCGCTCATCCAGAGATAGTTCGGAGAAACATCAGCATCGATCGATGCTGGCCAGCGA 1340
Db 831 GCGCTCATCCAGAGATAGTTCGGGCGCAATATCAGGCGCAAGATCTGGTGGCCAGCGA 890
Qy 1341 GCGTGGGCGAGCTCTCGCTCATTCGCAAGCCAGAGTACTTCCAGCTGGTGGCGGCGAC 1400
Db 891 GCGTGGGCGAGCTCTCTCTGATCGCCATGCTCTCAGTACTTCCAGCTGGTGGCGGCGAC 950
Qy 1401 CATGGGCTTCGCTCTCAGGCGGGGCTATCCAGGGTTCAACAAGTCTCTGAGAGAGGT 1460
Db 951 CATGGATTCGCTCTGAAGGCTGGGAGATCCAGGCTTCCGGGAAATCTCTGAGAGAGGT 1010
Qy 1461 CCACCCAGCAGGCTCTCGGACAAATGGTTTGTCAAGAGTCTCTGGGAGGAGACCTTCAA 1520

```

Db 1011 CCATCCCGAAGTCTGTCCAAATGGTTTTCGCAAGAGTTTGGGAAGAAACATTTAA 1070
Qy 1521 CTGCTACTTACCGAAGAGACCTCAGCAGCAGTGAAGAAATCCAAAGTGCCTCGCACGG 1580
Db 1071 CTGCCACCTCCAGA-----AGTGCAAAAGGACCTTTACCTGTGACACCTTTCTG 1122
Qy 1581 ACCGGGGCTCAAGGGGAGCGCTCAAGCGGGGAACTCCAGACGGAAGCCCTACGGCA 1640
Db 1123 AGAGG---TCACGAAGAAGTGGCGACAGGTTTAGCAACAGCTCGACAGCCTTCCGACC 1178
Qy 1641 CCCCTGCATCGGGAGGAGAAATCACCAGCGTGGAGACCCCTACCTGGATTATACACA 1700
Db 1179 CCTCTGTACAGGGGATGAACATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1238
Qy 1701 CTTGAGGATCTCCTCAATGTATAGTGGCGCTTACTCCATGCTCAGCCCTGCAAGA 1760
Db 1239 TTTACGGATATCTCAATGTGTACTTAGCAGTCTACTCCAATGCCACGCTTGAAGA 1298
Qy 1761 CATCCACTTTGCAAAACCGGACCGGATCTTTGCAACGAGATCTTGTGAGATTATAA 1820
Db 1299 TATATATACCTCTTACCTGGAGAGGGCTCTTACCAATGGCTCCTGTGAGACATCAA 1358
Qy 1821 AAAAGTTGAGGCTGGCAGGCTCTCAACCATCTGCTGCATCTGAAGTTTACCAACAGCAT 1880
Db 1359 GAAAGTTGAGGCTGGCAGGCTCTGAAGCACCTACGGCATCTAATCTTACAAACAATAT 1418
Qy 1881 GGTGAGCAGGTTGATTTGACATCAAGTGAACCTCAAGGGAACTACACATATACAA 1940
Db 1419 GGGGAGCAGGTGACCTTTGATGAGTGTGTGACCTGTGGGAACTATTCCATCATCAA 1478
Qy 1941 CTGGCAGCTCTCGCAGAGATGAATCGGTGTGTTTCCATGAGTGGGCACTACAAGC 2000
Db 1479 CTGGCACCTCTCCAGAGGATGGCTCCATCGTGTTTAAGNAAGTCGGGTATTACAGT 1538
Qy 2001 CTACGCTAAGCCAGTGACCGACTCAACATCAACGAAAGAAATCTCTGTGAGTGGCTT 2060
Db 1539 CTATGCAAGAAGGAGAGAAAGACTCTTCATCAACGAGGAGAAATCTCTGTGAGTGGCTT 1598
Qy 2061 CTCGAAAGTGTCTCTTCTCAACTGCAGTCGAGACTGTGCGGGGACACGAGAGGG 2120
Db 1599 CTCGAGGAGGTGCGCTTCTCAACTGTCAGCGGAGACTGCTGGCAGGAGCCAGGAAAG 1658
Qy 2121 GATCATCAGGGGGAGCCACCTGTCTTGAATGCATGGCATGTGAGAGGGAGATT 2180
Db 1659 GATCATGAGGGGAGCCACCTGTCTTGAAGTGTGTGGAGTGTCTGTATGGGAGTA 1718
Qy 2181 GAGTGAATGAACGATGCAAGTGGCTGTACAAAGTGGCCGATGATTTCTGTGCAATGA 2240
Db 1719 TAGTGATGAGACAGATGCCAGTGCCTGTAAACAGTGCCGAGATGACTTCTGTGTCGAATGA 1778
Qy 2241 GAACACACGTCGTGCATCGCAAGAGATCGAGTACCTGTGTCGAGCGAGCCCTTCGG 2300
Db 1779 GAACACACCTCTGCATTGCCAAGAGATCGAGTTCTGTCTGTGAGCGGAGCCCTTTGG 1838
Qy 2301 GATCGCTGTACCATCTTCCCGTACTGGGCATCTGTATCACTCTCTGTGCTGGGGT 2360
Db 1839 GATCGCACTCACCTCTTTCGGCTGTGGGCATTTTCTGACAGCCTTTGTGCTGGGT 1898
Qy 2361 CTTTCATGATTCAGGAACATCCCATCGTGAAGCCACCCACCGGAGTGTCTTACTCT 2420
Db 1899 GTTATCAAGTTCGGCAACACACCCATTTGTAAGGCCACCAACCGAGAGCTCTCTACT 1958
Qy 2421 GTGTCTCTTCTCCCTCATCTGTGTCTTCTCCAGCTCGCTCATCTTCATCGGCGAGCCAG 2480
Db 1959 CTTCTCTTCTCCCTGCTCTGTGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCA 2018
Qy 2481 GAGCTGAGCTGTGCGCTCGGCAACCGGCTTTGGCATCAGCTTGTGCTGTGATCTC 2540
Db 2019 GGATGAGAGTGGCGCTCGCCAGCGGCTTTGGCATCAGCTTGTGCTGTGATCTC 2078
Qy 2541 CTGCATCTCTGTAAGCAACCGGCTGTGTGCTTTCGAGGCAAGATCCCCACAG 2600
Db 2079 ATGCACTCTGTGTAACCAACCGTGTCTCTGTGTTGAGGCCAGATCCCCACAG 2138

Qy 2601 CTTCCACCGAAGTGGGTGGGCTCAACCTGCAAGTTCTCTGGTCTTCTCTGATCTCT 2660
Db 2139 CTTCCACCGAAGTGGGTGGGCTCAACCTGCAAGTTCTCTGGTCTTCTCTGATCTCT 2198
Qy 2661 GGTGCAATCGTCACTGTCATCTGGCTCTACACGGCGCTCCCTCCAGCTACAGGA 2720
Db 2199 CATGCAATGTCTCTGTGATCTGGCTCTACACGGCGCTCCCTCCAGCTACAGGA 2258
Qy 2721 CCATGAGCTGAGAGAGAGGTCTTTCATCAGCTGCGAGGGGTCTGCTCATGCGCT 2780
Db 2259 CCAGGAGCTGAGAGATGAGATCTTTCATCAGCTGCGAGGGGTCTCCTCATGCGCT 2318
Qy 2781 GGGCTTCTCATCGGCTACACCTGCTCTCCGCGCATCTGCTTCTTCTGCTTCAA 2840
Db 2319 GGGCTTCTCATCGGCTACACCTGCTGCTGCTGCTGCTGCTTCTTCTTCTGCTCAA 2378
Qy 2841 GTCCGCTAAGCTCGCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTTGAT 2900
Db 2379 GTCCGGAAGCTCGCGAGAACTTCAAGAGCAAGTTTCATCACCTTCAGCATGTTGAT 2438
Qy 2901 CTTCTTCATCGTGTGATCTCTTTCATCCCGCTTATGTGAGCACCTACGGCAAGTTGT 2960
Db 2439 CTTCTTCATCGTGTGATCTCTTTCATCCAGCTTATGCCAGCACCTATGGCAAGTTGT 2498
Qy 2961 GTCCGCTGAGGTGATTCGCTCTGCTTCCAGCTTCCGCTGCTGCTGCTGCTGCTTAA 3020
Db 2499 CTCTGCTGAGGTGATTCGCTTCCAGCTTCCGCTGCTGCTGCTGCTGCTGCTT 2558
Qy 3021 CTTCAACAAGTGTATCATCTCTTTCAGCGCTGCGCTTAAACCATCGAGAGGTGCG 3080
Db 2559 CTTCAACAAGTGTATCATCTCTTTCAGCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCG 2618
Qy 3081 CTGAGCACCGCGCCACCGCTTCAAGTGGCGCCCGGCGCACCTCCGCGCGAGCGC 3140
Db 2619 TTGAGCACCGCGCTTCAAGTGGCTTCAAGTGGCTGCGCGCGCACCTGCGCGCGAGAA 2678
Qy 3141 CGCTCTCGCAAGCGCTTCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 3200
Db 2679 CGTCTCCGCAAGCGCTTCCAGCGCTTGGAGCTTCCAGCGATCCACCCCTCTCTCTC 2738
Qy 3201 CACTGCGCGCGCGCTTCAACATGAGATGAGCTGAGCTGAGCGCTGAGCACGAGAGTTCAGCTT 3260
Db 2739 CATCAGCAGCAAGAGCAACA-----GCGAAGACCCATTCCTCCAGCGCGAGAGGAG 2793
Qy 3261 CGGCGAGCGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3320
Db 2794 CAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2853
Qy 3321 CAGCGCACGCGCGCGAGAGAACTGCGCGGATGCGCGAG 3362
Db 2854 CAGCAGCAAGATCTCAGCAGCAGCCAGATGCAAGCAGAAG 2895

RESULT 14
CO714283
LOCUS 3783 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 217 from Patent WO02068579.
ACCESSION CO714283
VERSION CO714283.1 GI:42275140
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams M.C., Li, P.W. and Myers, E.W.
TITLE Ktts, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 217 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers

QY 2541 CTGCTATCTGTTGAAGACCAACCGGGTGTCTGCTGTTCTTTCGAGGCCAAGATCCCCACCAG 2600
 Db 2451 ATGATCTCTGTTGAAGACCAACCGGTGTCTCTCTGTTGTTGAGGCCAAGATCCCCACCAG 2510
 QY 2601 CTTCAACCGCAAGTGGTGGGCTCAACCTGAGTCTCTCTGTTGTTCTCTCTCTCTCTCTCTCT 2660
 Db 2511 CTTCAACCGCAAGTGGTGGGCTCAACCTGAGTCTCTCTGTTGTTCTCTCTCTCTCTCTCTCT 2570
 QY 2661 GGTGAAATCTGTCACCTGATCATCTGCTCTACACCGGCTCTCTCTCTCTCTCTCTCTCTCTCT 2720
 Db 2571 CATGAGATGTCATCTGTTGATCTGCTCTACACCGGCTCTCTCTCTCTCTCTCTCTCTCTCT 2630
 QY 2721 CATGAGTGGAGGAGGATCATCTTCACTACCTGCGAGAGGCTCTCTCTCTCTCTCTCTCTCTCT 2780
 Db 2631 CCAGGAGTGGAGGATGAGATCATCTTCACTACCTGCGAGAGGCTCTCTCTCTCTCTCTCTCTCT 2690
 QY 2781 GGGCTTCCTCATCGGCTACACCTGCTCTCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2840
 Db 2691 GGGCTTCCTCATCGGCTACACCTGCTCTCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2750
 QY 2841 GTCCCGTAAGCTGCCGGAACCTTCAACGAGGCTAAGTTTCATCCTTCAGCATCTTTCAT 2900
 Db 2751 GTCCCGTAAGCTGCCGGAACCTTCAACGAGGCTAAGTTTCATCCTTCAGCATCTTTCAT 2810
 QY 2901 CTTCTTCATCTGATCT 2960
 Db 2811 CTTCTTCATCTGATCT 2870
 QY 2961 GTCCGCTGAGGCTGATTCCT 3020
 Db 2871 CTTCTTCATCTGATCT 2930
 QY 3021 CTTCAACAGTGTATCATCTCTGTTCAAGCGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3080
 Db 2931 CTTCAACAGTGTATCATCTCTGTTCAAGCGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2990
 QY 3081 CTGACGACGGGGCCAGCTTCAAGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 3140
 Db 2991 TTGACGACGGGGCCAGCTTCAAGTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 3050
 QY 3141 CGGCTCTGCAAGCGCTCAGCAGCGCTGTGGGCTCTCAACCATCTCTCTCTCTCTCTCTCTCTCT 3200
 Db 3051 CGTCTCCGCAAGCGGTGAGCAGCGCTTGGAGGCTCCAGGGATCCACCCCTCTCTCTCTCTCT 3110
 QY 3201 CACCTGGGGGGGGGCTCACCATGAGATGAGCGCTGAGCGCTGAGCGCGCAGAGGTCAGCTT 3260
 Db 3111 CATCAGCAGCAAGAGCAACA-----CGAAGAGCCCATCCACAGCCCGAGAGGAGAGAG 3165
 QY 3261 CGGACGCGGACCGCTCACCTGTCTGCTCAGCTTCGAGGAGACAGGCGCGGATAGCCACCCCT 3320
 Db 3166 CAGCAGCGCGGTGGCCCTTAACCCAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3225
 QY 3321 CAGCCGACGGCCCGCAGCAGGAACTCGGGGGATGGCCGGAG 3362
 Db 3226 CAGCAGCAACGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3287

RESULT 15
 AX548832
 LOCUS 3783 bp DNA linear PAT 26-NOV-2002
 DEFINITION Sequence 117 from Patent WO2061087.
 ACCESSION AX548832
 VERSION AX548832.1 GI:25613725
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE
 AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.
 TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides

JOURNAL Patent: WO 02061087-A 117 08-AUG-2002;
 Lifespan Biosciences, Inc. (US)
 FEATURES Location/Qualifiers
 1..3783
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 42.2%; Score 1745.2; DB 6; Length 3783;
 Best Local Similarity 76.4%; Pred. No. 7.6e-273;
 Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;
 QY 501 CTCAGGTTATGTTCCAAACCAAGGGCCAGAGAAAGAGAGATCATATCTGGAGGTCT 560
 Db 423 CTCTGGCTACGGGCGACAGCCAGAGCCAAAAGAGGGGACATTAATCTTGGGGGCT 482
 QY 561 CTTCCCAATACACTTCGAGTAGCGCCCAAGGACTCAGAGCTTAAATTCAGAGCCGAGGC 620
 Db 483 CTTTCTTATTCATTTTGGAGTAGAGCTAAGATCAAGATCTCAATCAAGGCGGAGTC 542
 QY 621 GACAAAATGTTATTCGGTACAAATTTTCGAGGCTTCGATGGCTCGAGCGATGATATTCGC 680
 Db 543 TGTGGAATGTTATCAGGTATAATTTCCGTTGGTTCGCTGCTTACAGGCTATGATATTCG 602
 QY 681 AATTGAAGAGATTAAACACAGATGATGCTTCTGCCCAATATCACCTCGGATATCGCAT 740
 Db 603 CATAGAGAGAGATAAACAGCAGCCAGCCCTTCTTCCCAACTTTCAGCGTGGATACAGAT 662
 QY 741 ATTTGACACGTTGAACACCGGTGTCGAAGGGCTAGAGGCAACACTCAGCTTTGTGGCCCA 800
 Db 663 ATTTGACACCTTGCAACACCGTTTCTAAGGCTTGGAGCCACCTGAGTTTGTGCTCA 722
 QY 801 GAACAAATTCGACTCGGTGAACTTAGATGATGTTCTGTAACTGCTCTGACATATCCCATC 860
 Db 723 AAACAAATTCGATTTCTTGAACCTTGATGATGTTCTGCAACTGCTCAGAGCAGATTCCTC 782
 QY 861 CACAAATGAGCTGTGCGGGCAACCGGTTCAGGAATCTCCACGGCTCTGGGCAATCTATT 920
 Db 783 TACGATTCGTTGTTGGAGCAACTGCTCAGGCTCTCCACGGCTGTCGCAATCTGCT 842
 QY 921 GGGATATTTTACATTCACAGTTCAGTATGCTCTCTCAGAGAGGTGCTCAGCAACAA 980
 Db 843 GGGGCTCTTCTACATTCCTCAGGTCAGTTATGCTCTCTCAGCAGAGACTCTCTCAGCAACA 902
 QY 981 GAATGAGTACAGGCTTCTCAGGACCATCCCAATGATGAGCAACAGGCGCCAGCAT 1040
 Db 903 GAATCAATTCAGTCTTCTCTCCGAACTTCCGCTGGAATCTGGTGGGCAATTCAGCTGATG 962
 QY 1041 GCGCAGATCATCAGCACTTCCAGTGGAACTGGGTGGGAACTCCCTGGCAGCGCAGTGA 1100
 Db 963 GGCAGACATCATCAGTATTTCCGCTGGAATCTGGTGGGCAATTCAGCTGATGACGA 1022
 QY 1101 CTATGGCGCGCCAGGCAATGACAGTTCCGGGAGAGGCGCTTAAGAGGACATCTGTAT 1160
 Db 1023 CTATGGCGCGCGGGGATGAGAAATTCGAGAGGAACTGAGGAAAGGGGATATCTGCAT 1082
 QY 1161 TGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAGCAGTTCGAGTTTCATCGCCGA 1220
 Db 1083 CGACTTCAGTGAATCTCATCTCCAGTACTCTGATGAGGAGAGATCCAGCATGTTGATGA 1142
 QY 1221 CGTCATCCAGAACTCTCTGGCCAAAGTCATGTTGGTCTTCTCCAAATGGCCCGACCTTGA 1280
 Db 1143 GGTGATTCAAAATTCACGGCCAAAGTCATGTTGGTCTTCTCCAGTGGCCAGATCTTGA 1202
 QY 1281 GCCCTCATCAGGAGATGTTCCGAGAAACATCACCGATCGGATCTGGCTGGCCAGCGA 1340
 Db 1203 GCCCTCATCAGGAGATGTTCCGCGGCAATATCACGGGCAAGATCTGGCTGGCCAGCGA 1262
 QY 1341 GGCCTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTACTTCCACGTGTCGGCGAC 1400
 Db 1263 GGCCTGGCCAGCTCTTCGCTCATTCGCTCATTCAGTACTTCCACGTGTTGGCGGAC 1322

QY 1401 CATCGGCTTGGCTCTAGGCGGGGCGTATCCAGGGTTCAACAGTTTCTGAGAGGT 1460
 Db 1323 CATTTGATTCGCTCTGAAGGCTGGGAGATCCAGGCTTCGGGAATTCCTGAAGAAGGT 1382
 QY 1461 CCACCCAGCAGGTCTCGACAAATGGGTTTGTCAAGGAGTTCTGGAGAGACCTTCAA 1520
 Db 1383 CCATCCAGGAAGTCTGTGCACAAATGGTTTGCRAAGAGTTTGGGAAGAACAATTAA 1442
 QY 1521 CTGCTACTTCCAGAGAAACCTGACGAGCTGAAGAAATTCOAAGTGCCTTCGACGG 1580
 Db 1443 CTGCCACTTCAAAGA-----AGGTGCAAAAGGACCTTTACCTGTGACACCTTTCTG 1494
 QY 1581 ACCGGGGCTCAAGGGAGCGCTCCAAAGCGGGGAACCTCCAGACGACAGCCCTAGCCA 1640
 Db 1495 AGAGG----TCAGAAAGAGTGGGACAGGTTTAGCAACAGCTCGACAGCCTTCGGACC 1550
 QY 1641 CCCTGCACTGGGAGAGAAATCAACAGCGTGGAGACCCCTACTCTGGATTATACACA 1700
 Db 1551 CCTCTGTACAGGGGATGAGAAATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1610
 QY 1701 CTTGAGATCTCTAATGATATACGTGGCGCTCTACTCTCATTTGCTCAGCCCTGCAAGA 1760
 Db 1611 TTTACGGATATCTCAAAATGTGTAATAGCAGTCTACTCOATTTGCCACGCGCTTGAAGA 1670
 QY 1761 CATCCACTCTTGAACACCCGGGACCGGCTCTTTGCAAAACGGATCTTTGTCAGATATTAA 1820
 Db 1671 TATATATACCTGTACCTTGGAGAGGGCTCTTCAACATGGCTCTGTGACAGATCAA 1730
 QY 1821 AAAAGTTAGGCTCTGAGGCTCTCAACCATCTGCTGATCTGAAGTTTACCAAGCAT 1880
 Db 1731 GAAAGTTGAGGCTGTCAGGCTCTGAAGCACCTTACGCGCATCTAAAGCTTTTACAAACAAT 1790
 QY 1881 GGGTGAAGCAGTTGACTTTGACCATCAAGTGAACCTCAAGGGGAACCTACACATTATCAA 1940
 Db 1791 GGGGAGACAGTGACCTTTGATGAGTGTGTTGACCTGTGTTGGGAATATTCATCATCAA 1850
 QY 1941 CTGGAGCTCTCGCAGAGAGTAATCGGTGTTGTTTCCATGAGGTGGGCAACTACAAAGC 2000
 Db 1851 CTGGACCTCTCCCGAGAGATGGCTCCATCGTGTAAAGGAAGTTCGGGTATTACAAGT 1910
 QY 2001 CTACGCTAAGCCAGTGAACGCTCAACATCAAGAAAGAAATCTCTGAGTGGCTT 2060
 Db 1911 CTATGCCAAGAGGGAAGAACTCTTCAACAGAGGAAATCTCTGAGTGGGT 1970
 QY 2061 CTCCAAAGTGGTTCTTCTCAACTGCAAGTGAAGTGTGTCGGGCAACAGGAGGG 2120
 Db 1971 CTCAGGAGGTGCTCTCTCAACTGCAAGTGAAGTGTGTCGGGCAACAGGAGG 2030
 QY 2121 GATCATGAGGGGAGCCACCTGCTGTTTGAATGATGGCATGTGACAGGGAGATT 2180
 Db 2031 GATCATGAGGGGAGCCACCTGCTGTTTGAATGATGGCATGTGACAGGGAGTA 2090
 QY 2181 CAGTGAATGAAGAGTGAAGTGCCTGTACAAAGTCCCGCAATGATTTCTGCTGCAATGA 2240
 Db 2091 TAGTGAATGAGACAGATGCGAGTGCCTGTAAAGTGGCCAGATGACTTCTGTCATATGA 2150
 QY 2241 GAACCAACAGTGTGATCCCAAGAGATGAGTACCTGTGTCGGAGCGGACCTTTCGG 2300
 Db 2151 GAACCAACAGTGTGATCCCAAGAGATGAGTACCTGTGTCGGAGCGGACCTTTCGG 2210
 QY 2301 GATCGCTCTGACCATCTTCCGCTGCTGGGATCCCTGATCCTCTTCTGCTGGGGT 2360
 Db 2211 GATCGCACTCACCTCTTTTGGGCTGCTGGGCAATTTTCTGACAGCTTTTGTCTGGGT 2270
 QY 2361 CTTTATCAAGTTTCAAGAACCTCCCATCTGTAAGGCCAACCAACCGGAGTTTCTCTACCT 2420
 Db 2271 GTTTATCAAGTTTCCGCAACACACCCATTTGTCAAGGCCAACCAACCGAGAGCTCTCTACT 2330
 QY 2421 GGTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTGCTCATCTTTCATCGGAGGCCAG 2480
 Db 2331 CTTCTCTTCTCTCCCTCTCTGCTGCTTCTCAGCTGCTCTGTTTCTTCTATCGGAGGCCCA 2390
 QY 2481 GGACTGGACCTGTGCGCTCCGGCAACCGGCTTTTGGCATCAGCTTCTGCTGTGATCTC 2540

Db 2391 GGACTGGAGTGGCGCTTGGCCAGCGGCTTTGGCATCAGCTTCTGCTGTGATCTC 2450
 QY 2541 CTGCACTCTGTGTAAGAACCAACCGGCTGCTGCTCTTTCAGGCGCAAGATCCCCACAG 2600
 Db 2451 ATGCATCTGTGTGAACCAACCGTGTCTCTCTGCTGTTTGAAGSACCAAGATCCCCACAG 2510
 QY 2601 CTTCAACGCAAGTGGTGGGCTCAACCTGCACTTCTCTGCTGCTCTCTCTGCTCTCT 2660
 Db 2511 CTTCAACGCAAGTGGTGGGCTCAACCTGCACTTCTCTGCTGCTCTCTCTGCTCTCT 2570
 QY 2661 GGTGCAAACTCGTCACTCTGCACTCATCTGGCTCTACACCGCGCTCTCTCTGCACTACAGAA 2720
 Db 2571 CATGCAAGTTGTCTCTGTGTGATCTGCTCTACACCGCGCTCTCTCTGCACTACAGAA 2630
 QY 2721 CCATGAGCTGGAGCAAGGTCATCTTCACTCATCTGCAAGGCTCTCTCTGCACTACAGAA 2780
 Db 2631 CCAGGAGCTGGAGGATGAGATCATCTTCACTCATCTGCAAGGCTCTCTCTGCACTACAGAA 2690
 QY 2781 GGGCTTCTCATCGGCTACACCTCTCTCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCT 2840
 Db 2691 GGGCTTCTCATCGGCTACACCTCTCTCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCT 2750
 QY 2841 GTCCCGTAAGTGTGCGGAGAACTTCAACGAGGCTAAGTTTCACTCACTTCAAGATTTGAT 2900
 Db 2751 GTCCCGTAAGTGTGCGGAGAACTTCAATGAAGCAAGTTTCACTCACTTCAAGATTTGAT 2810
 QY 2901 CTTCTTCTCATCGTCTGCT 2960
 Db 2811 CTTCTTCTCATCGTCTGCT 2870
 QY 2961 GTCCCGCTGTGAGGATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3020
 Db 2871 CTTCTCTGTAGAGTGTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2930
 QY 3021 CTTCAACAGTGTATCATCT 3080
 Db 2931 CTTCAACAGTGTATCATCT 2990
 QY 3081 CTGCAAGCAGCGGCGCCACCGCTTCAAGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 3140
 Db 2991 TTGCAAGCAGCGGCGCCACCGCTTCAAGTGGGCGCGCGCGCGCGCGCGCGCGCGCG 3050
 QY 3141 CGCTCTGCAAGCGCTTCAAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3200
 Db 3051 CGTCTCCGCAAGCGGCTTCAAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3110
 QY 3201 CACTCTGGGCGCGCGCTTCAAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3260
 Db 3111 CATCAGCAGCAAGAGCAACA-----GCGAAGACCCATTTCACAGCCCGAGAGGCAAG 3165
 QY 3261 CGGCAAGCGCGCGCTTCAAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3320
 Db 3166 CAGCAGCAGCGCTTGGCGCTTAAACCGCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3225
 QY 3321 CAGCGCAGCGCGCGCTTCAAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3380
 Db 3226 CAGCAGCAACGATCTCAGCAGCGCGCTTCAAGCGCTTCTCTCTCTCTCTCTCTCTCTCT 3280

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 20:20:06 ; Search time 1807 Seconds
(without alignments)
12009.467 Million cell updates/sec

Title: US-10-016-496-1
Perfect score: 4134
Sequence: 1 aatccgtgtgtcggttc.....aagcgccgcacagcaacgg 4134

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4134886 seqs, 2624710521 residues 8269772

Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 23sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4134	100.0	4134	6	Aad41631 SKCar DNA
2	4134	100.0	4134	6	Abk14910 DNA encod
3	4134	100.0	4134	6	AbL59964 Dogfish s
4	4134	100.0	4134	10	Adh10916 Shark pol
5	4134	100.0	4134	10	Aad64738 Dogfish s
6	4134	100.0	4134	12	Adi19962 Dogfish s
7	4098	99.1	4131	2	Aat89290 Dogfish s
8	1745.2	42.2	3234	2	Aaz31049 Human cal
9	1745.2	42.2	3234	2	Aax30922 Human cal
10	1745.2	42.2	3234	2	Aal43269 Human cal
11	1745.2	42.2	3237	12	Ado29824 Human GPC
12	1745.2	42.2	3237	8	Abz42663 Human cal
13	1745.2	42.2	3783	10	Abx74489 Human cdn
14	1745.2	42.2	3809	2	Aat61382 Parathyro
15	1745.2	42.2	3809	2	Aav26964 Human par
16	1745.2	42.2	3809	2	Aat95859 Human par
17	1745.2	42.2	3809	2	Aaz25055 Human par
18	1745.2	42.2	3809	2	Aav82485 Human par
19	1745.2	42.2	3809	3	Aaz89298 Human cal
20	1745.2	42.2	3809	5	Aaf86094 Small hum
21	1745.2	42.2	3809	6	Aai72122 cDNA enco

22	1743.6	42.2	3234	3	AAZ51398 Human wil
23	1743.6	42.2	3234	10	ACA56834 Human sig
24	1743.6	42.2	3234	12	ADI56630 Human pol
25	1743.6	42.2	3361	8	ABS57393 cDNA enco
26	1738	42.0	5275	2	AAV26962 Bovine pa
27	1738	42.0	5275	2	AAT95857 Bovine pa
28	1738	42.0	5275	2	AAZ25053 Bovine pa
29	1738	42.0	5275	2	AAV82483 Bovine pa
30	1738	42.0	5275	3	Aaz89296 Bovine ca
31	1738	42.0	5275	6	Aai72120 cDNA enco
32	1737.2	42.0	3237	4	AA506331 DNA enco
33	1703.6	41.2	5006	2	AAT61381 Parathyro
34	1703.6	41.2	5006	2	AAV26963 Human par
35	1703.6	41.2	5006	2	AAV25054 Human par
36	1703.6	41.2	5006	2	AAV82484 Human par
37	1703.6	41.2	5006	3	Aaz89297 Human cal
38	1703.6	41.2	5006	5	Aaf86093 Large hum
39	1703.6	41.2	5006	6	AAI72121 cDNA enco
40	1702	41.2	5006	2	AAT95858 Human par
41	1692.6	40.9	4550	12	ADO30115 Mouse GPC
42	1681.6	40.7	5046	4	AA501709 Chicken c
43	1678.2	40.6	4113	10	ABT41930 Toxicity
44	1678.2	40.6	4113	12	ADP72828 Renal tox
45	1678.2	40.6	4131	2	AAV26965 Rat kidne

ALIGNMENTS

RESULT 1
AAD41631
ID AAD41631 standard; DNA; 4134 BP.

XX AAD41631;

DT 30-OCT-2002 (first entry)

DE SKCar DNA of the invention.

KW Marine fish; fresh water; polyvalent cation sensing receptor; PVCr;

KW immune function; fat content; receptor; ds.

XX Unidentified.

XX WO200230215-A2.

XX 18-APR-2002.

PF 11-OCT-2001; 2001WO-US031625.

PR 12-OCT-2000; 2000US-00687373.

XX (AQUA-) AQUABIO PROD SCI LLC.

PA Harris HW, Russell DR, Nearing J, Betka M;

XX WPI; 2002-394428/42.

DR Growing marine fish in fresh water involves adding polyvalent cation receptor modulator and feed containing sodium chloride.

PT Disclosure; Fig 14; 71pp; English.

PS The invention relates to a method for growing marine fish in fresh water.
XX The method involves: adding at least one polyvalent cation sensing receptor (PVCr) modulator to fresh water to modulate or maintain expression and/or sensitivity of at least one PVCr in atleast one tissue; transferring the marine fish to the fresh water, modified according to the previous step; and adding feed containing NaCl to contribute to a significant increased level of the PVCr modulator in serum of the marine fish. The invention is useful for growing marine fish in freshwater e.g. mackerel, pollock, sea bass, sword fish, tuna, winter flounder and summer flounder. The marine fish cultured by the method have stronger immune

Db 1141 GTTAAAGGAGCATCTGTATTGACTTCAGTGTAGATGATCTCTCAGTACTACACCCAGAAG 1200
Qy 1201 CAGTTGGAGTTTCATCGCCAGAGCTCATCCAGAACTCTCGGCCAAGGTTCATCGTGTCTTC 1260
Db 1201 CAGTTGGAGTTTCATCGCCAGAGCTCATCCAGAACTCTCGGCCAAGGTTCATCGTGTCTTC 1260
Qy 1261 TCCAAATGGCCCCGAGCTGAGAGCGGTTCATCCAGGAGATAGTTTCGAGAGAAACATACCGAT 1320
Db 1261 TCCAAATGGCCCCGAGCTGAGAGCGGTTCATCCAGGAGATAGTTTCGAGAGAAACATACCGAT 1320
Qy 1321 CGGATCTGGCTGGCCAGAGAGCTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Db 1321 CGGATCTGGCTGGCCAGAGAGCTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Qy 1381 TTCCACGTGGTGGCCGAGCACCATCGGCTTCGCTTCAGGGCGGGCGGTATCCAGGGTTC 1440
Db 1381 TTCCACGTGGTGGCCGAGCACCATCGGCTTCGCTTCAGGGCGGGCGGTATCCAGGGTTC 1440
Qy 1441 AACAAAGTTCCCTGAAGAGGTCCACCCAGCAGGTCTCGGACAAATGGGTTTGTCAAGGAG 1500
Db 1441 AACAAAGTTCCCTGAAGAGGTCCACCCAGCAGGTCTCGGACAAATGGGTTTGTCAAGGAG 1500
Qy 1501 TTCTGGAGGAGACCTTCAACTGTACTTCAACGAGAGACCTTGACGAGCTGAAGAAT 1560
Db 1501 TTCTGGAGGAGACCTTCAACTGTACTTCAACGAGAGACCTTGACGAGCTGAAGAAT 1560
Qy 1561 TCCAAAGTTCCTCGCAGCAGACCGGCGCTCAAGGGAGCGGTCCAAAGCGGGGAACTCC 1620
Db 1561 TCCAAAGTTCCTCGCAGCAGACCGGCGCTCAAGGGAGCGGTCCAAAGCGGGGAACTCC 1620
Qy 1621 AGACGGAGACGCCCTACGCCACCCCTGCACTGGGAGGAGAACATCACAGCGGTGGAGACC 1680
Db 1621 AGACGGAGACGCCCTACGCCACCCCTGCACTGGGAGGAGAACATCACAGCGGTGGAGACC 1680
Qy 1681 CCTTACCTGGATTATACACACCTGAGGATCTCTCAATGATATAGTGGCCGTCTACTCC 1740
Db 1681 CCTTACCTGGATTATACACACCTGAGGATCTCTCAATGATATAGTGGCCGTCTACTCC 1740
Qy 1741 ATTGCTCAGCCCTCGAGAGATCACCTCTTGCRAACCGGACGGGATCTTTGCAAAAC 1800
Db 1741 ATTGCTCAGCCCTCGAGAGATCACCTCTTGCRAACCGGACGGGATCTTTGCAAAAC 1800
Qy 1801 GGATCTTGTGCAGATATTAATAAAGTTGAGGCGCTGGCAGGTCCTCAACCATCTGTGCAT 1860
Db 1801 GGATCTTGTGCAGATATTAATAAAGTTGAGGCGCTGGCAGGTCCTCAACCATCTGTGCAT 1860
Qy 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
Qy 1921 GGGAACTACACCATTTACACTGGCAGCTCTCCGAGAGGATGAATCGGTTGTTCAT 1980
Db 1921 GGGAACTACACCATTTACACTGGCAGCTCTCCGAGAGGATGAATCGGTTGTTCAT 1980
Qy 1981 GAGGTGGGCACTACAAGCCCTACGCTAAGCCAGTGACCGACTCAACATCAACGAAAAG 2040
Db 1981 GAGGTGGGCACTACAAGCCCTACGCTAAGCCAGTGACCGACTCAACATCAACGAAAAG 2040
Qy 2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCTTTCTCCAAGTCAAGTCGAGACTGT 2100
Db 2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCTTTCTCCAAGTCAAGTCGAGACTGT 2100
Qy 2101 GTGCCGGGACCCAGGAAGGGATCATCGAGGGGAGCCCACTGCTGCTTTGAATGCATG 2160
Db 2101 GTGCCGGGACCCAGGAAGGGATCATCGAGGGGAGCCCACTGCTGCTTTGAATGCATG 2160
Qy 2161 GCATGTGAGAGGAGTTCAGTGTGAAACAGATGCAAGTGGGTGACAAAGTGCCCG 2220
Db 2161 GCATGTGAGAGGAGTTCAGTGTGAAACAGATGCAAGTGGGTGACAAAGTGCCCG 2220
Qy 2221 AATGATTTCTGTGCAATGAGAAACACACGCTGTCATCGCCAGGAGATCGAGTACTCG 2280

Db 2221 AATGATTTCTGTGCAATGAGAAACACACGCTCGTGCATCGCCAAGGAGATCGAGTACTCG 2280
Qy 2281 TCGTGGACGAGCGCTTCGGGATCGCTCTCACCATCTTCGCCGTACTTGGGCATCCTGATC 2340
Db 2281 TCGTGGACGAGCGCTTCGGGATCGCTCTCACCATCTTCGCCGTACTTGGGCATCCTGATC 2340
Qy 2341 ACCTCTCTGTGTGGGGTCTTTCATCAAGTTTCAAGAACTATCCCATCTGTTGAAGGCCACC 2400
Db 2341 ACCTCTCTGTGTGGGGTCTTTCATCAAGTTTCAAGAACTATCCCATCTGTTGAAGGCCACC 2400
Qy 2401 AACCGGAGTTGCTCCTACCTGCTCTCTCTCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
Db 2401 AACCGGAGTTGCTCCTACCTGCTCTCTCTCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
Qy 2461 ATCTTATCGCGCAGCGCAGGGAATG9ACCTGTGGCTCGGCCAACACCGGCTTTTGGCATC 2520
Db 2461 ATCTTATCGCGCAGCGCAGGGAATG9ACCTGTGGCTCGGCCAACACCGGCTTTTGGCATC 2520
Qy 2521 AGCTTCGTCTGTGCATCTCTCCTGATCTCTGTTGAAGAACCAACCGGCTGCTGGTCTTC 2580
Db 2521 AGCTTCGTCTGTGCATCTCTCCTGATCTCTCTGATCTCTGTTGAAGAACCAACCGGCTGCTGGTCTTC 2580
Qy 2581 GAGGCCAAGATCCCCACACGAGCTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCTCTC 2640
Db 2581 GAGGCCAAGATCCCCACACGAGCTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCTCTC 2640
Qy 2641 CTGGTCTCTCTGATCTCTGTTGAAATCGTCACTGATCATCTGGCTCTACACCGG 2700
Db 2641 CTGGTCTCTCTGATCTCTGTTGAAATCGTCACTGATCATCTGGCTCTACACCGG 2700
Qy 2701 CCTCCCTCCAGCTACAGGAACCATGAGTGGAGGAGAGGTCTATCTTCACTACCTGGAC 2760
Db 2701 CCTCCCTCCAGCTACAGGAACCATGAGTGGAGGAGAGGTCTATCTTCACTACCTGGAC 2760
Qy 2761 GAGGGTCTGCTCATGCGCTGGGCTTCTCATCGGTACACCTGCTCTCGCCGCTATC 2820
Db 2761 GAGGGTCTGCTCATGCGCTGGGCTTCTCATCGGTACACCTGCTCTCGCCGCTATC 2820
Qy 2821 TGCTTCTTCTCGCTTCAAGTCCCGTAACTGCGCGGAGAACTTCAACGAGGCTAAGTTC 2880
Db 2821 TGCTTCTTCTCGCTTCAAGTCCCGTAACTGCGCGGAGAACTTCAACGAGGCTAAGTTC 2880
Qy 2881 ATCACTTCAAGCTGTGTGATCTTCTCATCGTCTGATCTCTTCTCATCTCCCGCTATGTC 2940
Db 2881 ATCACTTCAAGCTGTGTGATCTTCTCATCGTCTGATCTCTTCTCATCTCCCGCTATGTC 2940
Qy 2941 AGACCTACGGGAAGTTTGTGTCGGCGGTGGAGGTGATTCGATCTCTGCTCTCAGCTTC 3000
Db 2941 AGACCTACGGGAAGTTTGTGTCGGCGGTGGAGGTGATTCGATCTCTGCTCTCAGCTTC 3000
Qy 3001 GGGCTGTGGGCTGCAATTTACTTCAACAAAGTGTATCATCATCTGTTCAAGCGCTGCCGT 3060
Db 3001 GGGCTGTGGGCTGCAATTTACTTCAACAAAGTGTATCATCATCTGTTCAAGCGCTGCCGT 3060
Qy 3061 AACACCATCGAGAGGTGCGTGCAGCAGGGGGCCACCGCTTCAAGGTGGCGGCGCG 3120
Db 3061 AACACCATCGAGAGGTGCGTGCAGCAGGGGGCCACCGCTTCAAGGTGGCGGCGCG 3120
Qy 3121 GCCACCTCGGGCGCAGCGCGCTCGCAAGCGCTCCAGAGCTGTGGCTCCAC 3180
Db 3121 GCCACCTCGGGCGCAGCGCGCTCGCAAGCGCTCCAGAGCTGTGGCTCCAC 3180
Qy 3181 ATCTCTCTCGCCCGCTCTGCTCCACTCGGGCGGGGCTCACCATGAGATGAGCGCTGC 3240
Db 3181 ATCTCTCTCGCCCGCTCTGCTCCACTCGGGCGGGGCTCACCATGAGATGAGCGCTGC 3240
Qy 3241 AGCAGCAGAGGTGAGTTCGSCAGGCGCAGCTCACTGCTGCTGCTGCTGCTGAGGAG 3300
Db 3241 AGCAGCAGAGGTGAGTTCGSCAGGCGCAGCTCACTGCTGCTGCTGCTGCTGAGGAG 3300
Qy 3301 ACAGGCGGATACGCCACCTCAGCGCCGAGCGGCGCAGAGAACTCGGCGGATGCGCG 3360
Db 3301 ACAGGCGGATACGCCACCTCAGCGCCGAGCGGCGCAGAGAACTCGGCGGATGCGCG 3360

QY	3361	AGCGGCGACGACCTGCTGATCTAGACACACACACGAGGCGCGCTCAGAAATGGAGGCC	3420
DB	3361	AGCGGCGACGACCTGCTGATCTAGACACACACACGAGGCGCGCTCAGAAATGGAGGCC	3420
QY	3421	CAGCGCGCAACGATGCGCGATACAGGGGCGCGCGCAAGGGGACCTAGATCGCGG	3480
DB	3421	CAGCGCGCAACGATGCGCGATACAGGGGCGCGCGCAAGGGGACCTAGATCGCGG	3480
QY	3481	GCGGCGACGAGGAGCGCGCCCACTATGAGGAGAACTTAATCCAACTCTCTCCATCAAC	3540
DB	3481	GCGGCGACGAGGAGCGCGCCCACTATGAGGAGAACTTAATCCAACTCTCTCCATCAAC	3540
QY	3541	CCCAAGAACATCTCCAGCGACGACCGCTGCGCAACTGACATCAACTCTCAACGGTGGC	3600
DB	3541	CCCAAGAACATCTCCAGCGACGACCGCTGCGCAACTGACATCAACTCTCAACGGTGGC	3600
QY	3601	TGCGCAACCTCTCCCTCTCCGCGCACTTTGCGTTTGTGAAGATTGCGACATCTGCACT	3660
DB	3601	TGCGCAACCTCTCCCTCTCCGCGCACTTTGCGTTTGTGAAGATTGCGACATCTGCACT	3660
QY	3661	TGCTTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGGATGGAATATCAAC	3720
DB	3661	TGCTTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGGATGGAATATCAAC	3720
QY	3721	ATAATGAGTTGCAATATGAGTGACGAGGTTGTCTCAAGTATCTGAACTATCTGAAT	3780
DB	3721	ATAATGAGTTGCAATATGAGTGACGAGGTTGTCTCAAGTATCTGAACTATCTGAAT	3780
QY	3781	ATCTGAACCTATTTATCTCTGAAATTTGATTAACAACTTTTGAAGTATTTTGTAGTACA	3840
DB	3781	ATCTGAACCTATTTATCTCTGAAATTTGATTAACAACTTTTGAAGTATTTTGTAGTACA	3840
QY	3841	TTATGTTCAACATTTGTCAGATTAATTTGTTTACAACTATTAAGTACACCTGAGCAGT	3900
DB	3841	TTATGTTCAACATTTGTCAGATTAATTTGTTTACAACTATTAAGTACACCTGAGCAGT	3900
QY	3901	GACTGAGTTGCCACTGTGATGACGAGGTTGTTTATTAACATTTATCTGAACTCTGGA	3960
DB	3901	GACTGAGTTGCCACTGTGATGACGAGGTTGTTTATTAACATTTATCTGAACTCTGGA	3960
QY	3961	TTGCAACAGGAATATAATGACTGTAAACAAAAAATTTGTTGATTTCTTAAAAATGCAAT	4020
DB	3961	TTGCAACAGGAATATAATGACTGTAAACAAAAAATTTGTTGATTTCTTAAAAATGCAAT	4020
QY	4021	TGTAATCAGATGTGTAATTTGTTTATTTCTGTAATTAATGCAATTTCTTTGATA	4080
DB	4021	TGTAATCAGATGTGTAATTTGTTTATTTCTGTAATTAATGCAATTTCTTTGATA	4080
QY	4081	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCGCAGCAACGG	4134
DB	4081	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCGCAGCAACGG	4134

RESULT 3	
ID	ABL59964
XX	ABL59964 standard; DNA; 4134 BP.
AC	ABL59964;
XX	
DT	23-JUL-2002 (first entry)
XX	Dogfish shark kidney cation receptor (SKCar) DNA SEQ ID NO:17.
DE	Fish; polyvalent cation sensing receptor; PVCR; anadromous fish;
XX	polyvalent cation sensing receptor modulator; PVCR modulator; feed;
KW	atlantic salmon; arctic char; rainbow trout; gene; ds.
XX	Squalus acanthias.
OS	
XX	
PH	Key
FT	Location/Qualifiers
CD	439..3522
FT	/*tag= a

/product= "Dogfish shark kidney cation receptor"	
WO200230182-A2.	
18-APR-2002.	
11-OCT-2001; 2001WO-US031562.	
12-OCT-2000; 2000US-00687372.	
12-OCT-2000; 2000US-00687476.	
12-OCT-2000; 2000US-00687477.	
(AQUA-) AQUABIO PROD SCI LLC.	
Harris WH, Russell DR, Nearing J, Betka M;	
WPI; 2002-416815/44.	
P-PSDB; ABB78761.	
Improving the raising of pre-adult anadromous fish e.g. salmon involves adding polyvalent cation sensing receptor modulator and a feed containing an agent that increases level of modulator in serum of fish.	
Example 19; Fig 28; 201pp; English.	
The present invention describes a method for improving the raising of pre-adult anadromous fish maintained in fresh water prior to transfer to seawater. The method involves: (a) adding at least one polyvalent cation sensing receptor (PVCR) modulator to the fresh water; and (b) adding a feed containing an agent that increases the level of PVCR modulator in the serum of fish. The PVCR modulator has anabolic activity. The method can be used for improving the raising of pre-adult anadromous fish e.g. salmon, char and trout, maintained in fresh water prior to transfer to seawater. The present sequence encodes dogfish shark kidney cation receptor (SKCar), which is relative to the PVCRs from salmon, char and trout	
Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other;	
Query Match 100.0%; Score 4134; DB 6; Length 4134;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 AANTCCGTTCTGTCGGTTCAAGTCTCCTCCAGTGCAGAAATGAGAAATGGTGGTC 60	
DB 1 AANTCCGTTCTGTCGGTTCAAGTCTCCTCCAGTGCAGAAATGAGAAATGGTGGTC 60	
QY 61 GCCATTACAGGAACATGCTACATCTGTGTTAATGAATATTTGTCAGTTATCTGAAGGT 120	
DB 61 GCCATTACAGGAACATGCTACATCTGTGTTAATGAATATTTGTCAGTTATCTGAAGGT 120	
QY 121 TATTAATAATGTTTCTGCAAGGATGGTTTCAAGAGAAATCAATTTCTGACGTTTCCCAT 180	
DB 121 TATTAATAATGTTTCTGCAAGGATGGTTTCAAGAGAAATCAATTTCTGACGTTTCCCAT 180	
QY 181 GTCATTCTATGAATTAAGTACCAAGGATGTAAACAAATGGAACAGCTGAGGACCCAC 240	
DB 181 GTCATTCTATGAATTAAGTACCAAGGATGTAAACAAATGGAACAGCTGAGGACCCAC 240	
QY 241 GTTCACCCCTTTCTGGAGCATACGATCAACCCCTGAAGGAGATGGAAGATTTAGGAGGAA 300	
DB 241 GTTCACCCCTTTCTGGAGCATACGATCAACCCCTGAAGGAGATGGAAGATTTAGGAGGAA 300	
QY 301 ATGGGATTTGATCTTCCAGGATTTCTGTTAAAGCATCCCTCACCATTACAAAGATAA 360	
DB 301 ATGGGATTTGATCTTCCAGGATTTCTGTTAAAGCATCCCTCACCATTACAAAGATAA 360	
QY 361 GCAGAAATCTCCAGGATCTCTGTAAACGGGCTGGCGTAGTGTGGCTTTGGTCAAGGAA 420	
DB 361 GCAGAAATCTCCAGGATCTCTGTAAACGGGCTGGCGTAGTGTGGCTTTGGTCAAGGAA 420	
QY 421 CAGAGACAGGGCTGCACAAATGGCTCAGCTTCATCGCACTTATCTTGGATTTACA 480	

Db 421 CAGAGACAGGGGTCGACAAATGGCTCAGCTTCACCTGCCAACTCTTATTCTTGGGATTTACA 480
Qy 481 CTCCTACAGTCGTACAAATGCTCTCAGGGATGTTCCAAACCAAGAGGGGCCCAAGAAAGGA 540
Db 481 CTCCTACAGTCGTACAAATGCTCTCAGGGATGTTCCAAACCAAGAGGGGCCCAAGAAAGGA 540
Qy 541 GACATCATCTGGGAGGTCCTTCCCAATACATTTGAGTAGCGCCCAAGAGATCAGGAC 600
Db 541 GACATCATCTGGGAGGTCCTTCCCAATACATTTGAGTAGCGCCCAAGAGATCAGGAC 600
Qy 601 TTAATAATCGAGACCGGAGCGGACAAAATGTTATTCGGTACAAATTTTCGAGGGCTTCGGATGG 660
Db 601 TTAATAATCGAGACCGGAGCGGACAAAATGTTATTCGGTACAAATTTTCGAGGGCTTCGGATGG 660
Qy 661 CTCGAGGGATGATATTCGCAATTCGAATTAAGAGATTAAACAAGTAGCTTTCTGCGCCAAAT 720
Db 661 CTCGAGGGATGATATTCGCAATTCGAATTAAGAGATTAAACAAGTAGCTTTCTGCGCCAAAT 720
Qy 721 ATCACCTGGGATATCGATATTTACACAGCTGTACACCGTGTCCAAAGCGCTAGAGGCA 780
Db 721 ATCACCTGGGATATCGGATATTTGACACAGCTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780
Qy 781 ACACCTCAGCTTTGTGGCCGAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
Db 781 ACACCTCAGCTTTGTGGCCGAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
Qy 841 TGCTCTGACCATATCCATCCCAATAGCAGTGGTCCGGGCAACCGGCTCAGGATCTCC 900
Db 841 TGCTCTGACCATATCCATCCCAATAGCAGTGGTCCGGGCAACCGGCTCAGGATCTCC 900
Qy 901 ACGGCTGTGGCCAACTTATTTGGGATATTTTACATTTCCACAGGTGAGTATGCTCTCTCG 960
Db 901 ACGGCTGTGGCCAACTTATTTGGGATATTTTACATTTCCACAGGTGAGTATGCTCTCTCG 960
Qy 961 AGCAGGCTGCTCAGCAACAAGAAATGAGTACAAAGGCTTCTGAGGACCATCCCAATGAT 1020
Db 961 AGCAGGCTGCTCAGCAACAAGAAATGAGTACAAAGGCTTCTGAGGACCATCCCAATGAT 1020
Qy 1021 GAGCAACAGGCGCAGCGCATGCGCGAGATCATCGAGCATCTCCAGTGAACCTGGTGGA 1080
Db 1021 GAGCAACAGGCGCAGCGCATGCGCGAGATCATCGAGCATCTCCAGTGAACCTGGTGGA 1080
Qy 1081 ACCCTGGCAGCGGACGATGACTATGCGCGCCGAGCATTTGAAGTTCCGGGAGGAGGCC 1140
Db 1081 ACCCTGGCAGCGGACGATGACTATGCGCGCCGAGCATTTGAAGTTCCGGGAGGAGGCC 1140
Qy 1141 GTTAAGAGGACATCTGATTTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAG 1200
Db 1141 GTTAAGAGGACATCTGATTTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAG 1200
Qy 1201 CAGTTGGAGTTTCATCGCCGACGTCATCCAGAACTCCTCGGCAAGGTGATCGTGTCTTC 1260
Db 1201 CAGTTGGAGTTTCATCGCCGACGTCATCCAGAACTCCTCGGCAAGGTGATCGTGTCTTC 1260
Qy 1261 TCCAAATGGCCCGACCTGAGCGGCTCATCCAGAGAGATGATTCGAGAGAAATCACCGAT 1320
Db 1261 TCCAAATGGCCCGACCTGAGCGGCTCATCCAGAGAGATGATTCGAGAGAAATCACCGAT 1320
Qy 1321 CGGATCTGGCTGCGCAGAGGCTTTGGGCGAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Db 1321 CGGATCTGGCTGCGCAGAGGCTTTGGGCGAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Qy 1381 TTCCACGTTGGTCCGGGACCAATCGGCTTCGCTCTCAGGGGCGGCGTATCCAGGGTTC 1440
Db 1381 TTCCACGTTGGTCCGGGACCAATCGGCTTCGCTCTCAGGGGCGGCGTATCCAGGGTTC 1440
Qy 1441 AACAAAGTTCCCTGAAGGAGTCCACCCACAGGTCCTCGGCAATGGGTTTGTCAAGGAG 1500
Db 1441 AACAAAGTTCCCTGAAGGAGTCCACCCACAGGTCCTCGGCAATGGGTTTGTCAAGGAG 1500
Qy 1501 TTCTCGGAGGACCTTCAACTGCTACTTCAACGAGAGAGACCTTCAACGAGTGAAGAT 1560
Db 1501 TTCTCGGAGGACCTTCAACTGCTACTTCAACGAGAGAGACCTTCAACGAGTGAAGAT 1560

Qy 1561 TCCAAGGTGCCCTCGCACGACCGGCGGCTCAAGGGGACGGCTCCAAAGCGGGAACTCC 1620
Db 1561 TCCAAGGTGCCCTCGCACGACCGGCGGCTCAAGGGGACGGCTCCAAAGCGGGAACTCC 1620
Qy 1621 AGAGGACAGCCCTAGCCACACCTGCATCTGGGAGGAGAAACATCACAGCGTGGAGACC 1680
Db 1621 AGAGGACAGCCCTAGCCACACCTGCATCTGGGAGGAGAAACATCACAGCGTGGAGACC 1680
Qy 1681 CCCTACCTGATTTATACACACCTGAGGATCTCTCAAAATGTATACGTGGCGTCTACTCC 1740
Db 1681 CCCTACCTGATTTATACACACCTGAGGATCTCTCAAAATGTATACGTGGCGTCTACTCC 1740
Qy 1741 ATTGCTCAGCCCTGCAAGACATCCACTTTGAAACCCGGACCGGCATCTTTGCAAAAC 1800
Db 1741 ATTGCTCAGCCCTGCAAGACATCCACTTTGAAACCCGGACCGGCATCTTTGCAAAAC 1800
Qy 1801 GGATCTTGTGAGATTTAAAAAAGTTGAGCGCTGCGAGCTCTCAACCATCTGCTGCAT 1860
Db 1801 GGATCTTGTGAGATTTAAAAAAGTTGAGCGCTGCGAGCTCTCAACCATCTGCTGCAT 1860
Qy 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
Qy 1921 GGGAACTACACCATTTAATCGCAGCTCTCCGAGAGGATGAATCGGTGTTGTTCCAT 1980
Db 1921 GGGAACTACACCATTTAATCGCAGCTCTCCGAGAGGATGAATCGGTGTTGTTCCAT 1980
Qy 1981 GAGTGGGCAACTACAAACGCTACGTTAAGCCAGTGACCGACTCAACATCAACGAAAAG 2040
Db 1981 GAGTGGGCAACTACAAACGCTACGTTAAGCCAGTGACCGACTCAACATCAACGAAAAG 2040
Qy 2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTCCGAGCTGT 2100
Db 2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTCCGAGCTGT 2100
Qy 2101 GTGCGGGACACAGGAGGGGATCATCGAGGGGAGCCACCTGCTGCTTTGAAATGCATG 2160
Db 2101 GTGCGGGACACAGGAGGGGATCATCGAGGGGAGGGATCATCGAGGGGAGCCACCTGCTGCTTTGAAATGCATG 2160
Qy 2161 GCATGTTCGAGAGGAGTTCACTGATGATAAAGCATGATGATGCGTGTGTAAGAGTCCCG 2220
Db 2161 GCATGTTCGAGAGGAGTTCACTGATGATAAAGCATGATGATGCGTGTGTAAGAGTCCCG 2220
Qy 2221 AATGATTTCTGCTGATGAGAACACACGTCGTGATGCGCAAGGAGATCGAGTACCTG 2280
Db 2221 AATGATTTCTGCTGATGAGAACACACGTCGTGATGCGCAAGGAGATCGAGTACCTG 2280
Qy 2281 TCGTGAACGAGCCCTTCGGGATCGCTCTGACCATCTTGGCCGTAATCGGCACTCTGATC 2340
Db 2281 TCGTGAACGAGCCCTTCGGGATCGCTCTGACCATCTTGGCCGTAATCGGCACTCTGATC 2340
Qy 2341 ACCTCCTTCTGCTGGGGTCTTTCATCAGTTTCAAGAACACTCCCATCGTGAAGGCGACC 2400
Db 2341 ACCTCCTTCTGCTGGGGTCTTTCATCAGTTTCAAGAACACTCCCATCGTGAAGGCGACC 2400
Qy 2401 AACCGGAGTTGCTTCTACCTGCTGCTTCTTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460
Db 2401 AACCGGAGTTGCTTCTACCTGCTGCTTCTTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460
Qy 2461 ATCTTANTCGGAGAGCCAGGAGTGGACCTGTCGCTCGGCCAACCGGCTTTGGCATC 2520
Db 2461 ATCTTANTCGGAGAGCCAGGAGTGGACCTGTCGCTCGGCCAACCGGCTTTGGCATC 2520
Qy 2521 AGCTTGTCTGTGATCTCTCTGATCTCTGATGAGAACCAACCGGCTGCTGCTGCTTTC 2580
Db 2521 AGCTTGTCTGTGATCTCTCTGATCTCTGATGAGAACCAACCGGCTGCTGCTGCTTTC 2580
Qy 2581 GAGGCCAAGATCCCAACAGCTTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCCTC 2640
Db 2581 GAGGCCAAGATCCCAACAGCTTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCCTC 2640

CC The invention comprises the amino acid and coding sequences of polyvalent
 CC cation sensing receptor (PVCr) proteins from Atlantic salmon. The DNA and
 CC protein sequences of the invention are useful in the commercial raising
 CC of Atlantic salmon and the restoration of wild Atlantic salmon
 CC populations, especially in the transfer from freshwater to seawater with
 CC increased growth and reduced mortality. The present DNA sequence encodes
 CC a shark PVCr-related protein.

XX	Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other;	
QQ	Query Match 100.0%; Score 4134; DB 10; Length 4134;	
QQ	Best Local Similarity 100.0%; Pred. No. 0;	
QQ	Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AATTCGGTGTCTGGTTCAGTCCCAAGTCTCTCCAGTGCAGAAATGAGAATGGTGTGTC 60	
DB	1 AATTCGGTGTCTGGTTCAGTCCCAAGTCTCTCCAGTGCAGAAATGAGAATGGTGTGTC 60	
QY	61 GCATTACAGGAACATGCACTACATCTGTGTTAATGAATAATGTCATGTTGAAAGGT 120	
DB	61 GCATTACAGGAACATGCACTACATCTGTGTTAATGAATAATGTCATGTTGAAAGGT 120	
QY	121 TATTAATAATGTTTCTGCAAGGATGCTTCAAGAGAAATCAATTCGACGTTTTCCCAT 180	
DB	121 TATTAATAATGTTTCTGCAAGGATGCTTCAAGAGAAATCAATTCGACGTTTTCCCAT 180	
QY	181 GTCAATTGATGAATACTGACCAAGGATGTAACAAATGGAACAAAGCTGAGGACAC 240	
DB	181 GTCAATTGATGAATACTGACCAAGGATGTAACAAATGGAACAAAGCTGAGGACAC 240	
QY	241 GTTCAACCTTCTTGGAGCATACGATCAACCTGGAAGGATGGAAGACTTTGAGGAGAA 300	
DB	241 GTTCAACCTTCTTGGAGCATACGATCAACCTGGAAGGATGGAAGACTTTGAGGAGAA 300	
QY	301 ATGGGGATGATCTTCCAGGAGTCTGTGTAAAGCGATCCCTCAACCAATTAACAAGATA 360	
DB	301 ATGGGGATGATCTTCCAGGAGTCTGTGTAAAGCGATCCCTCAACCAATTAACAAGATA 360	
QY	361 GCAGAAATCTCTCAGGATCTCTGTAAACGGGCTGGGCTAGTGGCTTGGTCAAGGAA 420	
DB	361 GCAGAAATCTCTCAGGATCTCTGTAAACGGGCTGGGCTAGTGGCTTGGTCAAGGAA 420	
QY	421 CAGAGACAGGGGTGCACAAATGCTCAGCTTCACTGCCAACTCTTATCTTGGGATTTACA 480	
DB	421 CAGAGACAGGGGTGCACAAATGCTCAGCTTCACTGCCAACTCTTATCTTGGGATTTACA 480	
QY	481 CTCTACAGTCGTACAATGTCTCAGGATGTGTCCAAACCAAGGGCCCAAGAAAGGA 540	
DB	481 CTCTACAGTCGTACAATGTCTCAGGATGTGTCCAAACCAAGGGCCCAAGAAAGGA 540	
QY	541 GACATCATCTGGGAGGTCTCTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600	
DB	541 GACATCATCTGGGAGGTCTCTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600	
QY	601 TTAAATCGAGACCGGAGCGACAAAATGTATTTCGGTACAAATTTTCGAGGCTTCCGATGG 660	
DB	601 TTAAATCGAGACCGGAGCGACAAAATGTATTTCGGTACAAATTTTCGAGGCTTCCGATGG 660	
QY	661 CTCACGGGATGATATTGCAATTTGAAGAGATTAAACAAGTATGACTTTCTGCCCCAAT 720	
DB	661 CTCACGGGATGATATTGCAATTTGAAGAGATTAAACAAGTATGACTTTCTGCCCCAAT 720	
QY	721 ATCAACCTGGGATATCGGATATTCACACGCTGTAAACCGTGTCCAGGGCTAGAGGCA 780	
DB	721 ATCAACCTGGGATATCGGATATTCACACGCTGTAAACCGTGTCCAGGGCTAGAGGCA 780	
QY	781 ACACCTAGCTTTGTGGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840	
DB	781 ACACCTAGCTTTGTGGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840	
QY	841 TGCTCTGACCATATCCCATCCCAATAGCAGTGGTGGGGCAACCCGGGTGAGGAATCTCC 900	
DB	841 TGCTCTGACCATATCCCATCCCAATAGCAGTGGTGGGGCAACCCGGGTGAGGAATCTCC 900	

QY	901 ACGGCTGTGGCCAACTATTATGGGATATTTTACATTTCCACAGGTGAGTATGCTCTCTCG 960	
DB	901 ACGGCTGTGGCCAACTATTATGGGATATTTTACATTTCCACAGGTGAGTATGCTCTCTCG 960	
QY	961 AGCAGGCTGTCTAGCAACAAGATAGTACAAGGCTTCTCTGAGGACCATTCCTCAATGAT 1020	
DB	961 AGCAGGCTGTCTAGCAACAAGATAGTACAAGGCTTCTCTGAGGACCATTCCTCAATGAT 1020	
QY	1021 GAGCAACAGGCGCCATGGCCGAGATCATCAGACACTTCCAGTGGAACTCGGTGGGA 1080	
DB	1021 GAGCAACAGGCGCCATGGCCGAGATCATCAGACACTTCCAGTGGAACTCGGTGGGA 1080	
QY	1081 ACCCTGCGACCGACGATGACTATGCGCCGAGGATTCACAAAGTTTCGGGAGGAGGCC 1140	
DB	1081 ACCCTGCGACCGACGATGACTATGCGCCGAGGATTCACAAAGTTTCGGGAGGAGGCC 1140	
QY	1141 GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200	
DB	1141 GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200	
QY	1201 CAGTTGAGTTTCAATGCGCGACGTCATCCAGAACTCTCGGCCAAGGTTCATCGTGGTCTTC 1260	
DB	1201 CAGTTGAGTTTCAATGCGCGACGTCATCCAGAACTCTCGGCCAAGGTTCATCGTGGTCTTC 1260	
QY	1261 TCCAAATGGCCCGACCTGGAGCGCTCATCCAGAGATAGTTCGGAGAAACATCACCGAT 1320	
DB	1261 TCCAAATGGCCCGACCTGGAGCGCTCATCCAGAGATAGTTCGGAGAAACATCACCGAT 1320	
QY	1321 CGATCTGGCTGGCCAGCAGGAGCTTGGGCCAGCTCTTCGCTCATTCGCAAGCCAGAGTAC 1380	
DB	1321 CGATCTGGCTGGCCAGCAGGAGCTTGGGCCAGCTCTTCGCTCATTCGCAAGCCAGAGTAC 1380	
QY	1381 TTCCAGCTGTGCGCGGACCATCGGCTTCGCTCTCAGGGCGGGCGTATCCAGGAGTTC 1440	
DB	1381 TTCCAGCTGTGCGCGGACCATCGGCTTCGCTCTCAGGGCGGGCGTATCCAGGAGTTC 1440	
QY	1441 AACAAAGTTCTGAGGAGGTCCACCCAGCAGGCTCTCCGACAAATGGGTTTCGAGGAG 1500	
DB	1441 AACAAAGTTCTGAGGAGGTCCACCCAGCAGGCTCTCCGACAAATGGGTTTCGAGGAG 1500	
QY	1501 TTCTGGAGGAGACCTTTCAACTGCTACTTCCAGGAGAACCTCGACAGCTGAAGAAT 1560	
DB	1501 TTCTGGAGGAGACCTTTCAACTGCTACTTCCAGGAGAACCTCGACAGCTGAAGAAT 1560	
QY	1561 TCCAAAGTGTCTGCAAGGACCGGCGGTCAAGGGGACGGCTCCAAAGCGGGGAACTCC 1620	
DB	1561 TCCAAAGTGTCTGCAAGGACCGGCGGTCAAGGGGACGGCTCCAAAGCGGGGAACTCC 1620	
QY	1621 AGACGGACAGCCCTAGCCACCCCTGCACCTGGGGAGGAGAAACATCACAGCGTGGAGACC 1680	
DB	1621 AGACGGACAGCCCTAGCCACCCCTGCACCTGGGGAGGAGAAACATCACAGCGTGGAGACC 1680	
QY	1681 CCTACCTGGATTATACACACCTGAGGATCTCTCAAAATGTATACGTGGCCGTCTACTCC 1740	
DB	1681 CCTACCTGGATTATACACACCTGAGGATCTCTCAAAATGTATACGTGGCCGTCTACTCC 1740	
QY	1741 ATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCGGACGCGGATCTTTGCAAAAC 1800	
DB	1741 ATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCGGACGCGGATCTTTGCAAAAC 1800	
QY	1801 GGATCTTGTGAGATATTAAAAAAGTTGAGGCTGCGCAGTCTCAACCATCTGCTGCAT 1860	
DB	1801 GGATCTTGTGAGATATTAAAAAAGTTGAGGCTGCGCAGTCTCAACCATCTGCTGCAT 1860	
QY	1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACATCAAGGTGACCTCAAG 1920	
DB	1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACATCAAGGTGACCTCAAG 1920	
QY	1921 GGGAACTTACACCATTTCAACTGCGAGCTCTCCGAGAGGATGAATCGGTTGTTCCAT 1980	
DB	1921 GGGAACTTACACCATTTCAACTGCGAGCTCTCCGAGAGGATGAATCGGTTGTTCCAT 1980	

1981	Qy	GAGTGGGCAACTACAAACGGCTTACGCTTAAGCCAGCTGACCGATCAACATCAACGAAAG	2040
1981	Db		2040
		GAGTGGGCAACTACAAACGGCTTACGCTTAAGCCAGCTGACCGATCAACATCAACGAAAG	
2041	Qy	AAATCCTCTGGAGTGGCTTCTCCAAGTGGTTCTTTCTTCCAACTGCGAGTCGAGACTGT	2100
2041	Db		2100
		AAATCCTCTGGAGTGGCTTCTCCAAGTGGTTCTTTCTTCCAACTGCGAGTCGAGACTGT	
2101	Qy	GTCCGGGACCAAGGAAGGGATCATCGAGGGGAGCCCACTGTCTGCTTTGAATGCATG	2160
2101	Db		2160
		GTCCGGGACCAAGGAAGGGATCATCGAGGGGAGCCCACTGTCTGCTTTGAATGCATG	
2161	Qy	GCATGTGCAGAGGAGGTTCACTGATGAAACGATGCAAGTCGCTGTCAAAAGTCCCG	2220
2161	Db		2220
		GCATGTGCAGAGGAGGTTCACTGATGAAACGATGCAAGTCGCTGTCAAAAGTCCCG	
2221	Qy	AATGATTTCTGGTCGAATGAGAAACCAACGCTCGTCATCGCCAAAGGAGATCGAGTACCTG	2280
2221	Db		2280
		AATGATTTCTGGTCGAATGAGAAACCAACGCTCGTCATCGCCAAAGGAGATCGAGTACCTG	
2281	Qy	TCTGAGAGGAGCCCTTCGGGATCGCTCTGACCATCTTTCGCCGTACTGGGCATCTCTGATC	2340
2281	Db		2340
		TCTGAGAGGAGCCCTTCGGGATCGCTCTGACCATCTTTCGCCGTACTGGGCATCTCTGATC	
2341	Qy	ACTCTCTCTGTCTGGGGTCTTTCATCAAGTTCAGAAACACTCCCATCTGTGAAGGCCACC	2400
2341	Db		2400
		ACTCTCTCTGTCTGGGGTCTTTCATCAAGTTCAGAAACACTCCCATCTGTGAAGGCCACC	
2401	Qy	AAACGGAGTTGCTCACTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC	2460
2401	Db		2460
		AAACGGAGTTGCTCACTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC	
2461	Qy	ATCTTCATCGCGAGCCACAGGACTGACCTGTCCGCTCCGCCAAACCGGCTTTTGGCATC	2520
2461	Db		2520
		ATCTTCATCGCGAGCCACAGGACTGACCTGTCCGCTCCGCCAAACCGGCTTTTGGCATC	
2521	Qy	AGCTTCGCTCTGTCATCTCCTGCATCTCTGGTGAAGACCAACCGGCTGTCTGTGCTTC	2580
2521	Db		2580
		AGCTTCGCTCTGTCATCTCCTGCATCTCTGGTGAAGACCAACCGGCTGTCTGTGCTTC	
2581	Qy	GAGCCAGATCCCAACAGCTTCCACCGCAAGTGGTGGGCTCAACCTGCAAGTTCCTC	2640
2581	Db		2640
		GAGCCAGATCCCAACAGCTTCCACCGCAAGTGGTGGGCTCAACCTGCAAGTTCCTC	
2641	Qy	CTGCTCTCTCTGCACTCTCTGTGCAAACTCGTCACTGTCATCTGTGGCTCTACACCGCG	2700
2641	Db		2700
		CTGCTCTCTCTGCACTCTCTGTGCAAACTCGTCACTGTCATCTGTGGCTCTACACCGCG	
2701	Qy	CCTCCCTCAGCTACAGGAACCATGAGCTGGAGGACGAGTGCATCTTCATCACTCGGAC	2760
2701	Db		2760
		CCTCCCTCAGCTACAGGAACCATGAGCTGGAGGACGAGTGCATCTTCATCACTCGGAC	
2761	Qy	GAGGCTCGCTCATGGGCTTGGGCTTCTCATCGGCTACACCTGCTCTCGCGGCAATC	2820
2761	Db		2820
		GAGGCTCGCTCATGGGCTTGGGCTTCTCATCGGCTACACCTGCTCTCGCGGCAATC	
2821	Qy	TGCTTCTCTTCGCTTCAAGTCCCGTGAAGTCGCGGAGAACTTCAACAGGCTTAAGTTC	2880
2821	Db		2880
		TGCTTCTCTTCGCTTCAAGTCCCGTGAAGTCGCGGAGAACTTCAACAGGCTTAAGTTC	
2881	Qy	ATCACCTTCAGCATGTTGATCTTCTTCATCGTCTGGATCTCTTTCATCCCGGCTATGTC	2940
2881	Db		2940
		ATCACCTTCAGCATGTTGATCTTCTTCATCGTCTGGATCTCTTTCATCCCGGCTATGTC	
2941	Qy	AGCACCTACGGCAAGTTTGTTCGCGCTGGAGTGATTCGCACTCTGGCTCAAGCTTC	3000
2941	Db		3000
		AGCACCTACGGCAAGTTTGTTCGCGCTGGAGTGATTCGCACTCTGGCTCAAGCTTC	
3001	Qy	GGGCTGTGGCTGCATTTACTTCAACAGTGTACTCATCTGTTCAGCGCTGCCGT	3060
3001	Db		3060
		GGGCTGTGGCTGCATTTACTTCAACAGTGTACTCATCTGTTCAGCGCTGCCGT	
3061	Qy	AACACCATCGAGGAGTGCCTGACGACACGGCGCCACCGCTTCAAGTGGCGGCGCCG	3120

3061	Db	AAACACATCGAGGAGTGCGCTCAGCACGGCGGCCACGCGCTTCAAGTGGCGGCCGG	3121
3121	Qy	GCCACCTTCGGCGCAGCGCCGGTCTCGCAACGGCTTCAGCAGCTGTGCGGCTCCACC	3180
3121	Db	GCCACCTTCGGCGCAGCGCGCGTCTCGCAACGGCTTCAGCAGCTGTGCGGCTCCACC	3180
3181	Qy	ATTCTCTCGCCCGCTCTGCTCACCTCGGCGCGGGCTCACCATGGATGTCAGCGCTGC	3240
3181	Db	ATTCTCTCGCCCGCTCTGCTCACCTCGGCGCGGGCTCACCATGGATGTCAGCGCTGC	3240
3241	Qy	AGCACGCAGAAAGTTCAGCTTTCGGCAGCGGCACCGTCAACCTGTGCTCAGTTCGAGGAG	3300
3241	Db	AGCACGCAGAAAGTTCAGCTTTCGGCAGCGGCACCGTCAACCTGTGCTCAGTTCGAGGAG	3300
3301	Qy	ACAGGCGATACGCCACCTTCAGCGCAGCGCCGCGAGCAGGAACCTCGGCGGATGCGCGC	3360
3301	Db	ACAGGCGATACGCCACCTTCAGCGCAGCGCCGCGAGCAGGAACCTCGGCGGATGCGCGC	3360
3361	Qy	AGGGCGACACCTGCCATCTAGACACCAGCACAGGCGCCGCGCTCAGAAATCGAGCCC	3420
3361	Db	AGGGCGACACCTGCCATCTAGACACCAGCACAGGCGCCGCGCTCAGAAATCGAGCCC	3420
3421	Qy	CAGCGCGCAACGATGCCCGATACAGGCGCGCGCCAGCAGGCGCACCTTAGAGTCGCG	3480
3421	Db	CAGCGCGCAACGATGCCCGATACAGGCGCGCGCCAGCAGGCGCACCTTAGAGTCGCG	3480
3481	Qy	GGCGGACGAAGAGGCGCCCCACAATATGGAGGAACCTTAATCCAACTCTCTCCATCAAC	3540
3481	Db	GGCGGACGAAGAGGCGCCCCACAATATGGAGGAACCTTAATCCAACTCTCTCCATCAAC	3540
3541	Qy	CCCAAGAACATCTCCAGCGCAGCACCTTCGCGCTTTGCTGGAAGATTCGACATCTGCAGT	3600
3541	Db	CCCAAGAACATCTCCAGCGCAGCACCTTCGCGCTTTGCTGGAAGATTCGACATCTGCAGT	3600
3601	Qy	TGCCAACCTCTCCCTTCGCGACCTTTCGCGCTTTGCTGGAAGATTCGACATCTGCAGT	3660
3601	Db	TGCCAACCTCTCCCTTCGCGACCTTTCGCGCTTTGCTGGAAGATTCGACATCTGCAGT	3660
3661	Qy	TCCTTTTATCCCTGATTTCTCGACTTGATTTATCTAGTGTGCGATGGAATATCAAC	3720
3661	Db	TCCTTTTATCCCTGATTTCTCGACTTGATTTATCTAGTGTGCGATGGAATATCAAC	3720
3721	Qy	ATAATGAGTTGCACAAATAGGTGAGCAGAGTGTGTCAAAGTATCTGAACTATCTGAAAT	3780
3721	Db	ATAATGAGTTGCACAAATAGGTGAGCAGAGTGTGTCAAAGTATCTGAACTATCTGAAAT	3780
3781	Qy	ATCTGAACTACTTTATCTCTCGAATGTATTAACAAATTTGAAGTATTTTAGTGACA	3840
3781	Db	ATCTGAACTACTTTATCTCTCGAATGTATTAACAAATTTGAAGTATTTTAGTGACA	3840
3841	Qy	TTATGTTCTAACATGTTCAGATAATTTGTTTCAACATATAAGTACCACTCGAAGCAGT	3900
3841	Db	TTATGTTCTAACATGTTCAGATAATTTGTTTCAACATATAAGTACCACTCGAAGCAGT	3900
3901	Qy	GACTGAGATTCGCCACTGTGATGACAGAACTGTTTTTAACTTATCATTTGAAACCTGGA	3960
3901	Db	GACTGAGATTCGCCACTGTGATGACAGAACTGTTTTTAACTTATCATTTGAAACCTGGA	3960
3961	Qy	TTGCAACAGGAATATAATGATGTACAAAAAATTTGTTGATTTATCTTAAAAATGCAAT	4020
3961	Db	TTGCAACAGGAATATAATGATGTACAAAAAATTTGTTGATTTATCTTAAAAATGCAAT	4020
4021	Qy	TGTAATCAGATGTGTAATTTGGTAATTACTCTGTCAATTAATGATCATTTCTTGATA	4080
4021	Db	TGTAATCAGATGTGTAATTTGGTAATTACTCTGTCAATTAATGATCATTTCTTGATA	4080
4081	Qy	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCGCCCGCAGCAGCAACGG	4134
4081	Db	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCGCCCGCAGCAGCAGCGGG	4134


```

12-OCT-2000; 2000US-00687476.
12-OCT-2000; 2000US-00687477.
11-OCT-2001; 2001US-00975553.
11-OCT-2001; 2001WO-US031562.
XX (MARI-) MARICAL INC.
XX
XX Harris HW, Russell DR, Nearing J, Betka M;
PI
XX WPI; 2004-061122/06.
XX DR
XX P-PSDB; ADI19970.
XX
XX Growing pre-adult anadromous fish in freshwater comprises adding feed
PPT containing an amount of NaCl for fish consumption to the freshwater to
PPT increase the level of the Polyvalent Cation Sensing Receptor modulator in
PPT serum of the fish.
XX
XX Example 19; SEQ ID NO 17; 109pp; English.
XX
XX The present invention relates to methods for improving the raising of pre-
CC adult anadromous fish or preparing these fish for transfer to seawater
CC by modulating expression of a receptor referred to as the Polyvalent
CC Cation Sensing Receptor (PVCr). The invention is useful in increasing
CC survival and growth and reduce stress of the fish that have been
CC transferred to seawater. The present sequence is a dogfish shark cation
CC receptor (SKCar). DNA.
XX
XX Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 4134; DB 12; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATTCCGTTGCTGCGGTCAGTGCCAAAGTCTCTCCAGTGC AAAATGAGAAATGGTGTC 60
DB 1 AATTCCGTTGCTGCGGTCAGTGCCAAAGTCTCTCCAGTGC AAAATGAGAAATGGTGTC 60
QY 61 GCCATTACAGAAATGCACTACATCTGTGTTAAATGAAATATGTTCAGTTATCTGAAGGT 120
DB 61 GCCATTACAGAAATGCACTACATCTGTGTTAAATGAAATATGTTCAGTTATCTGAAGGT 120
QY 121 TATTAAATGTTTCTCAAGATGGCTTCCAGAGAAATCAATTCTGCACGTTTTCCCAATT 180
DB 121 TATTAAATGTTTCTCAAGATGGCTTCCAGAGAAATCAATTCTGCACGTTTTCCCAATT 180
QY 181 GTCATTGTATGAATAACTGACCAAAAGGATGTAAACAAAATGGAAACAAAGCTGAGACCAC 240
DB 181 GTCATTGTATGAATAACTGACCAAAAGGATGTAAACAAAATGGAAACAAAGCTGAGACCAC 240
QY 241 GTTCACCCCTTTCTGGAGCATCAGATCACCCTGAGGAGATGGAAGACTTGGAGAGAA 300
DB 241 GTTCACCCCTTTCTGGAGCATCAGATCACCCTGAGGAGATGGAAGACTTGGAGAGAA 300
QY 301 ATGGGGATTCATCTTCAGAGGTTCTGCTGTAAAGCGATCCCTCACCAATTACAAAGATAA 360
DB 301 ATGGGGATTCATCTTCAGAGGTTCTGCTGTAAAGCGATCCCTCACCAATTACAAAGATAA 360
QY 361 GCAGAAATCCCTCAGGATCTCTGTAAACGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
DB 361 GCAGAAATCCCTCAGGATCTCTGTAAACGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
QY 421 CAGAGACAGGCTGCACAAATGGCTCAGCTTCACTGCACACTCTTATTCTTGGGATTTACA 480
DB 421 CAGAGACAGGCTGCACAAATGGCTCAGCTTCACTGCACACTCTTATTCTTGGGATTTACA 480
QY 481 CTCCTACAGTCGTACAATGTCTCAGGGTATGFTCCAAACCAAAGGGCCAGAGAAAGGA 540
DB 481 CTCCTACAGTCGTACAATGTCTCAGGGTATGFTCCAAACCAAAGGGCCAGAGAAAGGA 540
QY 541 GACATCATCTGGGAGTCTCTTCCCAATACACTTTTGGAGTAGTCGCCAAGGATCAGCAC 600
DB 541 GACATCATCTGGGAGTCTCTTCCCAATACACTTTTGGAGTAGTCGCCAAGGATCAGCAC 600

```

601 TTAAATTCGAGACCGGAGCGCAAAATGTATTTCGGTACAAATTTTCGAGGCTTCGATGG 660
601 TTAAATTCGAGACCGGAGCGCAAAATGTATTTCGGTACAAATTTTCGAGGCTTCGATGG 660
661 CTCAGGCGATGATATTCCCAATTGAAGAGATTAAACAAGTATGACTTTCCTGCCCAAT 720
661 CTCAGGCGATGATATTCCCAATTGAAGAGATTAAACAAGTATGACTTTCCTGCCCAAT 720
721 ATCACCCTGGGATATCCGATATTGTACAGTGTAAACACCGTTCGCAAGCGCTAGAGCA 780
721 ATCACCCTGGGATATCCGATATTGTACAGTGTAAACACCGTTCGCAAGCGCTAGAGCA 780
781 AACTCAGCTTTGTGCGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAA 840
781 AACTCAGCTTTGTGCGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAA 840
841 TGCTTGACCATATCCCATCCCAATAGCAGTGGTTCGGGCGCAACCGGTCAGGAATCTCC 900
841 TGCTTGACCATATCCCATCCCAATAGCAGTGGTTCGGGCGCAACCGGTCAGGAATCTCC 900
901 ACGGCTGTGGCCNATCTATTGGGATTTATTTTACATTCACAGGTGAGTATGCTCTCTCG 960
901 ACGGCTGTGGCCNATCTATTGGGATTTATTTTACATTCACAGGTGAGTATGCTCTCTCG 960
961 AGCAGGCTGTGAGCAACAGAAATAGTACAAAGGCTTCCTGAGGACCATCCCAATGAT 1020
961 AGCAGGCTGTGAGCAACAGAAATAGTACAAAGGCTTCCTGAGGACCATCCCAATGAT 1020
1021 GAGCAACAGGCGCAACCGCCATGCGGAGATCATCGAGCACTTCAGTGGAACTGGGTGGGA 1080
1021 GAGCAACAGGCGCAACCGCCATGCGGAGATCATCGAGCACTTCAGTGGAACTGGGTGGGA 1080
1081 ACCCTGGAGCGAGCATGACTATGCGCGCCAGAGCATTTGCAAGTTCCGGAGGAGGCC 1140
1081 ACCCTGGAGCGAGCATGACTATGCGCGCCAGAGCATTTGCAAGTTCCGGAGGAGGCC 1140
1141 GTTAAGAGGAGCATCTGTATTGACTTTAGTGTAGTATGATCTCTCAGTACTACACCGAAG 1200
1141 GTTAAGAGGAGCATCTGTATTGACTTTAGTGTAGTATGATCTCTCAGTACTACACCGAAG 1200
1201 CAGTTGGAGTTATCGCCAGCTATCCAGAACTCTCGGCCAAGGTCAATGCTGTCTTC 1260
1201 CAGTTGGAGTTATCGCCAGCTATCCAGAACTCTCGGCCAAGGTCAATGCTGTCTTC 1260
1261 TCCAAATGGCCCGACCTGGAGCGGCTCATCCAGGAGATAGTTCCGAGAAACATACCCGAT 1320
1261 TCCAAATGGCCCGACCTGGAGCGGCTCATCCAGGAGATAGTTCCGAGAAACATACCCGAT 1320
1321 CGGATCTGCTGGCCAGCGAGGTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
1321 CGGATCTGCTGGCCAGCGAGGTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
1381 TTCCAGTGTGGCGGCAACATCGGCTTCGCTCTCAGGCGGGCGGTATCCAGGGTTC 1440
1381 TTCCAGTGTGGCGGCAACATCGGCTTCGCTCTCAGGCGGGCGGTATCCAGGGTTC 1440
1441 AACAAATTCCTGAAGAGTTCACCCCAAGAGGCTCTCGGCAATGGGTTTGTCAAGAG 1500
1441 AACAAATTCCTGAAGAGTTCACCCCAAGAGGCTCTCGGCAATGGGTTTGTCAAGAG 1500
1501 TTCTGGGAGAGACTTCAACTGTACTTACCGGAGAGACCTCAGCAGGTGAGAT 1560
1501 TTCTGGGAGAGACTTCAACTGTACTTACCGGAGAGACCTCAGCAGGTGAGAT 1560
1561 TCCAAAGTCCCTCGCACGGAACCGCGGCTCAAGGGGACGGTCCAAAGCGGGAACTCC 1620
1561 TCCAAAGTCCCTCGCACGGAACCGCGGCTCAAGGGGACGGTCCAAAGCGGGAACTCC 1620
1621 AGACGAGACGCTTACGCCACCCCTGCACTGGGAGGAGAACTACACAGGTGAGAGCC 1680
1621 AGACGAGACGCTTACGCCACCCCTGCACTGGGAGGAGAACTACACAGGTGAGAGCC 1680
1681 CCTACTCGATATATACACCTGAGGATCTCTCAATGTATAGTCTGGCGCTCTACTCC 1740

1681 CCCTACTCGATATATACACCTGAGGATCTCTACAATGTATATACGTGGCGCTCTACTCC 1740
1741 ATTCTCACCCTTCGAAAGACATCCACTCTTTGCAAAACCCGCGACGGGATCTTTGCAAAAC 1800
1741 ATTCTCACCCTTCGAAAGACATCCACTCTTTGCAAAACCCGCGACGGGATCTTTGCAAAAC 1800
1801 GGATCTTGTGAGATATATAAAAGTTGAGGCTTCGAGGTCTCTCAACATCTCTGCTCAT 1860
1801 GGATCTTGTGAGATATATAAAAGTTGAGGCTTCGAGGTCTCTCAACATCTCTGCTCAT 1860
1861 CTGAAGTTTACCAACAGCATGGGTGAGGAGTTGACTTTTACGATCAAGGTGAGCTCAAG 1920
1861 CTGAAGTTTACCAACAGCATGGGTGAGGAGTTGACTTTTACGATCAAGGTGAGCTCAAG 1920
1921 GGGAACTACACCATTTATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTTTCTCCAT 1980
1921 GGGAACTACACCATTTATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTTTCTCCAT 1980
1981 GAGTGGGCAACTACACCGCTAGCGTTAGCCCGAGTGACCGACTCAACATCAACGAAAG 2040
1981 GAGTGGGCAACTACACCGCTAGCGTTAGCCCGAGTGACCGACTCAACATCAACGAAAG 2040
2041 AAAATCCTCTGGAGTGGCTTTCTCAAAGTGGTTCTTTCTCCTCAACTGCGAGTGGTGT 2100
2041 AAAATCCTCTGGAGTGGCTTTCTCAAAGTGGTTCTTTCTCCTCAACTGCGAGTGGTGT 2100
2101 GTGCGGGGCAACGAGGAGTATCGAGGGGAGGCGCCACCTGCTGCTTTGATGCTCATG 2160
2101 GTGCGGGGCAACGAGGAGTATCGAGGGGAGGCGCCACCTGCTGCTTTGATGCTCATG 2160
2161 GCATGTGCAGAGGAGGATTCAGTGTGAAACGATGCAAGTGCCTGTGTAACAAAGTGGCGG 2220
2161 GCATGTGCAGAGGAGGATTCAGTGTGAAACGATGCAAGTGCCTGTGTAACAAAGTGGCGG 2220
2221 AATGATTTCTGCTGAAATGAGAAACCAAGCTGTGATCGCCAAAGGAGATCGAGTACCTG 2280
2221 AATGATTTCTGCTGAAATGAGAAACCAAGCTGTGATCGCCAAAGGAGATCGAGTACCTG 2280
2281 TCGTGGAGGAGCCCTTCGGGATCGCTGACCATCTTCGCGCTACTGGGCACTCTGATC 2340
2281 TCGTGGAGGAGCCCTTCGGGATCGCTGACCATCTTCGCGCTACTGGGCACTCTGATC 2340
2341 ACCTCTCTGCTGCTGGGGTCTTCATCAAGTTTCAGGAACAATCCCATCGTGAAGGCCACC 2400
2341 ACCTCTCTGCTGCTGGGGTCTTCATCAAGTTTCAGGAACAATCCCATCGTGAAGGCCACC 2400
2401 AACGGAGTGTCTTACCTGCTCTTCTCTCTCATCTGCTGCTCTCTCGAGCTCGCTC 2460
2401 AACGGAGTGTCTTACCTGCTCTTCTCTCTCATCTGCTGCTCTCTCGAGCTCGCTC 2460
2461 ATCTTCATCGCGAGCCAGGAGTGGACTGGACTGGCTCGGCTCGGCCAACCGGCTTTGSCATC 2520
2461 ATCTTCATCGCGAGCCAGGAGTGGACTGGACTGGCTCGGCTCGGCCAACCGGCTTTGSCATC 2520
2521 AGCTTGTCTGTGATCTCTGCTCATCTGCTGTAAGAACCAACCGGCTGCTGCTGCTTC 2580
2521 AGCTTGTCTGTGATCTCTGCTCATCTGCTGTAAGAACCAACCGGCTGCTGCTGCTTC 2580
2581 GAGGCCAAGATCCCAACCGAGCTCCCAAGTGGTGGGCTCAACTGCAAGTTCTCTC 2640
2581 GAGGCCAAGATCCCAACCGAGCTCCCAAGTGGTGGGCTCAACTGCAAGTTCTCTC 2640
2641 CTGGTCTTCTGTGATCTCTGCTCAAAATCGTCACTGATCATCTGGTCTTACACCGG 2700
2641 CTGGTCTTCTGTGATCTCTGCTCAAAATCGTCACTGATCATCTGGTCTTACACCGG 2700
2701 CCTCCCTCCAGCTTACAGGAGCATGAGTGGAGGAGGATCATCTTCACTCACTCGGAC 2760
2701 CCTCCCTCCAGCTTACAGGAGCATGAGTGGAGGAGGATCATCTTCACTCACTCGGAC 2760
2761 GAGGCTCGCTCATGCGCTGGGCTTCCTCATCGGCTACACCTGCTCTCGCGCATC 2820

Db	2761	GAGGGCTCGCTCATGGGGCTGGGCTTCTCTCATCGGCTACACCTGCGCTCTCTCGCGCGCATC	2822
Qy	2821	TGCTTCTTCTTCCGCTTCAAGTCCCGTAAGCTGCCGGAGAACTTCAACGAGGTAAGTTTC	2880
Db	2821	TGCTTCTTCTTCCGCTTCAAGTCCCGTAAGCTGCCGGAGAACTTCAACGAGGTAAGTTTC	2880
Qy	2881	ATCACCTTCAGCATGTGATCTTCTTCATCGTCTGGATCTCTTTCATCCCGGCTATGTC	2940
Db	2881	ATCACCTTCAGCATGTGATCTTCTTCTTCATCGTCTGGATCTCTTTCATCCCGGCTATGTC	2940
Qy	2941	AGCACCTTACGGCAAGTTTGTGTCGGCGTGAGAGTGATTGCCATCTCTGGGCTCCAGCTTC	3000
Db	2941	AGCACCTTACGGCAAGTTTGTGTCGGCGTGAGAGTGATTGCCATCTCTGGGCTCCAGCTTC	3000
Qy	3001	GGGCTGCTGGCTGTCATTACTTTCACAAAGTGTTATCATCTGTTTCAAGCGTCCCGT	3060
Db	3001	GGGCTGCTGGCTGTCATTACTTTCACAAAGTGTTATCATCATCTGTTTCAAGCGTCCCGT	3060
Qy	3061	AACACCATCAGGAGGTGCGCTCGACACCGCGGCCACCGCTTCAAGTGTGGCGGCCGG	3120
Db	3061	AACACCATCAGGAGGTGCGCTCGACACCGCGGCCACCGCTTCAAGTGTGGCGGCCGG	3120
Qy	3121	GCCACCTTCGGGGCAGCGCGGCTCTGCGAAGCGTTCAGAGCGTTCAGAGCTGTGCGGCTCCACC	3180
Db	3121	GCCACCTTCGGGGCAGCGCGGCTCTGCGAAGCGTTCAGAGCGTTCAGAGCTGTGCGGCTCCACC	3180
Qy	3181	ATCTCTCTCGGCGCTCGTCCACTGCTGGGCGCGGCGCTCACCATGGAGATGCAAGCGCTGC	3240
Db	3181	ATCTCTCTCGGCGCTCGTCCACTGCTGGGCGCGGCGCTCACCATGGAGATGCAAGCGCTGC	3240
Qy	3241	AGCACGCAAGAGTTCAGCTTTCGGCAGCGGCAACCGTCAACCTGTGCTCAGCTTCGAGGAG	3300
Db	3241	AGCACGCAAGAGTTCAGCTTTCGGCAGCGGCAACCGTCAACCTGTGCTCAGCTTCGAGGAG	3300
Qy	3301	ACAGGCGGATACGCCACCTTCAGCGGCACGGCCCGCAGCAGGAACTCGGCGGATGCGCGC	3360
Db	3301	ACAGGCGGATACGCCACCTTCAGCGGCACGGCCCGCAGCAGGAACTCGGCGGATGCGCGC	3360
Qy	3361	AGCGGCACCAACCTTGCCATCTAGACACCAAGAGCGCGCGCTCAGAAATGCGAGCCC	3420
Db	3361	AGCGGCACCAACCTTGCCATCTAGACACCAAGAGCGCGCGCTCAGAAATGCGAGCCC	3420
Qy	3421	CAGCCCGCCAAAGNATGCCGATACAGGGCGGCGCGACCAAGGCGCCCTTAGAGTGC	3480
Db	3421	CAGCCCGCCAAAGNATGCCGATACAGGGCGGCGCGACCAAGGCGCCCTTAGAGTGC	3480
Qy	3481	GGCGGCAGCAAGAGCGCCCCACAACCTATGGAGGAAACCTTAATCCAACTCCTCCATCAAC	3540
Db	3481	GGCGGCAGCAAGAGCGCCCCACAACCTATGGAGGAAACCTTAATCCAACTCCTCCATCAAC	3540
Qy	3541	CCCAGAACAATCTCCACGGGAGCACCGTCCAGCAACTGACATCAACTCTTAAACCGTGGC	3600
Db	3541	CCCAGAACAATCTCTCCACGGGAGCACCGTCCAGCAACTGACATCAACTCTTAAACCGTGGC	3600
Qy	3601	TGCCCAACCTCTCCCTCTCGGCACCTTGGGTTTCTGAAGATTCGACATCTGCAGT	3660
Db	3601	TGCCCAACCTCTCCCTCTCGGCACCTTGGGTTTCTGAAGATTCGACATCTGCAGT	3660
Qy	3661	TCTTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGTGGATGGAATATCAAC	3720
Db	3661	TCTTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGTGGATGGAATATCAAC	3720
Qy	3721	ATAATGAGTTGCCAAATTAGGTGACGAGGTTGTCAAPAGTATCTGAACTATCTGAAGT	3780
Db	3721	ATAATGAGTTGCCAAATTAGGTGACGAGGTTGTCTAAAAGTATCTGAACTATCTGAAGT	3780
Qy	3781	ATCTGAACTACTTTATCTCTCGAAATGTTATTACAAACATTTGAAGTATTTTAGTGACA	3840
Db	3781	ATCTGAACTACTTTATCTCTCGAAATGTTATTACAAACATTTGAAGTATTTTAGTGACA	3840
Qy	3841	TTATGTTCTTACAATGTGCAAGATAATTTGTTTACAAACATAAAGGTAACAACCTGAAGCAGT	3900
Db	3841	TTATGTTCTTACAATGTGCAAGATAATTTGTTTACAAACATAAAGGTAACAACCTGAAGCAGT	3900

[illegible]

RESULT 7

XX	AAT89290	
XX	ID	AAT89290 standard; cDNA; 4131 BP.
XX	XX	
XX	AC	AAT89290;
XX	DT	27-MAR-1998 (first entry)
XX	XX	Dogfish shark kidney calcium receptor related protein cDNA.
XX	DE	
XX	XX	Calcium receptor related protein; Car-RP; dogfish shark; SKCar-RP;
XX	KW	polycation-sensing receptor; aquaculture; fish farming;
XX	KW	salinity tolerance; ss.
XX	XX	
XX	OS	Squalus acanthias.
XX	XX	
XX	FH	Key
XX	FT	CDS
XX	FT	Location/Qualifiers
XX	FT	439..3519
XX	FT	/*tag= a
XX	FT	polyA_site
XX	FT	4076..4113
XX	FT	/*tag= b
XX	XX	
XX	PN	W09735977-A1.
XX	XX	
XX	PD	02-OCT-1997.
XX	XX	
XX	PF	27-MAR-1997; 97WO-US005031.
XX	XX	
XX	PR	27-MAR-1996; 96US-00622738.
XX	XX	
XX	PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.
XX	XX	
XX	PI	Harris HW, Brown E, Hebert S;
XX	XX	
XX	DR	WPI; 1997-489640/45.
XX	DR	P-PSDB; AAW32059.
XX	XX	
XX	PT	New isolated Aquatic polyvalent cation-sensing receptor - used to develop
XX	PT	products for increasing or decreasing the salinity tolerance of fish for
XX	PT	use in aquaculture.
XX	XX	
XX	PS	Claim 2; Fig 4A-F; 57bp; English.

This cDNA clone codes for dogfish shark kidney calcium receptor related protein (SKCaR-RP, see AAW32059), an aquatic polyvalent cation-sensing receptor (pVCR). It was isolated from a shark kidney cDNA library using a rat kidney calcium receptor cDNA as probe. Also claimed are: a probe comprising the 4131 bp SKCaR-RP sequence; an isolated pVCR present in the plasma membranes of aquatic species, especially on the apical membrane of epithelial cells of elasmobranch fish, particularly from cells found in the collecting duct or late distal tubule in the kidney; intestine, gall, rectal gland, gonad or brain; an antibody that specifically binds to a pVCR; and a method of screening for aquatic pVCR agonists and antagonists. Modulation of the expression of the aquatic pVCR activates or inhibits aquatic pVCR mediated ion transport and endocrine changes

CC that permit fish to adapt to fresh or salt water. The method facilitates
 CC the aquaculture of marine fish and can provide for the development of
 CC marine fish that are easily adaptable to fresh water aquaculture
 XX
 SQ Sequence 4131 BP; 1028 A; 1161 C; 1019 G; 923 T; 0 U; 0 Other;

Query Match 99.1%; Score 4098; DB 2; Length 4131;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4131; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY	1	AATTCGGTGTCTCGGTTTCAGTCCAAAGTCTCTCCAGTGCAGAAATGAGAAATGGTGGTC	60
DB	1	AATTCGGTGTCTCGGTTTCAGTCCAAAGTCTCTCCAGTGCAGAAATGAGAAATGGTGGTC	60
QY	61	GCATTACAGGAACATGCACTACATCTGTGTTAATGAATATATGTCAGTTATCTGAAGT	120
DB	61	GCATTACAGGAACATGCACTACATCTGTGTTAATGAATATATGTCAGTTATCTGAAGT	120
QY	121	TATTAATAATGTTTCTGCAAGGATGGCTTCAAGAGAAATCAATCTGCAGTCTTCCCAT	180
DB	121	TATTAATAATGTTTCTGCAAGGATGGCTTCAAGAGAAATCAATCTGCAGTCTTCCCAT	180
QY	181	GTCAATGTATGAATACTGCAAAAGGATGTAAACAAATGGAACAAAGCTGAGGACCA	240
DB	181	GTCAATGTATGAATACTGCAAAAGGATGTAAACAAATGGAACAAAGCTGAGGACCA	240
QY	241	GTTACCCCTTCTTGAGCATACGATCAACCTTGAGGAGATGGAAGCTTCAGAGGAA	300
DB	241	GTTACCCCTTCTTGAGCATACGATCAACCTTGAGGAGATGGAAGCTTCAGAGGAA	300
QY	301	ATGGGATGTATCTCCAGGATTTCTGTCTGTAAGCGATCCCTCAACATTAACAAGATA	360
DB	301	ATGGGATGTATCTCCAGGATTTCTGTCTGTAAGCGATCCCTCAACATTAACAAGATA	360
QY	361	GCAGAAATCTCCAGGATCTCTGTAAAGGGCTGGCTAGTGGTCTGTAAGGA	420
DB	361	GCAGAAATCTCCAGGATCTCTGTAAAGGGCTGGCTAGTGGTCTGTAAGGA	420
QY	421	CAGAGACAGGCTGCACATGCTCAGCTTCACTGCAACTCTTATCTTGGGATTTACA	480
DB	421	CAGAGACAGGCTGCACATGCTCAGCTTCACTGCAACTCTTATCTTGGGATTTACA	480
QY	481	CTCCTACAGTGTGAATGTCTCAGGATGTGTCCAAACCAAGGCTCCAGAAAGGA	540
DB	481	CTCCTACAGTGTGAATGTCTCAGGATGTGTCCAAACCAAGGCTCCAGAAAGGA	540
QY	541	GACATCATCTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGAC	600
DB	541	GACATCATCTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGAC	600
QY	601	TAAAAATCAGACCGGAGGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTCCGATGG	660
DB	601	TAAAAATCAGACCGGAGGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTCCGATGG	660
QY	661	CTCCAGGCTGATATTCGCAATTCAGAGATTAACACAGTATGACTTCTCGGCCAAT	720
DB	661	CTCCAGGCTGATATTCGCAATTCAGAGATTAACACAGTATGACTTCTCGGCCAAT	720
QY	721	ATCACCTCGGATATCGCATATTTGACACGTGTAAACCGTGTCCAAAGCGCTAGAGCA	780
DB	721	ATCACCTCGGATATCGCATATTTGACACGTGTAAACCGTGTCCAAAGCGCTAGAGCA	780
QY	781	ACACTCAGCTTTGTGGCCAGAACAAATTCGATCGTGAATAGATGATTCGTAAAC	840
DB	781	ACACTCAGCTTTGTGGCCAGAACAAATTCGATCGTGAATAGATGATTCGTAAAC	840
QY	841	TGCTCTGACCATATCCATCTCAATAGCAGTGGTTCGGGGCAACCGGGTCAGGAATCTCC	900
DB	841	TGCTCTGACCATATCCATCTCAATAGCAGTGGTTCGGGGCAACCGGGTCAGGAATCTCC	900
QY	901	ACGGCTGTGGCCAAATCTATTTGGGATTTATTTTACATTCACAGGTGATGCTTCCTCG	960
DB	901	ACGGCTGTGGCCAAATCTATTTGGGATTTATTTTACATTCACAGGTGATGCTTCCTCG	960

QY	961	AGCAGGCTGTCTACGAAACAGAAATGAGTACAAGGCTTCTCTGAGGACCATCCCAATGAT	1020
DB	961	AGCAGGCTGTCTACGAAACAGAAATGAGTACAAGGCTTCTCTGAGGACCATCCCAATGAT	1020
QY	1021	GAGCAACAGGCGCAGCGCATGGCCGAGATCATCGAGCACTTCAGTGGAACTGGTGGGA	1080
DB	1021	GAGCAACAGGCGCAGCGCATGGCCGAGATCATCGAGCACTTCAGTGGAACTGGTGGGA	1080
QY	1081	ACCCTGACGCGCAGTATGCGCCGCCAGGCAATCAAGTTCCGGGAGGAGGCC	1140
DB	1081	ACCCTGACGCGCAGTATGCGCCGCCAGGCAATCAAGTTCCGGGAGGAGGCC	1140
QY	1141	GTTAAGAGGACATCTGTATTTGACTTCAGTGAGATGATCTCTCAGTACTACCCAGAAG	1200
DB	1141	GTTAAGAGGACATCTGTATTTGACTTCAGTGAGATGATCTCTCAGTACTACCCAGAAG	1200
QY	1201	CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCTCGGCCAAGSTCATCTGTTCTTC	1260
DB	1201	CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCTCGGCCAAGSTCATCTGTTCTTC	1260
QY	1261	TCCAAATGGCCCGACCTGGAGCGCTCATCCAGAGATAGTTTCGGAGAAACATCCCGAT	1320
DB	1261	TCCAAATGGCCCGACCTGGAGCGCTCATCCAGAGATAGTTTCGGAGAAACATCCCGAT	1320
QY	1321	CGGATCTGGCTGGCCAGGAGGCTTGGCCGAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380
DB	1321	CGGATCTGGCTGGCCAGGAGGCTTGGCCGAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380
QY	1381	TTCCACTGTGGCGGCAACATCGGCTTCGCTCTCAGGGCGGGGCTATCCAGGGTTC	1440
DB	1381	TTCCACTGTGGCGGCAACATCGGCTTCGCTCTCAGGGCGGGGCTATCCAGGGTTC	1440
QY	1441	AACAAAGTTCTGAGGAGGTCACCCAGCAGGCTCTCGGACAAATGGTTTGTCAAGGAG	1500
DB	1441	AACAAAGTTCTGAGGAGGTCACCCAGCAGGCTCTCGGACAAATGGTTTGTCAAGGAG	1499
QY	1501	TTCTGGGAGGAGACCTTTCAAATCTCTTCAACGAGAGACCTCGACGAGCTGAAAGAT	1560
DB	1500	TTCTGGGAGGAGACCTTTCAAATCTCTTCAACGAGAGACCTCGACGAGCTGAAAGAT	1557
QY	1561	TCCAAAGTGTCTCGACGAGCGGGCTTCAGGGGACGGCTCCAAAGCGGGGAACTCC	1620
DB	1558	TCCAAAGTGTCTCGACGAGCGGGCTTCAGGGGACGGCTCCAAAGCGGGGAACTCC	1617
QY	1621	AGCAGACAGCCCTTACGCCACCTCTGACCTGGGGAGGAGAAACATCACACGCTGGAGACC	1680
DB	1618	AGCAGACAGCCCTTACGCCACCTCTGACCTGGGGAGGAGAAACATCACACGCTGGAGACC	1677
QY	1681	CCCTACCTGATTTATACACACCTGAGGATCTCTCAATGTATACGTTGGCGCTCTACTCC	1740
DB	1678	CCCTACCTGATTTATACACACCTGAGGATCTCTCAATGTATACGTTGGCGCTCTACTCC	1737
QY	1741	ATTGCTCAGCCCTCGCAAGACATCCACTCTTGCACACCGGACCGGCACTCTTTGCAAAAC	1800
DB	1738	ATTGCTCAGCCCTCGCAAGACATCCACTCTTGCACACCGGACCGGCACTCTTTGCAAAAC	1797
QY	1801	GGATCTTTGTGCAGATTTAAAAAAGTTGAGGCTGCGAGTCTCTCAACCATCTGCTGCAT	1860
DB	1798	GGATCTTTGTGCAGATTTAAAAAAGTTGAGGCTGCGAGTCTCTCAACCATCTGCTGCAT	1857
QY	1861	CTGAGTTTACCAACAGGCTGAGGAGGCTTGAATTTGACGATCAAGTCAAGCTCAAG	1920
DB	1858	CTGAGTTTACCAACAGGCTGAGGAGGCTTGAATTTGACGATCAAGTCAAGCTCAAG	1917
QY	1921	GGGAACTTACACCATTTAACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTGTTCCAT	1980
DB	1918	GGGAACTTACACCATTTAACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTGTTCCAT	1977
QY	1981	GAGGTGGGCAACTACAAAGCTTACGCTAAGCCAGTGACGAGTCAACATCAACGAAAG	2040
DB	1978	GAGGTGGGCAACTACAAAGCTTACGCTAAGCCAGTGACGAGTCAACATCAACGAAAG	2037

XX DT 07-JAN-2000 (first entry)

XX DE Human Car coding sequence.

XX KW G-protein fusion receptor; Car; calcium receptor; GluR; head injury; metatropic glutamate receptor; GABAR; chimeric receptor; stroke; gamma-aminobutyric acid receptor; allosteric modulator; antagonist; spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia; Alzheimer's disease; hyperparathyroidism; osteoporosis; depression; cognitive disorder; ss.

XX OS Homo sapiens.

XX PN W09951641-A1.

XX PD 14-OCT-1999.

XX PF 02-APR-1999; 99WO-US0007333.

XX PR 03-APR-1998; 98US-0080671P.

XX PA (NPSP-) NPS PHARM INC.

XX PI Stormann TM, Hammerland LG, Storjohann LL, Busby JG, Garrett JE, Simin RT;

XX DR MPI; 1999-610995/52.

XX DR P-PSDB; AAY49105, AAY49110, AAY49115.

XX PT New G-protein fusion receptors and chimeras containing domains from different receptors, used to screen for modulators, potentially useful e.g. for treating or preventing stroke or Alzheimer's disease.

XX PS Disclosure; Fig 5; 255pp; English.

XX CC The invention relates to G-protein fusion receptors (I) comprising: (1) in the N to C direction, extracellular (ECD), transmembrane (TMD) and intracellular (ICD) domains, each chosen independently from a CAR (calcium receptor), GluR (metatropic glutamate receptor) and GABAR (gamma-aminobutyric acid receptor); (2) an optional linker attached to the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the linker. (I), and recombinant chimeric receptors (CR) without the GP component, are used to assess function of the various domains and to identify compounds (e.g. allosteric modulators or antagonists) that act on these domains. The modulators are potentially useful for treating or preventing diseases associated with the receptors, e.g. stroke, head or spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia, Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive disorders and depression. Nucleic acid (II) that encodes (I) is used: (1) for recombinant production of corresponding proteins; and (2) to produce cells used in screening for modulators. Use of Car and mGluR domains allows presentation of GABAR domains, to a binding agent, in a form more like the natural domain structure compared with use of incomplete receptors, lacking one or more domains. By shuffling different domains, agents can be identified that affect particular domains of a receptor

XX SQ Sequence 3234 BP; 739 A; 931 C; 829 G; 735 T; 0 U; 0 Other;

Query Match 42.2%; Score 1745.2; DB 2; Length 3234;
Best Local Similarity 76.4%; Pred. No. 5.8e-300;
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;

QY 501 CTCAGGGTATGTCCTCAACCAAGGCGCCAGAGAAAGAGACATCATCTGGAGGGTCT 560

DB 51 CTCCTGCTACGGGCGACACAGCGGCCCAAGAGAGGGGACATATCTCTGGGGGCT 110

QY 561 CTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGACTTTAAATCGAGACCGAGGC 620

DB 111 CTTTCCTATTCTTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGCCGGAGTC 170

QY 621 GACAAATGTAATTCGGTACAAATTTTCGAGGCTTCGGATGGCTCCAGGGGATGATATTCG 680

DB 171 TGTGAATGATCAGGTATAATTTCCGTGGTTTCCGTGTTTACAGGCTATGATATTTGC 230

QY 561 AATTGAGAGATTAAACACAGATATGACTTTCTCGCCCAATATCACCTGGGATATCGCAT 740

DB 231 CATAGAGAGATAAACAGAGCCAGCCCTTTCTCCCACTTGACGCTGGGATACAGGAT 290

QY 741 ATTTGACACCTGTAAACACCGTGTCCAGGCGCTAGAGGCAACACTCAGCTTTTGTGCCCA 800

DB 291 ATTTGACACCTGTAAACACCGTGTCCAGGCGCTAGAGGCAACACTCAGCTTTTGTGCCCA 350

QY 801 GAACAAATGACCTCGCTGAACTTAGATGAGTTCTGTAACTGCTCTGACCAATATCCATC 860

DB 351 AACAAATGATTTCTTTGAACCTTGATGAGTTCTGCACTGCTCAGAGCACATTCCTC 410

QY 861 CACAATAGCAGTGGTCCGGGCAACCGGCTCAGGAATCTCCACGGCTGTGCCCAATCTATT 920

DB 411 TACGATTTGCTGGTGGAGCAACTGGCTCAGGCTCTCCACGGCAGTGCGCAATCTGCT 470

QY 921 GGGATTAATTTTACATTCACAGGTGAGCTATGCTCTCTGAGCAGGCTGCTCAGCAACAA 980

DB 471 GGGCTCTTTCTACATTTCCCGAGGTCAATGCTCTCTCAGCAGACTCTCTCAGCAACAA 530

QY 981 GAATGAGTACAAAGCCCTTCTGAGGACCAATCCCAATGATGAGCAACAGAGCCACGCCAT 1040

DB 531 GAATCAATTTCAAGTCTTTCTTCGACCACTCCCAATGATGAGCAACAGAGCCACTGCCAT 590

QY 1041 GGGCGAGATCATCGAGCACTTCCAGTGGAACTCGGTGGGAAACCTCGCAGCCGACATGA 1100

DB 591 GGCAGACATCATCGAGTATTTCCGCTGGAATCGGTGGGCAAAATTCGAGCTGATGACGA 650

QY 1101 CTATGGCGCCCGAGGATTCAGAGTTCCGGAGGAGGCGCTTAAGAGGACATCTGAT 1160

DB 651 CTATGGCGCCCGAGGATTCAGAGTTCCGGAGGAGGCTGAGGAAGGATATTCGAT 710

QY 1161 TGACTTCAGTGCAGATGATCTCTCAGTACTACACCCAGAGAGCAGTTGGAGTTTCATCCCGA 1220

DB 711 CGACTTCAGTGCAGTACTCTCTCCAGTACTCTGATGAGGAAGAGATCCAGCATGTGTAGA 770

QY 1221 GGTATCCAGAACTCTCTGGCCAAAGTTCATCGTGTCTTCTCCAAATGGCCCGACCTGA 1280

DB 771 GGTGATTTCAAATTTCCAGCCCAAGTTCATCGTGTCTTCTCCAGTGGCCCGACATCTGA 830

QY 1281 GCGCTCATCCAGAGATAGTTCGGGAAACATCAACCGATCGGATCTGGTGGCCAGCGA 1340

DB 831 GCGCTCATCCAGAGATAGTTCGGGAAACATCAACCGATCGGATCTGGTGGCCAGCGA 890

QY 1341 GGTGTTGGCCAGTCTCTCGTCTCATTTCCAAAGCCAGAGTACTTCCAGTGGTGGCGGAC 1400

DB 891 GGCCTGGCCAGTCTCTCTCGTCTCATTTCCCAATGCTCAGTACTTCCAGTGGTGGCGGAC 950

QY 1401 CACTCGCTTCGCTCTCAGGCGGGGATTCAGAGGTTCAACAACTTCTCTGAAGGAGT 1460

DB 951 CATTGGATTCGCTCTGAAGGCTGGGAGATCCAGGCTTCCGGGAATTCCTGAAGAGT 1010

QY 1461 CCACCCCGAGGCTCTCGGACAAATGGTGTTCGAAGGAGTCTCGGAGGAGACCTTCAA 1520

DB 1011 CCATCCCGAGGAGTCTGTCCCAATGGTTTTCGAAGGAGTTCCTGGGAACAAATTTAA 1070

QY 1521 CTGCTACTTCAGGAGAGACCTCTGAGGAGCTGAGAGATTCAGAGTGGCTTCGACCG 1580

DB 1071 CTGCCACCTTCAAAG-----AGTGTCAAAGGAGCTTTTACCTGTGACACTTTCTG 1122

QY 1581 ACCGGCGCTCAAGGGGACGGCTCCAGGCGGGGAACTCCAGAGCGAGACGCCCTAGCCCA 1640

DB 1123 AGAGG----TCAAGAGAAAGTGGCGGAGGTTTAGCAACAGCTCGACAGCTTCGACC 1178

QY 1641 CCCTGTCATGGGGGAGAGAAATCATACAGCGTGGAGACCCCTTACTCTGGATTTATACAA 1700

DB 1179 CCTCTGTACAGGGGATGAGAAATCAGCAGTGTGCGAGAGCCCTTTACATAGATTACACGA 1238

QY 1701 CCTGAGGATCTCTCAATGTATACGTGGCGGCTACTCCATTTGCTCAGCCCTGCAAGA 1760

DB 1239 TTTACGAGATCTCTCAATGTGTACTTAGCAGTCTACTTCCATTTGCCAGCCCTTGAAGA 1298

QY	2841	GTCCCGTAAGCTGCCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTTGAT	2900
Db	2379	GTCCCGAAGCTGCCGAGAACTTCAATGAAGCGAAGTTTCATCACCTTCAGCATGTTGAT	2438
QY	2901	CTTCTTCACTGCTGCTGATCTCTTCAATCCCGCTATGTCAGCACCTTCAGCAAGTTTGT	2960
Db	2439	CTTCTTCACTGCTGCTGATCTCTTCAATCCCGCTATGTCAGCACCTTCAGCAAGTTTGT	2498
QY	2961	GTCCGCGCTGAGGTTGATTGCCATCTGCTGCTTCCAGCTTTCGCGCTGCTGCTGCTGCT	3020
Db	2499	CTCTGCGTAGAGGTGATTGCCATCTGCTGCTTTCGCGCTGCTGCTGCTGCTGCTGCT	2558
QY	3021	CTTCAACAGTGTATCATCTCTGTTCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3080
Db	2559	CTTCAACAGTGTATCATCTCTGTTCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2618
QY	3081	CTGACAGCGCGCGCTGCTGCTTCAAGGTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT	3140
Db	2619	TTGACAGCGCGCTGCTGCTTCAAGGTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2678
QY	3141	CGCGTCTGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3200
Db	2679	CGTCTCCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2738
QY	3201	CACCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3260
Db	2739	CATCAGCAGCAAGCAACA-----CGAGACCCATTCCACAGCCCGAGAGGAGAG	2793
QY	3261	CGCAGCGCGCACCGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3320
Db	2794	CAGCAGCGCGCTGCTGCTTAAACCAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	2853
QY	3321	CAGCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3362
Db	2854	CAGCAGCAACGATCTCAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2895
RESULT 9			
AA90922			
ID	AA90922 standard; DNA; 3234 BP.		
XX	AA90922;		
AC	17-JAN-2000 (first entry)		
XX	Human calcium receptor nucleic acid sequence.		
DE	Human calcium receptor; GABABR modulator; GABABR receptor protein;		
KW	gamma-aminobutyric acid receptor; metabotropic receptor;		
KW	chimeric protein; synaptic transmission; extracellular binding domain;		
KW	antagonist activity; intracellular domain; intracellular effect; ds.		
XX	Homo sapiens.		
XX	Key		
XX	Location/Qualifiers		
FT	1..3234		
FT	/*tag= a		
FT	/product= "Human calcium receptor protein"		
XX	WO9951636-A2.		
XX	14-OCT-1999.		
XX	02-APR-1999; 99WO-US007352.		
XX	03-APR-1998; 98US-0080676P.		
XX	(NPS-1) NPS PHARM INC.		
XX	Garrett JE, Simin RT, Busby JG, Stormann TW;		
XX	WPI; 1999-610994/52.		
XX	P-PSDB; AAY28840.		

QY	1761	CATCACTCTTTGAAACCCGCGGATCTTTGAAACGATCTTTGCGAGATATTA	1820
Db	1299	TATATATACCTTCTTACCTGGAGAGGCTCTTCAACCAATGGCTCTGTCAGACATCA	1358
QY	1821	AAAGTTGAGCGCTGCGAGGCTCTCAACCAATCTGCTGATCTGAAGTTTACCAACGAT	1880
Db	1359	GAAAGTTGAGCGCTGCGAGGCTCTGAACCAATCTGCTGATCTGAAGTTTACCAACGAT	1418
QY	1881	GGGTGAGCAGGTGATCTTTGACGATCAAGGTGACCTCAAGGGGAATACACATTAACA	1940
Db	1419	GCGGAGCAGGTGACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG	1478
QY	1941	CTGCGAGCTCTCGCAGAGGATGAATCGGTGTTTCCATGAGTGGGCAACTACAACGC	2000
Db	1479	CTGCGAGCTCTCGCAGAGGATGAATCGGTGTTTCCATGAGTGGGCAACTACAACGC	1538
QY	2001	CTACGCTTAAGCCAGTGAACGACTCAACATCAACGAAAGAAATCTCTCGAGTGGCTT	2060
Db	1539	CTATGCCAAGAGGAGAAAGACTCTTCAACGAGGAGAAATCTCTGAGTGGGCTT	1598
QY	2061	CTCCAAAGTGGTCTCTTCTCAACTGCGAGTGGAGTGTGCGCGGCAACGAGGAAGG	2120
Db	1599	CTCCAGGAGGTCCTCTTCTCAACTGCGAGTGGAGTGTGCGCGGCAACGAGGAAGG	1658
QY	2121	GATCATCGAGGAGGAGCCCACTGCTGCTTTGAATGATGATGATGATGATGATGATGATG	2180
Db	1659	GATCATCGAGGAGGAGCCCACTGCTGCTTTGAGTGTGATGATGATGATGATGATGATG	1718
QY	2181	CAGTCAATCAACAGATGACGATGCTGACAAAGTCCCGAATGATTTCTGTCGAATGA	2240
Db	1719	TAGTCAATGACAGATGACGATGCTGACAAAGTCCCGAATGATTTCTGTCGAATGA	1778
QY	2241	GAAACACAGCTGTCATCGCAAGGAGATCGAGTACCTGCTGAGGAGGAGGCTTGG	2300
Db	1779	GAAACACAGCTGTCATCGCAAGGAGATCGAGTACCTGCTGAGGAGGAGGCTTGG	1838
QY	2301	GATCGCTGACATCTTCCGCTACTGGGATCTGATCACTCTCTGCTGCTGCTGCTGCTG	2360
Db	1839	GATCGCTGACATCTTCCGCTACTGGGATCTGATCACTCTCTGCTGCTGCTGCTGCTG	1898
QY	2361	CTTCAATCAAGTTTCAGAAACACTCCCATCGTGAAGGCCACCAACCGGGAGTTGTCTACCT	2420
Db	1899	GTTTATCAAGTTTCAGAAACACTCCCATCGTGAAGGCCACCAACCGGGAGTTGTCTACCT	1958
QY	2421	GCTGCTCTTCTCCATCTGCTGCTTCTCCAGTCTGCTCATCTTCATCGCGGAGCCAG	2480
Db	1959	CCTCCTCTTCTCCATCTGCTGCTTCTCCAGTCTGCTCATCTTCATCGCGGAGCCCA	2018
QY	2481	GGACTGGACCTGTCGCTCCGCAACCGGCTTTGGCATCAGCTTCGCTGCTGCTGCTGCTG	2540
Db	2019	GGACTGGACCTGTCGCTCCGCAACCGGCTTTGGCATCAGCTTCGCTGCTGCTGCTGCTG	2078
QY	2541	CTGCACTCTGGTGAAGACCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2600
Db	2079	ATGCACTCTGGTGAAGACCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2138
QY	2601	CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTTCCTCTGCTGCTGCTGCTGCTGCTGCTG	2660
Db	2139	CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTTCCTCTGCTGCTGCTGCTGCTGCTGCTG	2198
QY	2661	GGTGAATAATCGTCACTGATCATCTGGCTCTACACCGGCTCTCCCTCCAGTACAGGAA	2720
Db	2199	CATGCAAGTTGATCTGCTGATCTGGCTCTACACCGGCTCTCCCTCCAGTACAGGAA	2258
QY	2721	CCATGAGCTGGAGGAGGATCATCTTCACTGCGAGGAGGCTGCTCATGCGCT	2780
Db	2259	CCAGGAGCTGGAGGATGATCATCTTCACTGCGAGGAGGCTGCTCATGCGCT	2318
QY	2781	GGCTTCTCTCATCGGCTACACCTGCTCTCGCGCAATCTCTTCTTCTGCTGCTTCAA	2840
Db	2319	GGCTTCTCTCATCGGCTACACCTGCTCTCGCGCAATCTCTTCTTCTGCTGCTTCAA	2378

XX Novel nucleic acids, used to screen for specific modulators, e.g. for
 PT treating spasticity or Alzheimer's disease.
 XX Disclosure; Fig 3A-3D; 78pp; English.
 XX The present sequence is the human calcium receptor nucleic acid sequence.
 CC This is used in assaying for compounds modulating GABAB activity. GABAB
 CC receptors are metabotropic receptors that modulate synaptic transmission
 CC in brain. Portions of calcium receptor are swapped with portions of
 CC GABABR2 to create protein fusions. The agonist extracellular binding
 CC domain is swapped for measurement of antagonist activity. Intracellular
 CC domains are swapped for measuring intracellular effects caused by the
 CC different receptor
 XX Sequence 3234 BP; 739 A; 931 C; 829 G; 735 T; 0 U; 0 Other;

Query Match 42.2%; Score 1745.2; DB 2; Length 3234;
 Best Local Similarity 76.4%; Pred. No. 5.8e-300; Mismatches 658; Indels 17; Gaps 3;
 Matches 2187; Conservative 0;

QY 501 CTCAGGGTATGTTCCAAACCAAGGCGCCAGAGAAAGGAGACATCATACTGGGAGGTCT 560
 DB 51 CTCGTGCTACGGCCAGACAGCGAGCCCAAGAGAGGGGACATTATCTTGGGGGCT 110
 QY 561 CTTCCTCAATACACTTTGGAGTAGCCGCCAAGGATCAGNCTTAAATCGAGACCGGAGC 620
 DB 111 CTTTCCTATTCATTTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGGCCGGAGTC 170
 QY 621 GACAAATGATTCGGGTACAAATTTTCGAGGCTTCGGATGGCTCCAGGGCGATGATTCGC 680
 DB 171 TGTGGATGTATCAGGTAAATTTCCGTGGTTCGCTGGTTACAGGCTATGATTTGC 230
 QY 681 AATTGAAGAGATTAACAAGATGACTTTCTCGTGGGTTTCCGCTGATGATTCGATTCGGAT 740
 DB 231 CATAGAGGAGATAAACAGAGCCGACCTTCTTCCCACTTTGAGCTGGGATACAGGAT 290
 QY 741 ATTGACACGTGTAAACACCGTGTCAAGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA 800
 DB 291 AATTGACACTTGAACACCGCTTTCTAAGGCTTGAAGCCACCTGAGTTTGTGTCTCA 350
 QY 801 GAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAACTGCTCTGACCATATCCCATC 860
 DB 351 AAACAAATTTGATTTCTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACTTCCCTC 410
 QY 861 CACAAATAGCAGTGGTGGGGCAACCGGTTCAGGATCTCCAGGCTGGCCAACTATT 920
 DB 411 TAGGATGCTGTGGTGGGAGCACTGGCTCAGGCTTCCAGGCTGGGCAATCTGCT 470
 QY 921 GGGATTTATTTTACATTCACAGGTGAGCTATGCTCTCCAGCAGGCTGCTCAGCAACAA 980
 DB 471 GGGGCTCTTCTACATTTCCCGAGGTGAGTTATGCTCTCCAGCAGCTCTCAGCAACAA 530
 QY 981 GAATGATACAGGCTCTCAGAGCACTCCCAATGATGAGCAACAGGCAACGCGCAT 1040
 DB 531 GAATCAATTTCAAGTCTTTCTCCGAGCACTCCCAATGATGAGCAACAGGCACTGCGCAT 590
 QY 1041 GGGCAGATCATCGAGCACTTCCAGTGAATCTGGGTGGGAACCTTGGCAGCGCAGATGA 1100
 DB 591 GGCAGACATCATCGAGTATTTCCGTGGNACTGGGTGGGCACAAATTTGAGCTGATGAGA 650
 QY 1101 CTATGGCCGCCAGGCAATGAAGTTCCGGAGAGGCGGTTAAGAGGCACTCTGAT 1160
 DB 651 CTATGGCCGCCGGGGAATGAGAAATTCGAGAGGAAGCTGAGGAAGGATATCTGCAAT 710
 QY 1161 TGACTTCAGTGAGATCATCTCTCAGTACTACACCAGAGCAGTTTGGAGTTTCATCGCGCA 1220
 DB 711 CGACTTCAGTGAATCATCTCCAGTACTCTGATGAGGAAGATCCAGCATGTGGTAGA 770
 QY 1221 CGTATCCAGAACTCTCTGGCCAAAGGTATCATGTGCTTCTCCAAATGCCCCCGACCTGGA 1280
 DB 771 GGTGATTCAAATTCACGGCCAAAGTCACTGTGGTTTCTCCAGTGGGCCAGATCTTGA 830

QY 1281 GCCCTCATCCAGGAGATAGTTCCGAGAAACATCAACGATTCGATTCGGCTGGCCACGCA 1340
 DB 831 GCCCTCATCAAGGAGATTCGGGGGCAATACAGGGCAAGATTCGGCTGGCCACGCA 890
 QY 1341 GGCTTGGCCAGCTCTTCGCTCATTCGCCAGCCAGAGTACTCCAGCTGGTCCGGCCGAC 1400
 DB 891 GGCTTGGCCAGCTCTTCCTGATTCGCCATGCTCTAGTACTCCAGCTGGTGGCCGAC 950
 QY 1401 CATCGGCTTCGCTCTCAGGGCGGGGTATTCACAGGTTTCAACAAGTTCCTGAAGAGGT 1460
 DB 951 CATTTGATTCGCTCTGAAGCTGGGCAGATCCAGGCTTCGGGAATTCCTGAAGAAGGT 1010
 QY 1461 CCACCCAGCAGGTCCTCGGACAAATGGTTTGTCAAGGAGTTCCTGGAGGAGACCTTCAA 1520
 DB 1011 CCATCCAGGAGTCTGTCCACAATGGTTTTCGAAGGAGTTTGGGAAGAAACATTTAA 1070
 QY 1521 CTGCTACTTCCAGAGAAAGCCCTGACGAGCTGAAGAATTCGAAGTGGCTTCGCACGG 1580
 DB 1071 CTGCCACTCCAAGA-----AGTGCAAAAGGACCTTACTCTGGACACCTTCTG 1122
 QY 1581 ACCGCGGCTCAAGGGGACGGCTTCAAGCGGGGAACTCCAGACGGACAGCCCTACGCCA 1640
 DB 1123 AGAGG-----TCAGGAAGAAAGTGGCGACAGTTTAGCAACAGCTCGACAGCTTCGGACC 1178
 QY 1641 CCCTGCACTGGGAGGAGAAACATCACACGCTGGAGACCCCTACTCTGGATTATACACA 1700
 DB 1179 CCTCTGTACAGGGGATGAGAAACATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1238
 QY 1701 CCTGAGGATCTCCTCAATGTATACGTGGCGCTACTCTCAATGCTCAGCCCTCGAAGA 1760
 DB 1239 TTTACGGATATCTCAATGTGTACTTAGCAGTCTACTCCATTCGCCACGCTTGCAGA 1298
 QY 1761 CATCCACTCTTGCACAAACCGGACGGGCATCTTGCACAGGATCTTGTGCGAGATTTAA 1820
 DB 1299 TATATATACCTGTCTACCTGGGAGAGGGCTCTTCAACATGGCTCTCTGTGCGACATCAA 1358
 QY 1821 AAAAGTTGAGGCTTCGAGCTCTCAACCATCTGCTGCACTCTGAACTTTACCAACAGCAT 1880
 DB 1359 GAAAGTTGAGGCTTCGAGCTCTCAAGCACCTTACGGCATCTAAACTTTTACAAACAAT 1418
 QY 1881 GGTGAGCAGGTTGACTTTGACGATCAAGTGAACCTCAAGGGGAACTACACCATTTCAA 1940
 DB 1419 GGGGAGCAGGTCACCTTTGATGAGTGTGGTGAACCTTGGTGGGAACTATTTCCATCATCAA 1478
 QY 1941 CTGGCAGCTCTCCGACAGAGGATGAATCGGTGTTGTTTCCATGAGTGGGCAACTTACAACGC 2000
 DB 1479 CTGGCAGCTCTCCGACAGAGTGGCTCCATCGTGTTTAAGGAAGTCGGGTATTTACAACGT 1538
 QY 2001 CTAGCTTAAGCCCAAGTGAACGACTCAACATCAACGAAAGAAATCCTCTGAGTGGCTT 2060
 DB 1539 CTATGCAAGAGGAGAAAGACTCTTCACTCAACGAGGAGAAATCCTCTGAGTGGGT 1598
 QY 2061 CTCCAAAGTGGTTCCTTTCTCCAACTGCACTGAGACTGTGCGCGGACACGAGGAAGG 2120
 DB 1599 CTCAGGAGGTGCCCTTCTCCAACTGCAAGCCGAGACTGCTGGCAGGAGCAAGGAAGG 1658
 QY 2121 GATCATCGAGGGGAGCCCACTGCTGCTTGAATGCAATGGCATGTGACAGAGGAGATT 2180
 DB 1659 GATCATTTAGGGGGAGCCCACTGCTGCTTGAATGCTGAGTGTGGAGTGTCTGTAGTGGGAGTA 1718
 QY 2181 CAGTGTAGAAACGATGCAAGTGTGTAACAAGTCCCGAATGATTTCTGTGTCGATGA 2240
 DB 1719 TAGTGTATGACAGATGCGCAGTGCCTGTAAACAGTGGCCAGATGACTTCTGTGTCGAATGA 1778
 QY 2241 GAACCAACAGCTCTGTCATCGCCAAAGGAGATCGAGTACCTGTCTGTGACGAGGACCTTCGG 2300
 DB 1779 GAACCAACAGCTCTGTCATTTGCCAAGGAGATCGAGTTTCTGTGACGAGGACCTTTGG 1838
 QY 2301 GATCGCTGTGACCATCTTCGCGGTACTGGGCACTCTGATCACTCTTCTGCTGCTGGGGGT 2360
 DB 1839 GATCGCACTCACCTCTTTCCGCTGTGGGCAATTTTCTGTGACAGGCTTTGTCTGGGTGT 1898
 QY 2361 CTTTCATCAAGTTTCAAGAAACACTTCCCATCTGTGAAGGCCCAACACCGGAGTGTCTCTACCT 2420

OS	Homo sapiens.
XX	
PN	WC2004040000-A2.
XX	
PD	13-MAY-2004.
XX	
PP	09-SEP-2003; 2003WO-US028226.
XX	
PR	09-SEP-2002; 2002US-0409303P.
PR	09-APR-2003; 2003US-0461329P.
XX	
PA	{PRIM-} PRIMAL INC.
XX	
PI	Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI	Madisen L, McIlwain KL, Parlova MN, Vassilatis D, Zeng H;
XX	
XX	WPI; 2004-390329/36.
DR	P-PSDB; ADO29211.
XX	
XX	Novel mammalian G protein coupled receptors, useful for identifying
PT	compounds that modulates diagnosing and treating disease condition
PT	associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT	pectoris, Parkinson's disease.
XX	
XX	Claim 151; SEQ ID NO 926; 543pp; English.
PS	
XX	

Sequence 3237 BP: 741 A; 931 C; 829 G; 736 T; 0 U; 0 Other;

Qy	501	CTCAGGGTATGGTCCAAACCAAGGGCCCGAAGAAAGGACATCATCTGGAGGCT	560
Db	51	CTCTGCCTACGGCCAGACAGGAGGCCCAAGAAAGGGGACATTATCTTGGGGGCT	110
Qy	561	CTTCCCAATACACTTTTGGAGTAGCCGCCAAGGATCAGGACTTAAATTCGAGACCGGAGGC	620
Db	111	CTTTCTATTCTATTTGGAGTAGCAGTAAAGATCAAGATCTCAATCAAGGCCCGAGTC	170

22

T07

[illegible]

DB 351 AAACAAATATGATATCTTGGAACTTGGATGAGTTCGCACTGCTCAGAGCAGATTCCTTC 419

DB 411 TACGATTGCTGTGTGGTGGAGCAACTGGCTCAGGGGCTCTCCACGGGCAGTGGCAGATCTGCT 470

D5 471 GGGGCTCTTCTACATTCCTCCAGGTCAGTTATGCTTCCTCCAGCAGACTCCTCAGCAACA 530

Db 531 GAATCAATTCAAGTCTTTCTCCGAACCATCCCCAATGATGAGCACCAGGCCACTGGCAT 590

1041 GSCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGAACCTCGGAGCGCAGATGA 1100
Db
591 GCGAGACATATCGAGTATTTCCGTGGAACTGGGTGGGCAANTTGCAGCTGATGACGA 650
Qy
1101 CTATGCGCCGCCAGGCAATGACAAGTTCCGGAGGAGGCGGTTAAGAGGCAATCTGTAT 1160
Db
651 CTATGCGCGCCGGGATTTAGAAATTCGAGAGGAAGCTGAGGAAAGGATATCTGCAT 710
Qy
1161 TGACTTCAGTGAGATGATCTCTCAGTACTTACACCCAGAGAGTTGGAGTTCAATCGCGGA 1220
Db
711 CGACTTCAGTGAATCATCTCCAGTACTTCTGATGAGGAAGATCCAGCATGTGGTAGA 770
Qy
1221 CGTATCCAGAACTCTCCGCGCAAGTCACTGTGGTCTTCTCCAAATGGCCCGACCTCGA 1280
Db
771 GGTGATTCAAATTCACGCGCAAGTCACTGTGGTCTTCTCCAGTGGCCAGATCTTGA 830
Qy
1281 GCGCTCATCCAGGAGATAGTTCCGAGAGAAACATCAACGATCGGATCTGGCTGGCCAGGA 1340
Db
831 GCGCTCATCAAGGAGATTTCCGCGCAATATACGCGCAAGATCTGGCTGGCCAGGA 890
Qy
1341 GCGTGGGCGAGCTCTTCCGCTAATTCGCAAGCAGAGTACTTCCAGCTGGTGGCGGCAC 1400
Db
891 GCGCTGGGCGAGCTCTTCCGCTAATTCGCAAGCAGAGTACTTCCAGCTGGTGGCGGCAC 950
Qy
1401 CATCGCTTCGCTCTAAGCGCGGCGTATCCAGGGTTCAACAGTTCTTGAAGAGGT 1460
Db
951 CATTTGATTCGCTCTCAAGGCTGGGCGAGATCCAGGCTTCGGGAATTCCTGAAGAGGT 1010
Qy
1461 CCACCCAGAGTCTCGGCAATGGGTTTCTCAGAGTTCTGGGAGGAGCTTCAAC 1520
Db
1011 CCATCCAGAGTCTGTCCCAATGGTTCGCAAGGATTTGGGAGAGAAATTTAA 1070
Qy
1521 CTGCTACTTCACGAGAGAACCTCAGCGAGCTGAAGAAATTCAGAGTGCCTCGCAGG 1580
Db
1071 CTGCCACCTCCAAGA-----AGTGCAAGAGACCTTTACCTGTGCACACCTTTCTG 1122
Qy
1581 ACGGCGGCTCAAGGGAGCGCTCAAGCGGGAACTCCAGAGGAGAGCTTACGCCA 1640
Db
1123 AGAGG----TCAGAGAGAAAGTGGGAGAGGTTTAGCAACAGCTCGACAGCTTCGGACC 1178
Qy
1641 CCGCTGCACTGGGAGGAGAAATCAACAGCGTGAGACCCCTACCTGGATTATACAA 1700
Db
1179 CTTGTGACAGGGATGAGAAATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1238
Qy
1701 CTTGAGGATCTCTCAATGATATAGTGGCGCTTACTTCCATTTGCTCAAGCCCTGCAAGA 1760
Db
1239 TTTACGGATATCTCAATGTGTACTTTAGCAGTCTACTCCATTTGCCACGCGCTTGAAGA 1298
Qy
1761 CATCACTCTTCAAAACCGGACCGGATCTTTGCAAAAGGATCTTGTGCAGATATTAA 1820
Db
1299 TATATATCTCTTACCTGGAGAGGGCTCTTACCAATGGCTCTGTGCAGACATCAA 1358
Qy
1821 AAAAGTTAGGCTGGCAGGCTCTCAACCAATCTGTGCTGATGAGTTTACCAAGCAT 1880
Db
1359 GAAAGTTAGGCGTGGCAGGCTCCTGAAGCACCTACGGCATCTAAACTTTACAAACAATAT 1418
Qy
1881 GGTGAGGAGTTGATTTGAGATCAAGGTGACCTCAAGGGGACTACACATTTCAA 1940
Db
1419 GGGGAGCAGGTTGACCTTTGATGTGTGTGACCTGTGGGGAACCTATTCCATCATCAA 1478
Qy
1941 CTGGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCATAGGTGGGCAACTCAACGCG 2000
Db
1479 CTGGCAGCTCTCCGAGAGGATGGCTCCATCGTGTTTAAGGAAGTCCGGTATTACAAGT 1538
Qy
2001 CTACGCTAAGCCAGTACCGCATCAACATCAACGAAAGAAATCTCTGAGTGGCTT 2060
Db
1539 CTATGCCAAGAGGAGGAGAAAGTCTTTCAACAGGAGGAAATCTCTGTGAGTGGGTT 1598
Qy
2061 CTCCAAAGTGGTCTCTTTCTCCAACTGAGTCTGAGACTGTGTGCGGCGCACAGGAAGG 2120
Db
1599 CTTCAGGAGGTTGCCCTTCTCCAACTGAGCGGAGACTGCTTGGCAGGACCAAGGAAGG 1658

2121 GATCATCGAGGGAGGCCACCTGCTGCTTTGAATGATGGCATGTGCAGAGGAGGTT 2180
Db
1659 GATCATTTAGGGGGAGGCCACCTGCTGCTTTGAGTGTGTGGAGTGTCTGATGGGAGTA 1718
Qy
2181 CAGTGATGAAAACGATGCAAGTGGTGTACAAAGTCCCGAATGATTTCTGTTCGATGA 2240
Db
1719 TAGTGATGACAGAGATGCCAGTGCCTGTAAACAGTGCCAGATGACTTTGTGTCCAATGA 1778
Qy
2241 GAACCAACGCTGCTGATCGCCAAAGAGATCGAGTACTGTCTGTGACGAGAGCCCTTCGG 2300
Db
1779 GAACCAACGCTGCTGATTTGCCAAAGAGATCGAGTTTCTGTGTGACGAGAGCCCTTCGG 1838
Qy
2301 GATGCTCTGACCATTTTCCGCGTATCTGGGCACTCTGATCACTCTTCTGTGTCTGGGGT 2360
Db
1839 GATGCACTCACCTCTTTCGCGTGTGGGCAATTTCTTGCAGAGCTTTGTGTGGGTGT 1898
Qy
2361 CTTTATCAAGTTCCAGGAACATCTCCATCTGTGAAGGCCAACCCGGAGTTGTCTTACCT 2420
Db
1899 GTTTATCAAGTTCCGCAACACACCCATTTGTCAAGGCCAACCCGAGAGCTCTTCTTACT 1958
Qy
2421 GCTGCTCTTCTCCCTCATCTGTGCTTCTCCAGCTCGCTCATCTTTCATCGGAGAGCCAG 2480
Db
1959 CTTCTCTTCTCCCTGCTCTGTGCTTCTCCAGCTCCCTGTTCTTTCATCGGAGAGCCCA 2018
Qy
2481 GATGAGACCTGTGCGCTCGGCCAACCGGCTTTGGCATCAGTTGCTCTGTGATCTC 2540
Db
2019 GACTGGAGGTGCGGCTCGGCCAGCGGCTTTGGCATCAGCTTGTGCTCTGTGATCTC 2078
Qy
2541 CTGCATCTTGTGAAGAACCAACCGGCTGTGTGTCTTTCGAGGCCAAGATCCCCACCAAG 2600
Db
2079 ATGCATCTTGTGAAGAACCAACCGTGTCTCTGTGTGTTTGAAGGCCAAGATCCCCACCAAG 2138
Qy
2601 CTTCCACCGCAAGTGGTGGGCTCAACCTGCAAGTTCTCTGCTGTCTCTGTGATCTC 2660
Db
2139 CTTCCACCGCAAGTGGTGGGCTCAACCTGCAAGTTCTCTGCTGTGTTTCTCTGTGACCTT 2198
Qy
2661 GGTGCAAACTGTCACCTGATCATCTGTGCTTACACCGGCTCTCCCTCCAGCTACAGGAA 2720
Db
2199 CATGAGATTTGATCTGTGTGATCTGTGCTTACACCGGCGCCCTCAAGTACCGGAA 2258
Qy
2721 CCAATGAGCTGGAGGACGAGTCTATCTTCACTGCTGCAAGAGGCTCGCTCATGGCGT 2780
Db
2259 CCAGGAGCTGGAGGATGAGATCATCTTCACTGCTGCAAGAGGCTCGCTCATGGCGCT 2318
Qy
2781 GGGCTTCTTCACTGCTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2840
Db
2319 GGGCTTCTTCACTGCTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2378
Qy
2841 GTCCGCTTAAAGTCTCCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTGAT 2900
Db
2379 GTCCGAGAGCTGCGGAGAACTTCAATGAAGCAAGTTTCATCACCTTCAGCATGTGAT 2438
Qy
2901 CTTCTTCACTGCTGATCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2960
Db
2439 CTTCTTCACTGCTGATCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2498
Qy
2961 GTCCGCTTAAAGTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3020
Db
2499 CTTCTGCTGATGAGTGTGATTTGCCATCTTGGCAGGAGCTTTGCTGCTGCTGCTGCTGCT 2558
Qy
3021 CTTCAACAAAGTGTATCATCTGTTCAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3080
Db
2559 CTTCAACAAAGTGTATCATCTTCAAGCCATCCCGCAACATCCCGCAAGCTGCTGCTGCTGCT 2618
Qy
3081 CTTGAGGAGCGGCGGCGGCGGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3140
Db
2619 TTTGAGGAGCGGCGGCGGCGGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2678
Qy
3141 CCGGCTTCCGAGAGGCTTCCAGGAGGCTGTGCGGCTTCCAGCTCTCTGCTGCTGCTGCTGCT 3200
Db
2679 CGTCTCCGCAAGCGGCTCAGCAGGCTTGGAGGCTCCAGGAGTCCACCCCTCTCTCTCTC 2738
Qy
3201 CACTCGGCGGCGGCGGCTCAGCATGGAGATGACGCGCTGCAGCAGCAGAGGTCAGCTT 3260

QY 1341 GGCTGGGCGAGCTCTTCCTCATTCGCAAGCCAGGAGTACTTCCAGCTGGTGGCGGCAC 1400
 Db 1263 GGCTGGGCGAGCTCTTCCTCATTCGCAAGCCAGGAGTACTTCCAGCTGGTGGCGGCAC 1322
 QY 1401 CATCGGCTTCGCTCTCAGGCGGGGGGATCCAGGGTTCAACAAGTTCTCCTGAAGAGGT 1460
 Db 1323 CATGGAATCGCTCTGAAGGCTGGGAGATCCAGGCTTCGAGGAAATCCTGAAGAGGT 1382
 QY 1461 CACCCAGAGGTCTCTCGAACAATGGGTTTGTCAAGAGTTCTGGAGAGACCTTCAA 1520
 Db 1383 CCATCCAGAGAGTCTGTCCAAATGGTTTTCAGAGGTTTTCGGAAGAAATTTAA 1442
 QY 1521 CTGCTACTTCCAGGAGAGACCTGACGAGCTGAAGAAATTCAGAGGTCCTCCAGCG 1580
 Db 1443 CTGCCACCTCCAGA-----AGTGCAAGAGACCTTTACCTGTGGACACCTTTCTG 1494
 QY 1581 ACCGCGGCTCAAGGGAGCGGTCCAGAGCGGGGAACTCCAGAGCAGCCCTACGCCA 1640
 Db 1495 AGAGG----TCAGAGAAAGTGGGACAGAGTTTAGCAACAGCTCGACAGCCTTCGACC 1550
 QY 1641 CCCTGCACTGGGAGGAGAAATCACAGAGCTGGAGACCCCTACCTGGATTATACACA 1700
 Db 1551 CTTCTGTACAGGGAGTGAAGAAATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1610
 QY 1701 CTTGAGGATCTCTCAATGTATAGTGGCGGTCTACTCCATTTGCTCAAGCCCTGCAAGA 1760
 Db 1611 TTTAGGATATCTCAATGTGTACTTAGCAGTCTACTCCATTGGCCACGCTTGCAAGA 1670
 QY 1761 CATCACTCTTGAACCCGACCGGATCTTTCGAACGATCTTGTGAGATATTAA 1820
 Db 1671 TATATATACCTCTTACCTGGAGAGGGCTCTACCAATGGCTCCTGTGACAGATCAA 1730
 QY 1821 AAAAGTTGAGGCTGGCAGGCTCTCAACCATCTGTGATCTGAAGTTTACCAACAGAT 1880
 Db 1731 GAAAGTTGAGGCTGGCAGGCTCTGAGACCTACGGCATCTAAATTTTACAAACAAT 1790
 QY 1881 GGGTGAAGGTTGATTTGAGCATCAAGGTGACCTCAAGGGGAACTACCATTTATCAA 1940
 Db 1791 GGGGAGCAGAGTGACCTTTGATGAGTGTGTGACCTGGTGGGAACTATTTCATCATCAA 1850
 QY 1941 CTGGCAGCTCTCGGAGAGAGTGAATCGGTGTTGTTCCATGAGTGGGCAACTCAAGC 2000
 Db 1851 CTGGCACCTCTCCAGAGAGTGGTCCATCGTGTGTAAGAGTGGGATTTACAGCT 1910
 QY 2001 CTACGCTAAGCCAGTGCAGCTCAACATCAACAGAAAGAAATCTCTGGAGTGGTT 2060
 Db 1911 CTATGCCAAGAGGAGAAAGACTCTTCAACAGAGGAGAAATCTCTGGAGTGGTT 1970
 QY 2061 CTCGAAGTGGTTCTTTCTCACTGAGTGCAGTGTGTCGGGACCCAGGAGGG 2120
 Db 1971 CTCAGGAGGTTGCCCTTCTCACTGACGCGAGACTGCTGGCAGGACAGGAAAG 2030
 QY 2121 GATCATCGAGGGGAGCCACCTGCTGCTTTGAATGCAATGCGCATGTGAGAGGAGATT 2180
 Db 2031 GATCATGAGGGGAGCCACCTGCTGCTTTGAGTGTGTGGAGTCTCTGATGGGAGTA 2090
 QY 2181 CAGTGTGAAGAGTGAAGTGTGTACAAAGTGCAGGATGATTTCTGTCGAATGA 2240
 Db 2091 TAGTGATGAGACAGATGCCAGTGCCTGTAAAGTGCAGGATGATTTCTGTCGAATGA 2150
 QY 2241 GAACACACGCTGTCATGCCAAGAGATCAGTACCTGTGTCGAGCAGGAGCCCTTCGG 2300
 Db 2151 GAACACACCTCTGCAATGCCAAGAGATCAGTGTGTGGAGTCTCTGATGGGAGTTGG 2210
 QY 2301 GATGCTCTGACCATCTTCGCGTACTGGGCATCTGTATACCTCTTCTGCTGGGGGT 2360
 Db 2211 GATGCACTACCCCTCTTTCGCGTGTGGGCATTTTCTGACAGCCTTTGTGCTGGGTGT 2270
 QY 2361 CTTTCATCAAGTTTCAGAACACTCCCATCTGTGAAGGCCCAACCGGGAGTTGTCTACT 2420
 Db 2271 GTTTATCAAGTTTCGGAACACACCATTTGTCAAGGCCCAACCGAGAGCTCTCTACT 2330
 QY 2421 GCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTGCTCATCTTTCATCGGAGCCAG 2480

Db 2331 CTTCTCTTCTCCTGCTGCTGCTTCTTCCAGTCCCTGTTCTTTCATCGGAGGCCCA 2390
 QY 2481 GGAATGACCTGTGCGGCTCGCCAAACCGGCTTTTGGATCAGCTTCTGTCGATCTC 2540
 Db 2391 GGAATGACCTGTGCGGCTCGCCAAACCGGCTTTTGGATCAGCTTCTGTCGATCTC 2450
 QY 2541 CTGCATCCTGCTGAAGACCAACCGGCTGCTGCTGCTTTCGAGGCCAAGATCCCAACAG 2600
 Db 2451 ATGCATCCTGCTGAAGAACCAACCGTGTCTCTCTGCTGTTTGGAGCCAGATCCCAACAG 2510
 QY 2601 CTTCCACCGCAAGTGGGCTGCTCAACCTGCACTTCTCTGCTGCTTCTCTGCACTCT 2660
 Db 2511 CTTCCACCGCAAGTGGGCTGCTCAACCTGCACTTCTCTGCTGCTTCTCTGCACTCT 2570
 QY 2661 GGTGCAATCTGCTCACTGATCATCTGGCTCTACCGGCGCTCCCTCCAGCTACAGGA 2720
 Db 2571 CATGCAATTTGTCATCTGTGTGATCTGGCTCTACCGGCGCTCCCTCAAGCTACCGCA 2630
 QY 2721 CCATGAGCTGGAGAGAGGTCTATCTTTCATCACTGCGAGGAGGCTCGCTCATGGCGT 2780
 Db 2631 CCAGGAGCTGGAGATGAGATCATCTTTCATCACTGCGAGGAGGCTCCCTCATGGCGCT 2690
 QY 2781 GGGCTTCTCATCGGCTACACCTGCTCTCTGCGGCGATCTGCTTCTTCTGCTCTCA 2840
 Db 2691 GGGCTTCTCATCGGCTACACCTGCTGCTGCTGCTGCTTCTTCTTCTGCTCTCA 2750
 QY 2841 GTCCGCTAAGCTCCCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGATGTTAT 2900
 Db 2751 GTCCGAGAGCTCCCGAGAACTTCAATGAGCAAGTTTCATCACCTTCAGATGTTAT 2810
 QY 2901 CTTCTTCATCTGATCTCTTTCATCCCGCTTATGTCAGCACTACCGCAAGTTGT 2960
 Db 2811 CTTCTTCATCTGATCTCTTTCATCCCGCTTATGTCAGCACTATGCGCAAGTTGT 2870
 QY 2961 GTCCGCTGAGGATGATTTGCCATCTGCGCTCCAGCTTCCAGCTTCCGCTGCTGCTT 3020
 Db 2871 CTTCTGCTGAGGATGATTTGCCATCTGCGCTCCAGCTTCCGCTGCTGCTTCTT 2930
 QY 3021 CTTCAACAAGTTTATCATCTCTTTCAGCGCTGCTTCAACCATCCAGGAGTGG 3080
 Db 2931 CTTCAACAAGATCTACATCATCTTTCAGCGCTTCCCGCAACACCATCCAGGAGTGG 2990
 QY 3081 CTGAGCAAGGCGGCGCAAGCTTCAAGTGGGCGGCGGCGCAACCTCCGCGGAGCGC 3140
 Db 2991 TTGAGCAAGGCGGCGCAAGCTTCAAGTGGGCGGCGGCGCAACCTCCGCGGAGCA 3050
 QY 3141 CGGCTCTCGCAAGGCTTCCAGCAGCTGTCGCGCTCCAGCATCTCTCTCGCGGCTCTGTC 3200
 Db 3051 CTTCTCCGAGAGGCTCCAGCAGCTTGGAGGCTCCAGGATCCACCTCTCTCTCTC 3110
 QY 3201 CACTCGGCGCGGCGCTTACCATGAGATGAGCTGAGCTGAGCAGCAGAGGTGAGTT 3260
 Db 3111 CATCAGCAGCAAGAGCAACA-----GCGAAGACCATTCACAGCCCGAGGAGCAAG 3165
 QY 3261 CGCAGCGGCGCAGCTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3320
 Db 3166 CAGCAGCGGCTGCGCTTACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3225
 QY 3321 CAGCGCGCAGCGCGGCGGAGAACTCGCGGAGTGGCGGAG 3382
 Db 3226 CAGCAGCAAGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3267

RESULT 13
 ABX74489
 ID ABX74489 standard; cDNA; 3783 BP.
 XX
 AC ABX74489;
 XX
 DT 21-MAR-2003 (first entry)
 XX
 DE Human cDNA sequence #32 down-regulated in CC-RCC patients.

CC using pBopCar1 as a hybridisation probe. mRNA was isolated from a 39 year
CC old caucasian male diagnosed with primary hyperparathyroidism and two
CC clones of approx. 5 and 4 kb were identified. These cDNA's were injected
CC into Xenopus oocytes which were assayed for the presence of functional
CC calcium receptors. Both clone types gave rise to functional calcium
CC receptors as assessed by the stimulation of calcium-activated chloride
CC currents upon addition of appropriate calcium receptor agonists, e.g. NPS
CC R-467 and NPS R-568. Sequence analysis of the two cDNA clones indicated
CC the existence of at least two sequence variants differing in the 3',
CC untranslated region and which may result from alternative
CC polyadenylation. Sequence variation also exists in the 5' end of the
CC inserts. These sequence differences may have arisen due to alternative
CC transcription initiation and/or splicing. Three additional sites of
CC sequence variation occur within the coding regions of cDNA clones
CC pBopCar5.2 and pBopCar4.0 demonstrating that they encode distinct
CC proteins. Sequence analysis of the human Car gene indicates that the
CC additional 30 bp in clone pBopCar5.2 as compared to pBopCar4.0, results
CC from alternative mRNA splicing. This alternative splicing is predicted to
CC insert 10 additional amino acids into the Car protein encoded by
CC pBopCar5.2 between residues 536 and 537 of the protein encoded by
CC pBopCar4.0. In addition pBopCar4.0 encodes Gln at position 925 and Gly at
CC position 930, whereas pBopCar5.2 encodes Arg at both equivalent
CC positions. The human Car gene encodes for Gln and Arg respectively at
CC these positions. These two receptor isoforms may be functionally and/or
CC pharmacologically distinct

XX
SQ Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T; 0 U; 0 Other;
Query Match 42.2%; Score 1745.2; DB 2; Length 3809;
Best Local Similarity 76.4%; Pred. No. 66-300;
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;

QY 501 CTCAGGGTATGTCCTCAACCAAGAGGGCCGAGAGAGAGACATCATCTATCGGGAGGTCT 560
DB 423 CTCCTCCCTACGGGCCAGACCCAGCGAGCCCAAGAGAGGGGACATATCTCTTGGGGGGCT 482
QY 561 CTTCCCAATACACTTTGGAGTAGCCGCGCAAGATCAGGACTTAAATCGACACGGAGGC 620
DB 483 CTTTCTTATTCAATTTGGAGTAGAGCTAAGATCAAGATCTCAATCAAGCCGGAGTC 542
QY 621 GACAAAATGATTCGGTCAAAATTTTCGAGGCTTCGATGGTTCAGGCGATGATTTGCG 680
DB 543 TGTGAAATGATCAGGTATAATTTCCGTGGTTCGCTGGTTACAGGCTATCATATTTGC 602
QY 681 AATTCAGAGATTAACAAGATGACTTTCTGCGCCCAATATCACCTCGGATATCGCAT 740
DB 603 CATAGAGAGATAAAGAGAGCCAGCCAGCCCTTTCCCACTTGAAGCCACCTGAGTATCAGGAT 662
QY 741 ATTTGACAGGTAAACACCGTCTCCAGGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA 800
DB 663 ATTTGACACTTCAACACCGTTTCTAAGCCCTTGAAGCCACCTGAGTTTGTGCTCA 722
QY 801 GAACAAATCGACTGCTGAATTTAGATGAGTTCTGTAACTGCTTGACCATATCCCATC 860
DB 723 AAACAAAATTGATTTTGAACCTTTGATGAGTTCTGCAACTGCTCAGAGACATTCCTC 782
QY 861 CACAATAGCAGTGTGCGGGCAACCGGTGAGGAATCTCCAGGCTGTGGCCAAATCTATT 920
DB 783 TACGATGCTGTGGTGGAGCAACTGGCTCAGGCGCTCTCCAGGCGAGTGGCAATCTGCT 842
QY 921 GGGATTAATTTTCAATTCACAGGTGAGTATGCTTCCTCGAGAGCGGTGCTCAGCAACAA 980
DB 843 GGGGCTCTTCTCAATTCCTCCAGTTCAGTTATGCTCTCTCCAGCACTCTCTCAGCAACAA 902
QY 981 GAATGAGTACAGGCTTCTCGAGGACCATCCCAATATGATGAGCAACAGGCCAGGCCAT 1040
DB 903 GAATCAATTCAGTCTTCTCCGAAACCATCCCAATGATGAGCAACAGGCCAGGCCAT 962
QY 1041 GCGCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGAAACCTTGGCAGCGCAGATGA 1100
DB 963 GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCAAAATTGAGCTGATGACGA 1022
QY 1101 CTATGGCCGCCAGGCATTTGACAAAGTTCCGGGAGAGAGCCGCTTAAGAGGAGCATCTGTAT 1160

DB 1023 CTATGGCCGCCGGGATTCAGAAAATTCGAGAGAGAGCTGAGAAAGGATATCTGCAT 1082
QY 1161 TGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAGACAGTGGAGTTCTATCGCCGA 1220
DB 1083 CGACTTCAGTGAACTCATCTCCAGTACTCTGTATGAGGAGAGATCCAGATCTGTAGA 1142
QY 1221 CGTCATCCAGAACTCTCGGCCCAAGGTCTATCGTGTCTTCTCCAAATGGCCCGACCTGGA 1280
DB 1143 GGTGATTCAAAATTCACAGGCCAAAGTCTATCGTGGTGTCTTCAGTGGCCAGATCTTGA 1202
QY 1281 GCCGCTCATCCAGAGATAGTTCGGAGAAACATCACCGATCGATCTGCTGCTGCCAGCGA 1340
DB 1203 GCCCTCATCAAGAGATTTCCGGCGCAATATCACGGCAAGATCTGGCTGGCCAGCGA 1262
QY 1341 GGTGTGGCCAGCTCTTCGCTATTGCCAAGCCAGAGTACTTCCACGTGTGTCGCGGCAC 1400
DB 1263 GGCTGGGCCAGCTCTCTCCCTGATCGCATGCTCAGTACTTCCACGTGTGTTGGCGCAC 1322
QY 1401 CATCGGCTTCGCTCTCAGGGCGGGCGTATCCAGGGTTCAACAAGTTCTCTGAAGAGGT 1460
DB 1323 CATTTGATTCGCTCTGAAGGCTGGCGAGATCCAGGCTTCCGGGAAATCTCTGAAGAAGT 1382
QY 1461 CCACCCAGCAGGTCTCTCGGACAAATGGTGTTCAGAGGTTCTGGAGAGAGACCTTCAA 1520
DB 1383 CCATCCAGGAAGTCTGTCCACAATGGTTTTCAGAGGAGTTTGGGAGAAACATTTAA 1442
QY 1521 CTGCTACTTCAACCGAAGACCTCGCAGCTGAAAGATTCCAAGTGCCTTCGACGG 1580
DB 1443 CTGCCACCTTCAAAGA-----AGGTGCAAAAAGGACCTTTACCTGTGGACACCTTTCTG 1494
QY 1581 ACCGGCGGCTCAAGGGGACGGCTCCRAAGGGGGGNACTCCAGACGGAGACAGCCCTAGCCCA 1640
DB 1495 AGAGG----TCACGAAGAAAGTGGCGACAGGTTTAGCAAGCTCGACAGCCTTCGACC 1550
QY 1641 CCCTGCACTGGGGAGAGAAATCACAGCGTGGAGACCCCTACTCGATTTATACACA 1700
DB 1551 CCTCTGTACAGGGGATGAGAAATCAGCAGTGTGAGAGACCTTACATAGATTACAGCA 1610
QY 1701 CTTGAGGATCTCTACAAATGATATAGTGGCGCTACTCCATGCTCAGCCCTGCAAGA 1760
DB 1611 TTTACGATATCTTACAAATGTACTTTAGCAGTCTACTCCATTTGCCACGCTTGAAGA 1670
QY 1761 CATCCACTCTTTCAAAACCCGGCACGGGCATCTTTGAAAACGGATCTTGTGCAGATTTAA 1820
DB 1671 TATATATACCTGTACTCTGGAGAGGGCTCTTCACAATGGCTCTGTGCGACATCAA 1730
QY 1821 AAAAGTTAGGCTTGGCAGGTCTCAACCAATCTGCTGCATCTGAAATTTACCAACAGCAT 1880
DB 1731 GAAAGTTAGGCGTGGCAGGTCTCTGAAGCACCTACGCGCATCTAAACTTTACAAACAATAT 1790
QY 1881 GGGTGCAGGTTGACTTTTGAACGATCAAGGTGACCTCAAGGGGAACTACACCAATTTCAA 1940
DB 1791 GGGGAGCAGTGACCTTTTATGAGTGTGTGACCTGTGGTGGGAACTATTTCCATCATCAA 1850
QY 1941 CTGCGAGCTCTCCGCGAGAGATGAATCGGTGTGTGTTTTCATAGAGTGGGCAACTTCAACGC 2000
DB 1851 CTGGCACCTCTCCCGCAGAGATGGCTCCATCGTGTTTTAAAGAAAGTCGGGTATTACAACT 1910
QY 2001 CTAGCTTAAGCCAGTGACCGACTCAACATCAACGAAGAAAGAAATCTCTGGAGTGGCTT 2060
DB 1911 CTATGCCAAGAGGGGAAAGACTTTTCATCAACGAGGAGAAATCTCTGTGGAGTGGGT 1970
QY 2061 CTCCAAAGTGGTTCCTTTCTCCAACTGCGAGTCCAGACTGTGTGCCGGGACCAAGGAGGG 2120
DB 1971 CTCGAGGAGTGGCTTTCTCCAACTGCGAGCGAGACTGCTCGCAGGAGGACCAAGGAGG 2030
QY 2121 GATCATCGAGGGGAGCCCACTGCTGCTTTTGAATGATGGCATGGCATGTGAGAGGAGAGTT 2180
DB 2031 GATCATTTAGGGGAGGCCCACTGCTGCTTTTGAATGATGGAGTGTGCTGATGGGAGTA 2090
QY 2181 CAGTGATGAAACGATGCAAGTGGGTGTACAAAGTGCAGGATGATTTCTGTGTCGATGA 2240

Db 2091 TAGTGATGAGACAGATGCCAGTGCCTGTGTAACAAGTGCCAGATGACTTCTGTGTCACATGA 2150
 QY 2241 GAACACACAGTGGTGCATGCCAAGAGAGATCAGTACCTGTGCTGGAGGAGCCCTTCGG 2300
 Db 2151 GAACACACACTCTGTGATGCCAAGAGATCAGTTCGTGCTGGAGGAGCCCTTCGG 2210
 QY 2301 GATGCTGTGACCACTCTGCGCGTACTGGGCACTCCTGATCAGCTCCTTCGTGCTGGGGT 2360
 Db 2211 GATGCACTCAGCCCTCTTTGCGGCTGTGGGCACTTTTCTGACAGCCTTTGTGCTGGGT 2270
 QY 2361 CTTTCAATCAAGTTTCAGGAACACTCCCATCGTGAAGGCCAACACCGGAGTTGTCTACT 2420
 Db 2271 GTTTATCAAGTTTCGGCAACACACCATTTGTCAAGGCCAACACGAGACTCTCTACT 2330
 QY 2421 GTGCTCTTCTCCCTCATCTGCTGCTTCCAGTGGTCTCATCTTCATCGGCGAGCCAG 2480
 Db 2331 CTTCTCTTCTCCCTGCTGCTGCTTCCAGTGGTCTCATCTTCATCGGCGAGCCAG 2390
 QY 2481 GGAAGTGGCTGTGGCTCGGCTCGGCAACCGGCTTTGGCATCAGCTTCGCTGCTGCTG 2540
 Db 2391 GGAAGTGGCTGTGGCTCGGCTCGGCAACCGGCTTTGGCATCAGCTTCGCTGCTGCTG 2450
 QY 2541 CTGATCTCTGTTGAAGCAACCAACCGGCTGTGCTGCTTTCGAGGCCAAGATCCCAACAG 2600
 Db 2451 ATGATCTCTGTTGAAGCAACCAACCGGCTGTGCTGCTTTCGAGGCCAAGATCCCAACAG 2510
 QY 2601 CTTCAACCGAAGTGGTGGGCTCAACCTGAGTTCCTCTGCTTCTCTCTGCTGCTGCT 2660
 Db 2511 CTTCAACCGAAGTGGTGGGCTCAACCTGAGTTCCTCTGCTTCTCTCTGCTGCTGCT 2570
 QY 2661 GGTGCAATCTGTCACCTGCTCATCTGCTGTACACCGGCTCTGCTGCTGCTGCTGCTG 2720
 Db 2571 CATGCAATCTGTCATCTGCTGCTGTGCTGTACACCGGCTCTGCTGCTGCTGCTGCT 2630
 QY 2721 CATGAGCTGGAGGAGGAGTTCATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2780
 Db 2631 CCAGGAGCTGGAGGATGAGATCATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2690
 QY 2781 GGGCTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2840
 Db 2691 GGGCTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2750
 QY 2841 GTCCCGTGAAGCTGCGGAGAACTTCAACGAGGCTAAGTTTCATCTGCTGCTGCTGCTGCT 2900
 Db 2751 GTCCCGGAGCTGCGGAGAACTTCAATGAAGCAAGTTTCATCTGCTGCTGCTGCTGCT 2810
 QY 2901 CTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2960
 Db 2811 CTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2870
 QY 2961 GTCCGCTGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3020
 Db 2871 CTTCTGCTGAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2930
 QY 3021 CTTCAACAGTGTATCATCTGCTTCAAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3080
 Db 2931 CTTCAACAGTGTATCATCTGCTTCAAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2990
 QY 3081 CTTCAACAGTGTATCATCTGCTTCAAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3140
 Db 2991 TTGCAACAGTGTATCATCTGCTTCAAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3050
 QY 3141 CGGCTTCGAGAGCTTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3200
 Db 3051 CGGCTTCGAGAGCTTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3110
 QY 3201 CACCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3260
 Db 3111 CATTCAGAGAGAGAGCAACA-----CGAAGACCATTCCTCCACGCGGAGGAGGAGAG 3165
 QY 3261 CGGAGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3320
 Db 3166 CAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3225

QY 3321 CAGCGCACGCGCGCGAGCAAGTCTCGCGGATGCGCGCAG 3362
 Db 3226 CAGCAGCAAGATCTCAGCAGCAGCCAGATGCAAGCAAG 3267

RESULT 15
 AAV26964
 ID AAV26964 standard; cDNA to mRNA; 3809 BP.
 XX AAV26964;
 XX 01-SEP-1998 (first entry)
 XX Human parathyroid calcium receptor 4.0 gene 4Kb fragment.
 XX ss; calcium ion concentration; parathyroid hormone; homeostasis; kidney;
 XX calcium receptor; detection.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 373..3609
 FT /*tag= a
 FT /product= "phuPCar 4.0 4Kb fragment"
 XX US5763569-A.
 XX 09-JUN-1998.
 XX 07-JUN-1995; 95US-00484565.
 XX 23-AUG-1991; 91US-00749451.
 XX 11-FEB-1992; 92US-00834044.
 XX 21-AUG-1992; 92US-00934161.
 XX 12-FEB-1993; 93US-00017127.
 XX 23-FEB-1993; 93US-00009389.
 XX 22-OCT-1993; 93US-00141248.
 XX 19-AUG-1994; 94US-00292827.
 XX 21-OCT-1994; 94WO-US012117.
 XX 08-DEC-1994; 94US-00353784.
 XX (NPSP-) NPS PHARM INC.
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX Hebert SC, Brown EM, Garrett JE;
 XX WPI; 1998-347412/30.
 XX P-FSDB; AAW54846.
 XX Calcium receptor poly:peptide(s) - useful for drug screening or antibody production.
 XX Example 27; Fig 49; 174pp; English.
 XX The Human parathyroid calcium receptor gene encodes a 1078 amino acid protein. The tissue from which the receptor and receptors from bovine parathyroid and rat kidney are derived, respond to changes, and control changes, in calcium ion concentration, e.g. parathyroid hormone regulates Ca2+ homeostasis in blood and extracellular fluid, and kidney function alters through changes in Ca2+ levels in juxtaglomerular and proximal tubule cells in the kidney. The purified receptors (produced recombinantly) can be used to screen for compounds that modulate calcium receptor activity, especially those that can be used to treat diseases associated with the receptors in these tissues. They can also be used to raise antibodies for use in detection assays
 XX Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T; 0 U; 0 Other;

Query Match 42.2%; Score 1745.2; DB 2; Length 3809;
 Best Local Similarity 76.4%; Pred. No. 6e-300;
 Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;

QY 501 CTCAGGATATGTTCCAAACCAAGGGCCCGAGAAAGAGACATCATCTAGGAGGTCT 560
DB 423 CTCTGCTTACAGGCGCCAGACCCAGCGAGCCCAAGAGGGGACATTAATCTTGGGGGCT 482
QY 561 CTTCCCAATACATTTTGGAGTAGCGCCCAAGGATCAGACTTAAATCGAGACCGGAGGC 620
DB 483 CTTTCTCTATCTATTTTGGAGTAGAGCTTAAGATCAGATCTCAATCAAGCCGGAGTC 542
QY 621 GACAAAATGATTCGGTCAAAATTTTCGAGGCTTCGATGGCTCCAGGCGATGATATTCG 680
DB 543 TGTGGAATGATCAGGTATAATTTCCGTGGGTTTCGCTGGTTACAGGCTATGATATTTGC 602
QY 681 RAATGAGAGATTAACACAGATGACTTTCTGCGCCCAATATCAACCTGGGATATTCGAT 740
DB 603 CATAGAGAGATAAACAGAGCCCGAGCCCTTCTCCCAACTTTGACGCTGGGATACAGGAT 662
QY 741 ATTTGACACGTTAAACACCGTGTCCAAGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA 800
DB 663 ATTTGACACTTCCAAACACCGTTTCAAGCCCTTGAAGCCACCTGAGTTTGTGCTCA 722
QY 801 GAAACAAATCGACTCGTGAATTAAGATGAGTTCTGTAAGTCTGTGACCATATCCCATC 860
DB 723 AAACAAAATTTGATTTTGAACCTTTGATGAGTTCTGCAACTGCTCAGAGCAATCCCTC 782
QY 861 CACAATAGCAGTGTTCGGGCAACCGGCTCAGGAATCTCCAGCGCTGTGGCAATCTATT 920
DB 783 TAGGATGCTGTGGTGGAGCACTGGCTCAGGCGCTCTCCAGCGAGTGGCAATCTGCT 842
QY 921 GGGATATTTTACATTCACAGGTGAGTATGCTCTCTCGAGAGGCTGTCTCAGCAAA 980
DB 843 GGGGCTCTTACATTCGCCAGGTGAGTTATGCTTATGCTTCTCCAGCAGACTCTCAGCAAA 902
QY 981 GAATGAGTACAGGCTTCTTGGAGCACTCCCAATGATGAGCAACAGGCAAGCCCAT 1040
DB 903 GAATCAATCAAGTCTTCTCCGAAACCATCCCAATGATGAGCAACAGGCACTGCCAT 962
QY 1041 GSCGAGATCATCGAGCACTTCCAGTGAACCTGGGTGGGAACCTTGGCAGCGCAGATGA 1100
DB 963 GGCAGACATCATCGAGTATTTCCGCTGGAACCTGGGTGGGCAAAATTCAGCTGATGAGA 1022
QY 1101 CTATGGCGCCAGCATATGACAAATTCGGGAGGAGCGGTTAAGAGGACATCTGTAT 1160
DB 1023 CTATGGCGCGCGGGATTTGAATAATCCGAGAGGAAGCTGAGGAAGGAGATATCTGCAT 1082
QY 1161 TGACTTCAGTGAAGTATCTCTCAGTACTACACCCAGAGAGGATTTGGAGTTTCTCGCGCA 1220
DB 1083 GCAGTTCAGTGAACATCTCCAGTACTCTGATGAGGAGAGATCCAGCATGTGTAGA 1142
QY 1221 GGTATCCAGAACTCTCTCGGCCAAGGTATCGTGTGTCTTCTCCAAATGCGCCCGACCTGGA 1280
DB 1143 GGTGATTCAAAATTCACGGCCCAAGTATCATGTGTGTCTTCTCCAGTGGCCAGATCTTGA 1202
QY 1281 GCGGCTCATCCAGGAGATAGTTTCGAGAAACATACCGATCGGATCTGCTGGCCAGCA 1340
DB 1203 GCGCTCATCAAGAGATTTGTCGGCGCAATATACGGGCAAGATCTGCTGGCCAGCA 1262
QY 1341 GGCCTGGGCGAGCTCTCTCCATTTGCCAAGCAGAGTACTTCCACGTGTTCGCGGCA 1400
DB 1263 GGCCTGGGCGAGCTCTCTCCATGATCGCATGCTCAGTACTTCCACGTGTTCGCGGCA 1322
QY 1401 CATCGCTTCGCTTCAGGGCGGGGCTATCCAGGTTTCAACAGTTCTCTGAAGAGGT 1460
DB 1323 CATTGATTCGCTCTGAAGGCTGGGAGATCCAGGCTTCCGGGAATTTCTGGAAGAGGT 1382
QY 1461 CCACCCCGAGAGCTCTCGCAATGGGTTTGTCAAGGAGTTCTGGGAGGAGACCTTCAA 1520
DB 1383 CCATCCCGAGGATCTGTCCCAATGTTTTCGCAAGGAGTTTGGGAGAAACATTTAA 1442
QY 1521 CTGCTACTTTCACCGAAGACCCCTGACGAGCTGAAGAAATTCGAAGTGCCTTCGACGG 1580
DB 1443 CTGCCACCTTCCAAGA-----AGGTGCAAAAGACCTTTTACCTGTGTGACACCTTTCTG 1494
QY 1581 ACCGGCGCTCAAGGGAGCGGCTCCAGGCGGGGAACCTCCAGACGAGACGCTTACGGCA 1640

DB 1495 AGAGG-----TCACGAAGAAAGTGGCGACAGGTTTAGCAACAGCTCAGACGCTTCCGACC 1550
QY 1641 CCCTGCTACCTGGGAGGAGAAACATCACCAGCGTGGAGAGCCCCCTACTGGAATATACACA 1700
DB 1551 CTTCTGTACAGGGGATGAGAAACATCAGCAGTGTGAGAGCCCCCTTACATAGATTACAGCA 1610
QY 1701 CTTGAGGATCTCTACAAATGATACGTGGCGCTTACTTCAATTTGCTCAGCCCTGCAAGA 1760
DB 1611 TTTACGGATATCTTACAAATGTACTTAGCAGTCTACTCCATTTGCCCGCTTGAAGA 1670
QY 1761 CATCCACTCTTGCAAAACCCGGCACGGCATCTTTGCAAAACGGATCTTGTGCAGATTTAA 1820
DB 1571 TATATATACCTGTACTTACCTGGGAGAGGGCTCTTCACAATAGGCTCTGTGCAGACATCAA 1730
QY 1821 AAAAGTTGAGCCTGGCAGGTCTCAACCATCTGTCGATCTGAAATCTGAAATTTACCAACAGCAT 1880
DB 1731 GAAAGTTGAGCGCTGGCAGGTCTTGAAGCACCTTACGCGATCTAACTTTACAAACAATAT 1790
QY 1881 GGGTGAAGGTTGACTTTTGACGATCAAGGTGACCTCAAGGGGAACCTACACCAATTTCAA 1940
DB 1791 GGGGAGCAGGTGACCTTTGATGAGTGTGTGACCTGGTGGGAACTATTTCCATCATCAA 1850
QY 1941 CTGCGAGCTCTCCGCGAGAGATGAATCGGTGTTTGTTCATGAGTGGGCAACTACAACGC 2000
DB 1851 CTGCGACTCTCTCCGAGAGGATGCTCCATCGTGTTTAAGGAAGTCGGGTATTACAAGCT 1910
QY 2001 CTAGCTAAGCCAGTGACCGACTCAACATCAACGAAGAAATAATCTCTGAGAGTGGCTT 2060
DB 1911 CTATGCCAAGAGGAGAAAGACTTCTCATCAACGAGGAAATAATCTCTGAGAGTGGCTT 1970
QY 2061 CTCAAGTGGTTCCTTTCTCCAACTGCGAGTCTGTCGCGGCGCACAGGAGAGG 2120
DB 1971 CTCAGGAGTGGCTTCTCCAACTGCGAGTCTGCGAGTCTGCGAGGACGAGGAAAG 2030
QY 2121 GATCATCGAGGGAGCCACCTGCTGCTTTTGAATGATGCGATGCGAGAGGAGGAT 2180
DB 2031 GATCAITAGGGGAGGCCACCTGCTGCTTTGAGTGTGGAGTGTCTGATGGGAGTA 2090
QY 2181 CAGTGATGAACAGATCGAGTGGTGTACAAAGTCCCGAATGATTTCTGTCGAATGA 2240
DB 2091 TAGTGATGAGACAGATGCCAGTGCCTGTAAAGTGGCCAGATGATCTCTGTCGAATGA 2150
QY 2241 GAACCAACATCTGTCATCGCCAAAGAGATCGAGTACCTGTCGTGAGCGAGGCTTCGG 2300
DB 2151 GAACCAACATCTGTCATTTGCCAAGAGATCGAGTTTCTGTCGTGAGCGAGCCCTTGG 2210
QY 2301 GATCGCTGACCATCTTTCGCGCTACTGGGCTCTGATCACTCTCTTCTGTCGTGGGCT 2360
DB 2211 GATCGCATCACTCCCTCTTTTCGCGCTGTCGGCATTTTCTGACAGCCTTTTGTGTCGGTGT 2270
QY 2361 CTTTCATCAAGTTTCAGGAACACTCCCATCGTGAAGGGCCACCAACCGGGAGTTGCTACCT 2420
DB 2271 GTTTATCAAGTTTCGCAACACACCCATTTGCAAGGCCACCAACCGAGAGCTCTCTACCT 2330
QY 2421 GCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTCGCTCATCTTATCGGCGAGCCAG 2480
DB 2331 CTTCTCTTCTCCCTGCTCTGCTGCTTCTCAGCTCCCTGTTCTTATCGGGAGCCCCA 2390
QY 2481 GGAATGACCTGTCGGCTCGCCCAACCGGCTTTTGGCATCAGCTTCTGTCGTGATCTC 2540
DB 2391 GGAATGACCTGTCGGCTCGCCCGAGCGGCTTTTGGCATCAGCTTCTGTCGTGATCTC 2450
QY 2541 CTGCATCTCTGGTGAAGAACCAACCGGCTGCTGCTGTTCTTCGAGGCCAAGATCCCCACAG 2600
DB 2451 ATGCATCTCTGGTGAAGAACCAACCGGCTGCTTCTCTGGTGTTCGAGGCCAAGATCCCCACAG 2510
QY 2601 CTTCCACCGCAAGTGGGTGGGCTCAACCTGAGTTCTCTCTGCTTCTCTGTCGATCTC 2660
DB 2511 CTTCCACCGCAAGTGGGTGGGCTCAACCTGAGTTCTCTGCTGCTTCTCTGTCGACCTT 2570
QY 2661 GGTGCAATCTGCTCACTGATCATCTGGGTCTACACCGGCGCTCTCCCTCAGAGTACAGGAA 2720

Db	2571	CATGCAGATTGTATCTGTGTGATCTGGCTCTACACCGCGCCCCCTCAAGCTACCGCAA	2630
Qy	2721	CGATGAGCTGGAGGAGGAGTCTTTCATACCTGCGACGAGGGCTCGCTCATGGCGCT	2780
Db	2631	CCAGGAGCTGGAGGATGAGATCATCTTCATACGTGCCACGAGGGCTCCCTCATGGCCCT	2690
Qy	2781	GGGCTTCCTTCATCGGCTACACCTGCTCTCTCGCCGCACTGCTCTCTCTCTGGCTTCAA	2840
Db	2691	GGGCTTCCTTCATCGGCTACACCTGCTCTCTCGCCGCACTGCTCTCTCTCTGGCTTCAA	2750
Qy	2841	GTCCCGTAAGCTGCCGGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCAATGTCAT	2900
Db	2751	GTCCCGTAAGCTGCCGGAGAACTTCAATGAGCCAAAGTTTCATCACCTTCAGCAATGTCAT	2810
Qy	2901	CTTCTTCATCTGCTGTGATCTCTCTTCATCCCGCCCTATGTTCAGCACCTACGGCAAGTTTGT	2960
Db	2811	CTTCTTCATCTGCTGTGATCTCTCTTCATCCAGCCCTATGCCAGCACCTATGGCAAGTTTGT	2870
Qy	2961	GTCCGCGTGGAGGTGATTCATCTCTGCTCTCCAGCTTCGGGCTGCTGGGCTGCATTTTA	3020
Db	2871	CTCTGCGTAGAGGTGATTCATCTCTGCTCTCCAGCTTCGGGCTGCTGGGCTGCATTTT	2930
Qy	3021	CTTCAACAGTGTATCATCATCTCTGTTCAAGCCGTGCGTAAACACCATCGAGGAGTGGC	3080
Db	2931	CTTCAACAGTGTATCATCATCTCTGTTCAAGCCGTGCGTAAACACCATCGAGGAGTGGC	2990
Qy	3081	CTGCAGCAGCGCGGCCACGCTTCAAGTGGCGCGCGGCCACCTCCGGCGCAGCGC	3140
Db	2991	TTGCAGCAGCGCGGCCACGCTTCAAGTGGCGCGCGGCCACCTCCGGCGCAGCAA	3050
Qy	3141	CGGCTCTCGAAGCGCTCCAGCAGCTGTGGGCTCCACCATCTCTCTCGCCGCTCGTC	3200
Db	3051	CGTCTCCGCAAGCGGTCCAGCAGCTTGGAGGCTCCAGGGATCCACCCCTCTCTCTC	3110
Qy	3201	CACCTCGGGCGCGGCTCACCATGGAGATGAGCGGTGCGAGCAGCAGAAAGTTCAGCTT	3260
Db	3111	CATCAGCAGCAGAGCAACA----GCGAAGACCCATTCCACAGCCCGAGAGGCAGAG	3165
Qy	3261	CGGAGCGGCGACGCTACCTCTGCTCAGCTTCGAGGAGCAGGCGGATAGCCACCT	3320
Db	3166	CAGCAGCAGCGCTGGCCCTTAACCCAGCAAGAGCAGCAGCAGCCCTGACCCCTCCCA	3225
Qy	3321	CAGCCGACCGCGCGCAGAGAACTCGGCGGATGGCGCGAG	3362
Db	3226	CAGCAGCAACGATCTCAGCAGCAGCCAGATGCAAGCAGAG	3267

Search completed: November 16, 2004, 22:55:41
Job time : 1831 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 22:20:13 ; Search time 317 Seconds
(without alignments)
9269.405 Million cell updates/sec

Title: US-10-016-496-1

Perfect score: 4134

Sequence: 1 aattccgttgcgtgcgttc.....aagcgccgacagcaacgg 4134

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4134	100.0	4134	3	US-09-162-021B-1
2	4134	100.0	4134	4	US-09-687-477-17
3	4134	100.0	4134	4	US-09-687-476-17
4	4134	100.0	4134	4	US-09-687-372-17
5	4134	100.0	4134	4	US-09-975-553-17
6	4134	100.0	4134	4	US-10-270-795-17
7	4134	100.0	4134	4	US-10-270-876-17
8	4134	100.0	4134	4	US-10-268-051-7
9	1745.2	42.2	3809	1	US-08-485-588-3
10	1745.2	42.2	3809	1	US-08-484-585-3
11	1745.2	42.2	3809	2	US-08-480-751-3
12	1745.2	42.2	3809	2	US-08-943-986-3
13	1745.2	42.2	3809	3	US-08-353-784-3
14	1745.2	42.2	3809	3	US-08-484-719B-3
15	1745.2	42.2	3809	3	US-08-546-998-2
16	1745.2	42.2	3809	3	US-08-484-159-3
17	1743.6	42.2	3234	4	US-09-016-434-1432
18	1738	42.0	5275	1	US-08-485-588-1
19	1738	42.0	5275	1	US-08-484-565-1
20	1738	42.0	5275	2	US-08-480-751-1
21	1738	42.0	5275	2	US-08-943-986-1
22	1738	42.0	5275	3	US-08-353-784-1
23	1738	42.0	5275	3	US-08-484-719B-1
24	1738	42.0	5275	3	US-08-484-159-1
25	1703.6	41.2	5006	1	US-08-485-588-2
26	1703.6	41.2	5006	1	US-08-484-565-2
27	1703.6	41.2	5006	2	US-08-480-751-2

```

US-09-162-021B-1
; Sequence 1, Application US/09162021B
; Patent No. 6337391
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/09/162,021B
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: squalus acanthias
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (439)...(3522)
US-09-162-021B-1

Query Match      100.0%; Score 4134; DB 3; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTCGTTGCTCGGTTCCAGTCCAAAGTCTCTCCAGTGCAAAATGAGAAATGGTGC 60
Db 1 AATTCGTTGCTCGGTTCCAGTCCAAAGTCTCTCCAGTGCAAAATGAGAAATGGTGC 60
Qy 61 GCCATTACAGAAATGCACTACATCTGTTTAATGAAATATGTCAGTTATCTGAAGGT 120
Db 61 GCCATTACAGAAATGCACTACATCTGTTTAATGAAATATGTCAGTTATCTGAAGGT 120
Qy 121 TATTAATAATGTTTCTCAAGGATGGCTTCCAGGAAATCAATTTCTCAGTTTCCATT 180
Db 121 TATTAATAATGTTTCTCAAGGATGGCTTCCAGGAAATCAATTTCTCAGTTTCCATT 180
Qy 181 GTCAATTGTAATACTGACCAAGGATGTAACAAAATGGAACAAAGCTGAGGACCAC 240
Db 181 GTCAATTGTAATACTGACCAAGGATGTAACAAAATGGAACAAAGCTGAGGACCAC 240
Qy 241 GTTCAACCTTTCTTGGAGCATACGATCAACCCCTGAAGGAGATGGAAGACTTGAGGAGAA 300
Db 241 GTTCAACCTTTCTTGGAGCATACGATCAACCCCTGAAGGAGATGGAAGACTTGAGGAGAA 300

```

ALIGNMENTS

```

RESULT 1
US-09-162-021B-1
; Sequence 1, Application US/09162021B
; Patent No. 6337391
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/09/162,021B
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: squalus acanthias
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (439)...(3522)
US-09-162-021B-1

```

Db 241 GTTCACCCCTTTCTTGGAGCATACGATCAACCTGAGGAGATGGAAGACTTTGAGAGGAA 300
QY 301 ATGGGGAATGATCTTCCAGGAGTTCCTGCTGTAAGACGATCCCTCACCATTACAAAGATAA 360
Db 301 ATGGGGAATGATCTTCCAGGAGTTCCTGCTGTAAGACGATCCCTCACCATTACAAAGATAA 360
QY 361 GCAGAAATCTCCAGGATCTCTCTCTAAACGGCTGGGCTAGTGTGGCTTGGTCAAGGAA 420
Db 361 GCAGAAATCTCCAGGATCTCTCTCTAAACGGCTGGGCTAGTGTGGCTTGGTCAAGGAA 420
QY 421 CAGACAGGGCTGCACAAATGGCTCAGCTTCACTCCAACTCTTATTTCTGGGATTTACA 480
Db 421 CAGACAGGGCTGCACAAATGGCTCAGCTTCACTCCAACTCTTATTTCTGGGATTTACA 480
QY 481 CTCCTACAGTGTACAATGTCTCAGGCTATGCTCCAAACCAAGGGCCCAAGAAAGGA 540
Db 481 CTCCTACAGTGTACAATGTCTCAGGCTATGCTCCAAACCAAGGGCCCAAGAAAGGA 540
QY 541 GACATCATCTGGGAGGCTCTTCCCAATACACTTTGGAGTAGCGGCCAAGGATCAGGAC 600
Db 541 GACATCATCTGGGAGGCTCTTCCCAATACACTTTGGAGTAGCGGCCAAGGATCAGGAC 600
QY 601 TTAATAATCGAGACCGGAGCGCAAAATGTATTCTGGTACAAATTTTCGAGGCTTCGGATGG 660
Db 601 TTAATAATCGAGACCGGAGCGCAAAATGTATTCTGGTACAAATTTTCGAGGCTTCGGATGG 660
QY 661 CTCAGGGGATGATATTTCGAATTGAAGAGATTAAACAAGTATGACTTTCCTGCCCAAT 720
Db 661 CTCAGGGGATGATATTTCGAATTGAAGAGATTAAACAAGTATGACTTTCCTGCCCAAT 720
QY 721 ATCAACCTGGGATATCGCATATTGACACGCTGTAAACCGCTGTCCAGGCGCTAGAGGCA 780
Db 721 ATCAACCTGGGATATCGCATATTGACACGCTGTAAACCGCTGTCCAGGCGCTAGAGGCA 780
QY 781 ACACCTCAGCTTTGGCCAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
Db 781 ACACCTCAGCTTTGGCCAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
QY 841 TGCTCTGACCATATCCCATPCCAAATAGCAGTGGTGGGGCAACCGGCTCAGGAATCTCC 900
Db 841 TGCTCTGACCATATCCCATPCCAAATAGCAGTGGTGGGGCAACCGGCTCAGGAATCTCC 900
QY 901 AGGGCTGGCCAAATCTATTGGGATTTTACATTCACAGGTCAGCTATGCTCTCTCG 960
Db 901 AGGGCTGGCCAAATCTATTGGGATTTTACATTCACAGGTCAGCTATGCTCTCTCTCG 960
QY 961 AGCAGGCTCTCAGCAACAAAGATGATCAAGGCGCTTCTTGGAGCACCATCCCAATGAT 1020
Db 961 AGCAGGCTCTCAGCAACAAAGATGATCAAGGCGCTTCTTGGAGCACCATCCCAATGAT 1020
QY 1021 GAGCAACAGGCCACGGCCATGCGAGATCATCGAGGACTTCCAGTGAACTGGGTGGGA 1080
Db 1021 GAGCAACAGGCCACGGCCATGCGAGATCATCGAGGACTTCCAGTGAACTGGGTGGGA 1080
QY 1081 ACCCTGGCAGCGACGATCACTATGGCCGCCAGGCAATGACAACTTCGGGAGGAGGCC 1140
Db 1081 ACCCTGGCAGCGACGATCACTATGGCCGCCAGGCAATGACAACTTCGGGAGGAGGCC 1140
QY 1141 GTTAAGAGGGAATCTGATTTGACTTCACTAGTGAATGATCTCTCAGTACTACACCCAGAG 1200
Db 1141 GTTAAGAGGGAATCTGATTTGACTTCACTAGTGAATGATCTCTCAGTACTACACCCAGAG 1200
QY 1201 CAGTTGGAGTTCATCGCCAGCTCATCCAGAACTCTCGGCCAAGTCACTGTGCTCTTC 1260
Db 1201 CAGTTGGAGTTCATCGCCAGCTCATCCAGAACTCTCGGCCAAGTCACTGTGCTCTTC 1260
QY 1261 TCCAAATGGCCCGGACCTGGAGCGGCTCATPCCAGGAGATAGTTTCGAGAAACATCACCGAT 1320
Db 1261 TCCAAATGGCCCGGACCTGGAGCGGCTCATPCCAGGAGATAGTTTCGAGAAACATCACCGAT 1320
QY 1321 CGGATCTGGCTGGCCAGCGAGCTTGGGCGAGCTCTTCGCTCATTTGCCAGCCAGGATAC 1380
Db 1321 CGGATCTGGCTGGCCAGCGAGCTTGGGCGAGCTCTTCGCTCATTTGCCAGCCAGGATAC 1380

QY 1381 TTCCACGTGTGGCGGCACCATCGCTTTCGCTCTCAGGCGGGGGCTATCCAGGGTTC 1440
Db 1381 TTCCACGTGTGGCGGCACCATCGCTTTCGCTCTCAGGCGGGGGCTATCCAGGGTTC 1440
QY 1441 AACAAATCTCTGAAGAGGTTCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG 1500
Db 1441 AACAAATCTCTGAAGAGGTTCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG 1500
QY 1501 TTCTGGAGGAGACCTTCAACTGCTACTTTCACCGGAAGACCTGACGAGCTGAAGAAT 1560
Db 1501 TTCTGGAGGAGACCTTCAACTGCTACTTTCACCGGAAGACCTGACGAGCTGAAGAAT 1560
QY 1561 TCCAAGGTGCTTCGCACGAGCCGGCGCTCAAGGGAGCGGCTCCAAGCGGGGAACTCC 1620
Db 1561 TCCAAGGTGCTTCGCACGAGCCGGCGCTCAAGGGAGCGGCTCCAAGCGGGGAACTCC 1620
QY 1621 AGACGACAGCCCTACGCCACCCCTGCACTGGGGAGGAGAAATCACCAGCGTGGAGACC 1680
Db 1621 AGACGACAGCCCTACGCCACCCCTGCACTGGGGAGGAGAAATCACCAGCGTGGAGACC 1680
QY 1681 CCCTACTGGAATTATACACACCTGAGGATCTCTACAATGTATATAGTGGCCCTCTACTCC 1740
Db 1681 CCCTACTGGAATTATACACACCTGAGGATCTCTACAATGTATATAGTGGCCCTCTACTCC 1740
QY 1741 ATTGCTCAGCCCTGCAAGACATCCACTCTTGGCAACCCGGCACGGGCACTTTGGCAAC 1800
Db 1741 ATTGCTCAGCCCTGCAAGACATCCACTCTTGGCAACCCGGCACGGGCACTTTGGCAAC 1800
QY 1801 GGATCTTGTGCAGATTTAAATAAGTTGAGGCTGGCAGGTCTCTCAACCATCTGTGCTAT 1860
Db 1801 GGATCTTGTGCAGATTTAAATAAGTTGAGGCTGGCAGGTCTCTCAACCATCTGTGCTAT 1860
QY 1861 CTGAAGTTTACCAACAGCATTGGGTAGCGAGTGTACTTTTTCGATCAAGGTGACTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATTGGGTAGCGAGTGTACTTTTTCGATCAAGGTGACTCAAG 1920
QY 1921 GGGAACTACACATTTCACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTGTTCAT 1980
Db 1921 GGGAACTACACATTTCACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTGTTCAT 1980
QY 1981 GAGGTGGGCAATPACACCGCTACGCTAAGCCAGTGACCGACTCAACATCAACGAAAG 2040
Db 1981 GAGGTGGGCAATPACACCGCTACGCTAAGCCAGTGACCGACTCAACATCAACGAAAG 2040
QY 2041 AAAATCTCTGAGTGGCTTCTCAAAGTGGTTCCTTCTCAAAGTGGTTCCTTCTCAAAGTGGCT 2100
Db 2041 AAAATCTCTGAGTGGCTTCTCAAAGTGGTTCCTTCTCAAAGTGGTTCCTTCTCAAAGTGGCT 2100
QY 2101 GTCCGGGACACAGGAGGGGATCATCGAGGGGAGGCCACCTGTCTGTCTTGAATGCAATG 2160
Db 2101 GTCCGGGACACAGGAGGGGATCATCGAGGGGAGGCCACCTGTCTGTCTTGAATGCAATG 2160
QY 2161 GCATGTGAGAGGAGGATTCAGTGTAAACAGATGCAAGTGCCTGTGTAACAAGTGCCTCG 2220
Db 2161 GCATGTGAGAGGAGGATTCAGTGTAAACAGATGCAAGTGCCTGTGTAACAAGTGCCTCG 2220
QY 2221 AATGATTTCTGTCGAATGAGAACACACGCTGTCATCGCAAGGAGATCGAGTACCTG 2280
Db 2221 AATGATTTCTGTCGAATGAGAACACACGCTGTCATCGCAAGGAGATCGAGTACCTG 2280
QY 2281 TCCTGGAAGGAGCCCTTCGGGATCGTCTGACCATCTTCGCGCTACTGGGCACTCTGATC 2340
Db 2281 TCCTGGAAGGAGCCCTTCGGGATCGTCTGACCATCTTCGCGCTACTGGGCACTCTGATC 2340
QY 2341 ACCTCTTCTGTGTGGGCTCTTCACTCAAGTTTCAGGAACATCCCATCTGTGAGGCGCAC 2400
Db 2341 ACCTCTTCTGTGTGGGCTCTTCACTCAAGTTTCAGGAACATCCCATCTGTGAGGCGCAC 2400
QY 2401 AACCGGAGTGTCTTACCTGTCTCTTCTCCCTCATCTGTGCTTCTTCCAGTCTCGTTC 2460
Db 2401 AACCGGAGTGTCTTACCTGTCTCTTCTCCCTCATCTGTGCTTCTTCCAGTCTCGTTC 2460

Db	61	GCCATTACAGGAACATGCATACATCTGTGTTAAATGAAATATCTCAGTTTACTCTGTAAGGT	120
Qy	121	TATTAAAAATGTTTCTGCAAGGATGGCTTTCAGAGAAATCAATTTCTGCACGTTTTCCTCCATT	180
Db	121	TATTAAAAATGTTTCTGCAAGGATGGCTTTCAGAGAAATCAATTTCTGCACGTTTTCCTCCATT	180
Qy	181	GTCATTGTATGAATAACTGACCAAGGGATGTAAACAAAATGGAACAAAGCTGAGGACAC	240
Db	181	GTCATTGTATGAATAACTGACCAAGGGATGTAAACAAAATGGAACAAAGCTGAGGACAC	240
Qy	241	GTTCCACCTTTCTTGGAGCATACCATCAACCCCTCAAGGAGATGGAAGACTTTGAGGAGAA	300
Db	241	GTTCCACCTTTCTTGGAGCATACCATCAACCCCTCAAGGAGATGGAAGACTTTGAGGAGAA	300
Qy	301	ATGGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCAATTACAAAGATAA	360
Db	301	ATGGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCAATTACAAAGATAA	360
Qy	361	GCAGAAATCCTCCAGGATCCTCTGTAAACGGCTGGCTAGTGTGGCTTGGTCAAGAA	420
Db	361	GCAGAAATCCTCCAGGATCCTCTGTAAACGGCTGGCTAGTGTGGCTTGGTCAAGAA	420
Qy	421	CAGAGACAGGGCTGCACAAATGGCTCAGCTTCACCTGCCAATCTTATTCTTTGGGATTTACA	480
Db	421	CAGAGACAGGGCTGCACAAATGGCTCAGCTTCACCTGCCAATCTTATTCTTTGGGATTTACA	480
Qy	481	CTCCTACAGTCGTACATGTCTCAGGGTATGGTCCAAACCAAGGGCCCAAGAAAGGA	540
Db	481	CTCCTACAGTCGTACATGTCTCAGGGTATGGTCCAAACCAAGGGCCCAAGAAAGGA	540
Qy	541	GACATCATCTCGGAGGTCTCTTCCCAATACACTTTGGAGTAGCGGCCAAGGATCAGGAC	600
Db	541	GACATCATCTCGGAGGTCTCTTCCCAATACACTTTGGAGTAGCGGCCAAGGATCAGGAC	600
Qy	601	TTAAAAATCGAGACCGGAGGCGACAAAATGTATTTCGGTACAAATTTTCAGGGCTTCGGATGG	660
Db	601	TTAAAAATCGAGACCGGAGGCGACAAAATGTATTTCGGTACAAATTTTCAGGGCTTCGGATGG	660
Qy	661	CTCCAGGCGATGTATTTCGCAATTTGAAGAGATTAAACAACAGTATGACTTTCTCTGCCCAAT	720
Db	661	CTCCAGGCGATGTATTTCGCAATTTGAAGAGATTAAACAACAGTATGACTTTCTCTGCCCAAT	720
Qy	721	ATCACCTCTGGGATATCGCATATTTGACACGFTGTAAACACCGFTGCCAGGCGCTTAGAGCA	780
Db	721	ATCACCTCTGGGATATCGCATATTTGACACGFTGTAAACACCGFTGCCAGGCGCTTAGAGCA	780
Qy	781	ACACTCAGCTTTGTGGCCCGAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC	840
Db	781	ACACTCAGCTTTGTGGCCCGAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC	840
Qy	841	TGCTCTGACCATATCCCATCCCAATATGACGTGTTCCGGGCAACCGGTCAGGAATCTCC	900
Db	841	TGCTCTGACCATATCCCATCCCAATATGACGTGTTCCGGGCAACCGGTCAGGAATCTCC	900
Qy	901	ACGGCTGTGGCAATCTATTGGGATATTTTACATTCACAGGTCAGCTATGCTCTCTCG	960
Db	901	ACGGCTGTGGCAATCTATTGGGATATTTTACATTCACAGGTCAGCTATGCTCTCTCG	960
Qy	961	AGCAGGCTGTCTCAGCAACAAGATGAGTACAAAGGCTTCTCTGAGGACCATCCCCAATGAT	1020
Db	961	AGCAGGCTGTCTCAGCAACAAGATGAGTACAAAGGCTTCTCTGAGGACCATCCCCAATGAT	1020
Qy	1021	GAGCAACAGGCGATGGCCGAGATCATCGACACTTTCAGTGGAACTGGGTGGGA	1080
Db	1021	GAGCAACAGGCGATGGCCGAGATCATCGACACTTTCAGTGGAACTGGGTGGGA	1080
Qy	1081	ACCTTGGCAGCGCAGATGACTATTGGCCGCCAGGCATTGACAAAGTTCCGGGAGAGGCC	1140
Db	1081	ACCTTGGCAGCGCAGATGACTATTGGCCGCCAGGCATTGACAAAGTTCCGGGAGAGGCC	1140
Qy	1141	GTTAAGAGGGACATCTGTATTGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG	1200
Db	1141	GTTAAGAGGGACATCTGTATTGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG	1200

Qy	1201	CAGTTGGAGTTCAATCGCCGACGTCATCCAGAACTCCTCGGCCCAAGTGTCATCGTGGTCTTC	1261
Db	1201	CAGTTGGAGTTCAATCGCCGACGTCATCCAGAACTCCTCGGCCCAAGTGTCATCGTGGTCTTC	1260
Qy	1261	TCCAAATGGCCCGCCGACCTTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAA.CATCAACCGAT	1320
Db	1261	TCCAAATGGCCCGCCGACCTTGGAGCCGCTCATCCAGGAGATAGTTCGGAGAAA.CATCAACCGAT	1320
Qy	1321	CGAATCTGGCTGCGCAGCAGGGCTTGGCCAGACTCTTCGCTCATTCGCCAAGCCAGAGTAC	1380
Db	1321	CGAATCTGGCTGCGCAGCAGGGCTTGGCCAGACTCTTCGCTCATTCGCCAAGCCAGAGTAC	1380
Qy	1381	TTCCACGTGCTCGGCGGCAACCATCGGCTTCGCTCTCAGGGCGGGCGTATCCCAAGGGTTC	1440
Db	1381	TTCCACGTGCTCGGCGGCAACCATCGGCTTCGCTCTCAGGGCGGGCGTATCCCAAGGGTTC	1440
Qy	1441	AACAAGTTCCTGAAGAGGTCACCCAGAGTCTCGACACATGGGTTTGTCAAGGAG	1500
Db	1441	AACAAGTTCCTGAAGAGGTCACCCAGAGTCTCGACACATGGGTTTGTCAAGGAG	1500
Qy	1501	TTCTGGGAGGAGACCTTCAACTGCTACTTCCACGAGAAGACCTCGACGCTGAAGAAT	1560
Db	1501	TTCTGGGAGGAGACCTTCAACTGCTACTTCAACCGAGAAGACCTCGACGCTGAAGAAT	1560
Qy	1561	TCCAAGTGCCCTCGACGAGCCGCGGCTCAAGGGGACGGCTCCAAGGCGGGAACTCC	1620
Db	1561	TCCAAGTGCCCTCGACGAGCCGCGGCTCAAGGGGACGGCTCCAAGGCGGGAACTCC	1620
Qy	1621	AGACGGACACCCCTAGCCACCCCTGCACCTGGGGAGAGAAATCAACACGCTGGAGACC	1680
Db	1621	AGACGGACACCCCTAGCCACCCCTGCACCTGGGGAGAGAAATCAACACGCTGGAGACC	1680
Qy	1681	CCCTACTCGGATTATACACACCTGAGGATCTCCTACAACTATACGTGGCGGCTACTCC	1740
Db	1681	CCCTACTCGGATTATACACACCTGAGGATCTCCTACAACTATACGTGGCGGCTACTCC	1740
Qy	1741	ATTGCTCACGCCCTGCAAGACATCCACTCTTGAAACCCGGCACGGGCATCTTTTGCAAAC	1800
Db	1741	ATTGCTCACGCCCTGCAAGACATCCACTCTTGCAACCCGGCACGGGCATCTTTTGCAAAC	1800
Qy	1801	GGATCTTGTCAGATATTAAAAAGTTGAGGCTCGCAGGTCCTCAACCATCTGCTGCAT	1860
Db	1801	GGATCTTGTCAGATATTAAAAAGTTGAGGCTCGCAGGTCCTCAACCATCTGCTGCAT	1860
Qy	1861	CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACCATCAAGTGACCTCAAG	1920
Db	1861	CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACCATCAAGTGACCTCAAG	1920
Qy	1921	GGNACTACACCAATTATCACTCGCAGCTCTCGCAGAGAGATCAATCGGTTGTTCCAT	1980
Db	1921	GGNACTACACCAATTATCACTCGCAGCTCTCGCAGAGAGATCAATCGGTTGTTCCAT	1980
Qy	1981	GAGGTGGGCAACTACAAACCGCTTACGCTTAAGCCCAAGCTGACCGACTCAACATCAACGAAAG	2040
Db	1981	GAGGTGGGCAACTACAAACCGCTTACGCTTAAGCCCAAGCTGACCGCGACTCAACATCAACGAAAG	2040
Qy	2041	AAATCCTCTGGAGTGCTTCTCCAAGTGTTTCCCTTCTCCAACCTGCAGTCGAGACTGT	2100
Db	2041	AAATCCTCTGGAGTGCTTCTCCAAGTGTTTCCCTTCTCCAACCTGCAGTCGAGACTGT	2100
Qy	2101	GTCCGGGCAACCAAGGAGGATCATCGAGGGGAGCCCACTGCTGCTTTGTAATGATG	2160
Db	2101	GTCCGGGCAACCAAGGAGGATCATCGAGGGGAGCCCACTGCTGCTTTGTAATGATG	2160
Qy	2161	GCATGTCGAGGGAGGTTTCAGTGATGAAAAAGATGCGAGTCGGTGTAACAAAGTGCCCG	2220
Db	2161	GCATGTCGAGGGAGGTTTCAGTGATGAAAAAGATGCGAGTCGGTGTAACAAAGTGCCCG	2220
Qy	2221	AATGATTTCTGGTTCGAATGAGAACCAACGCTCGTGATCGCCCAAGGAGATCGAGTACCTG	2280
Db	2221	AATGATTTCTGGTTCGAATGAGAACCAACGCTCGTGATCGCCCAAGGAGATCGAGTACCTG	2280

2281 TCGTGGACGAGCCCTTCGGGATCGCTCTGACCAATCTTTCGGCGTACTGGGCAATCCTGATC 2340
2281 TCGTGGACGAGCCCTTCGGGATCGCTCTGACCAATCTTTCGGCGTACTGGGCAATCCTGATC 2340
2341 ACCTCTCTTCTGCTGGGGTCTTCAATCAAGTTCAGGACATCCCACTGTCGAAGGCCACC 2400
2341 ACCTCTCTTCTGCTGGGGTCTTCAATCAAGTTCAGGACATCCCACTGTCGAAGGCCACC 2400
2401 AACCGGAGTGTCTTCTACTGCTGCTCTTCTCCCTCATCTGCTCTTCTCCAGCTCGCTC 2460
2401 AACCGGAGTGTCTTCTACTGCTGCTCTTCTCCCTCATCTGCTCTTCTCCAGCTCGCTC 2460
2461 ATCTTATCTGGGAGCCAGGACTGAGCTGTGGCTCCGCGCAACCGGCTTTGGGATC 2520
2461 ATCTTATCTGGGAGCCAGGACTGAGCTGTGGCTCCGCGCAACCGGCTTTGGGATC 2520
2521 AGCTTCTGCTGTGATCTCTGCAATCTGTTGAAGACCAACCGGCTCTGCTGCTCTC 2580
2521 AGCTTCTGCTGTGATCTCTGCAATCTGTTGAAGACCAACCGGCTCTGCTGCTCTC 2580
2581 GAGGCCAAGATCCCAACAGGCTCCACCGCAAGTGGTGGGCTCAACCTGCAGTTCCTC 2640
2581 GAGGCCAAGATCCCAACAGGCTCCACCGCAAGTGGTGGGCTCAACCTGCAGTTCCTC 2640
2641 CTGGTCTTCTGCTGATCTCTGCAATCTGTTGAAGACCAACCGGCTCTGCTGCTCTC 2700
2641 CTGGTCTTCTGCTGATCTCTGCAATCTGTTGAAGACCAACCGGCTCTGCTGCTCTC 2700
2701 CCTCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCACTTTCATCAGCTGGAC 2760
2701 CCTCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCACTTTCATCAGCTGGAC 2760
2761 GAGGCTGCTCATGGGCTGGGCTTCTCATGCTGACCTGCTGCTGCTGCTGCTGCTGCT 2820
2761 GAGGCTGCTCATGGGCTGGGCTTCTCATGCTGACCTGCTGCTGCTGCTGCTGCTGCT 2820
2821 TCGTCTTCTTCTGCTTCAAGTCCGCTAAGCTGCGGGAACCTTCAACGAGGCTAAGTTC 2880
2821 TCGTCTTCTTCTGCTTCAAGTCCGCTAAGCTGCGGGAACCTTCAACGAGGCTAAGTTC 2880
2881 ATCACTTCAGCATGTTGATCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2881 ATCACTTCAGCATGTTGATCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2941 AGCACTACGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
2941 AGCACTACGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
3001 GGGCTGCTGGGCTGATTTACTTCAACAGTGTATCATCTGTTCAAGCCGCTGCGGT 3060
3001 GGGCTGCTGGGCTGATTTACTTCAACAGTGTATCATCTGTTCAAGCCGCTGCGGT 3060
3061 AACACCATGAGAGTGGCTGCGAGCAGCGGGCCGAGCCCTTCAAGGTGGCGGCGCG 3120
3061 AACACCATGAGAGTGGCTGCGAGCAGCGGGCCGAGCCCTTCAAGGTGGCGGCGCG 3120
3121 GGCACCTCCGCGGAGCGCGGCTTCCGACAGCGCTCCAGAGCGCTGTGGGCTCCACC 3180
3121 GGCACCTCCGCGGAGCGCGGCTTCCGACAGCGCTCCAGAGCGCTGTGGGCTCCACC 3180
3181 ATCTCTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
3181 ATCTCTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
3241 AGCAGCAGAGTCAAGTTCGCGAGCGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
3241 AGCAGCAGAGTCAAGTTCGCGAGCGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
3301 ACAGGCGGATAGCCACCTCAGCGGACCGGCGGAGGAACTCGGCGGATGCGCG 3360
3301 ACAGGCGGATAGCCACCTCAGCGGACCGGCGGAGGAACTCGGCGGATGCGCG 3360
3361 AGCGGCGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420

3361 AGCGGCGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
3421 CAGCCCGCAACCATGATCCGATACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3480
3421 CAGCCCGCAACCATGATCCGATACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3480
3481 GCGGCGAGCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3540
3481 GCGGCGAGCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3540
3541 CCCAAGAACATCTCCACGCGCAGCAGCGCTGACAACTGACATCAACTCTTAACTGCGTGC 3600
3541 CCCAAGAACATCTCCACGCGCAGCAGCGCTGACAACTGACATCAACTCTTAACTGCGTGC 3600
3601 TGCCCAACCTCTCCCTCTCCGCGCATTTTGGGTTTCTGAGATTGCGAGCATCTCGAGT 3660
3601 TGCCCAACCTCTCCCTCTCCGCGCATTTTGGGTTTCTGAGATTGCGAGCATCTCGAGT 3660
3661 TCCCTTTATCCCTGATTTTCTGACATTTTCTGATTTTCTAGTGTGCGATGGAATATCAAC 3720
3661 TCCCTTTATCCCTGATTTTCTGACATTTTCTGATTTTCTAGTGTGCGATGGAATATCAAC 3720
3721 ATATGAGTTGCAAAATAGGTGAGCAGAGTTCGTCAAAGTATCTGAACTATCTGAAGT 3780
3721 ATATGAGTTGCAAAATAGGTGAGCAGAGTTCGTCAAAGTATCTGAACTATCTGAAGT 3780
3781 ATCTGAATCTTATCTCTGAAATGATATCAACATTTTGAAGTATTTTGAAGTATTTTGAAGT 3840
3781 ATCTGAATCTTATCTCTGAAATGATATCAACATTTTGAAGTATTTTGAAGTATTTTGAAGT 3840
3841 TTATGTTTCAATTTGTAAGATAATTTGTTTACAACATATAAGGTACCACCTGAAGCAGT 3900
3841 TTATGTTTCAATTTGTAAGATAATTTGTTTACAACATATAAGGTACCACCTGAAGCAGT 3900
3901 GACTGAGATTGCCACTGTGATGACAGACTGTTTATTAACATTTATCAATTTATCAATTTATCAAT 3960
3901 GACTGAGATTGCCACTGTGATGACAGACTGTTTATTAACATTTATCAATTTATCAATTTATCAAT 3960
3961 TTGCAACAGGAATATAATGATCTGTAACAAAATTTGTTGATTTATCTTAAATGCAAT 4020
3961 TTGCAACAGGAATATAATGATCTGTAACAAAATTTGTTGATTTATCTTAAATGCAAT 4020
4021 TGTAATCAGATGTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAAT 4080
4021 TGTAATCAGATGTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAAT 4080
4081 AAAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAAT 4134
4081 AAAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAAT 4134

RESULT 3
US-09-687-476-17
; Sequence 17, Application US/09687476
; Patent No. 6475792
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2001-000
; CURRENT APPLICATION NUMBER: US/09/687,476
; CURRENT FILING DATE: 2000-10-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark

US-09-687-476-17

Query Match 100.0%; Score 4134; DB 4; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AATTCGGTTCGTGCTCAGTCCAAAGTCTCTCCAGTGCAGGATGAGAAATGTTGTC	60
DB	1	AATTCGGTTCGTGCTCAGTCCAAAGTCTCTCCAGTGCAGGATGAGAAATGTTGTC	60
QY	61	GCATTACAGGACATGCATCATCTGTTAAATGAAATATTTGTCAGTTATCTCAAGT	120
DB	61	GCATTACAGGACATGCATCATCTGTTAAATGAAATATTTGTCAGTTATCTCAAGT	120
QY	121	TATTAATAATGTTTCTGCAAGGATGGCTTCAAGAGAAATCAATCTGCAGTTTCTCCAT	180
DB	121	TATTAATAATGTTTCTGCAAGGATGGCTTCAAGAGAAATCAATCTGCAGTTTCTCCAT	180
QY	181	GTCAATGTTATGAATACCTACCAAGGATGTAACAAATGAAACAAAGCTGAGGACAC	240
DB	181	GTCAATGTTATGAATACCTACCAAGGATGTAACAAATGAAACAAAGCTGAGGACAC	240
QY	241	GTTCAACCTTTCTTGGAGCATACGATCAACCTGAAAGGATGGAAGACTTGGAGGAA	300
DB	241	GTTCAACCTTTCTTGGAGCATACGATCAACCTGAAAGGATGGAAGACTTGGAGGAA	300
QY	301	ATGGGATTTGATCTTCAGGAGTTCTGCTGTAAGAGGATCCCTCAACATTAACAAGATA	360
DB	301	ATGGGATTTGATCTTCAGGAGTTCTGCTGTAAGAGGATCCCTCAACATTAACAAGATA	360
QY	361	GCAGAAATCCTCCAGGATCTCTGTAACGGCTGGGCTAGTGTGGTTCGTAAGGAA	420
DB	361	GCAGAAATCCTCCAGGATCTCTGTAACGGCTGGGCTAGTGTGGTTCGTAAGGAA	420
QY	421	CAGAGACAGGCTGCAATGCTCAGTTCTACTGCCAACTCTTATTTCTGGGATTTACA	480
DB	421	CAGAGACAGGCTGCAATGCTCAGTTCTACTGCCAACTCTTATTTCTGGGATTTACA	480
QY	481	CTCCTACAGTCTCAATGCTCAGGATGCTGTCACCAAGGCTGCAAGGCTGCAAGGAA	540
DB	481	CTCCTACAGTCTCAATGCTCAGGATGCTGTCACCAAGGCTGCAAGGCTGCAAGGAA	540
QY	541	GACATCATCTGGGAGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGAC	600
DB	541	GACATCATCTGGGAGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGAC	600
QY	601	TTAAATCAGACCGGAGGCTGCAAAATGATTCGGTACAAATTTTCGAGGCTTCGATGG	660
DB	601	TTAAATCAGACCGGAGGCTGCAAAATGATTCGGTACAAATTTTCGAGGCTTCGATGG	660
QY	661	CTCCAGGCTGATATTCGCAATTCAGAGATTAACAAGATGATGATCTTCTGCCCAAT	720
DB	661	CTCCAGGCTGATATTCGCAATTCAGAGATTAACAAGATGATGATCTTCTGCCCAAT	720
QY	721	ATCACCTCGGATATGCAATTTGACAGGTTAAACCGTGTCAAGGCTGAGGCA	780
DB	721	ATCACCTCGGATATGCAATTTGACAGGTTAAACCGTGTCAAGGCTGAGGCA	780
QY	781	ACACTCAGCTTTGGGCTGCAAGGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	840
DB	781	ACACTCAGCTTTGGGCTGCAAGGATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	840
QY	841	TGCTCTGACCATATCCCATCCCAATAGCAGTGGTTCGGGCAACCGGCTCAGGATCTCC	900
DB	841	TGCTCTGACCATATCCCATCCCAATAGCAGTGGTTCGGGCAACCGGCTCAGGATCTCC	900
QY	901	ACGGCTGTGGCAATCTATTGGGATTTATTTACATTTCCAGGCTCAGTATGCTCTCCG	960
DB	901	ACGGCTGTGGCAATCTATTGGGATTTATTTACATTTCCAGGCTCAGTATGCTCTCCG	960
QY	961	AGCAGGCTCTCAGCAACAAAGATGATACAGGCTTCTCAGGACCATCCCAATGAT	1020
DB	961	AGCAGGCTCTCAGCAACAAAGATGATACAGGCTTCTCAGGACCATCCCAATGAT	1020

QY	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTCGGTGGGA	1080
DB	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTCGGTGGGA	1080
QY	1081	ACCTGCGACCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1140
DB	1081	ACCTGCGACCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1140
QY	1141	GTTAAGAGGACATCTGTTATGATCTTCAAGTATGATGATGATGATGATGATGATGATGAT	1200
DB	1141	GTTAAGAGGACATCTGTTATGATCTTCAAGTATGATGATGATGATGATGATGATGATGAT	1200
QY	1201	CAGTTGAGTTCTATGCGCGACGTCATCCAGAACTCTCGGCCAAGGTCTATCGTGTCTTC	1260
DB	1201	CAGTTGAGTTCTATGCGCGACGTCATCCAGAACTCTCGGCCAAGGTCTATCGTGTCTTC	1260
QY	1261	TCCAAATGGCCCGACCTGGAGCGCTCATCCAGAGATAGTTCGAGAAACATCACCGAT	1320
DB	1261	TCCAAATGGCCCGACCTGGAGCGCTCATCCAGAGATAGTTCGAGAAACATCACCGAT	1320
QY	1321	CGATCTGGCTGCGCGACGAGGCTTGGCCAGCTCTTCGCTCAATTCGCAAGCCAGAGTAC	1380
DB	1321	CGATCTGGCTGCGCGACGAGGCTTGGCCAGCTCTTCGCTCAATTCGCAAGCCAGAGTAC	1380
QY	1381	TTCCAGTGTGCGCGACCATCGGCTTGGCTCTCAGGCGGGGCTATCCGAGGTTTC	1440
DB	1381	TTCCAGTGTGCGCGACCATCGGCTTGGCTCTCAGGCGGGGCTATCCGAGGTTTC	1440
QY	1441	AACAAGTTCCTGAAGAGGTCCTCAACCGACAGGTCCTCGGACAAATGGTTCGTAAGGAG	1500
DB	1441	AACAAGTTCCTGAAGAGGTCCTCAACCGACAGGTCCTCGGACAAATGGTTCGTAAGGAG	1500
QY	1501	TTCTGGAGGAGACCTTCAACTGCTACTTCAACCGAGAAACCTGACGAGCTGAGAT	1560
DB	1501	TTCTGGAGGAGACCTTCAACTGCTACTTCAACCGAGAAACCTGACGAGCTGAGAT	1560
QY	1561	TCCAAAGTGTGCGCGACCGGCTTCAAGGCGGCTCAAGGCGGCTCAAGGCGGCTCAAGG	1620
DB	1561	TCCAAAGTGTGCGCGACCGGCTTCAAGGCGGCTCAAGGCGGCTCAAGGCGGCTCAAGG	1620
QY	1621	AGACGACAGCCCTACGCGCCCTGCACTGGGAGGAGAAACATCACAGGCTGAGAC	1680
DB	1621	AGACGACAGCCCTACGCGCCCTGCACTGGGAGGAGAAACATCACAGGCTGAGAC	1680
QY	1681	CCCTACCTGGATATACACAGCTGAGATCTCTCAATGATATAGTGGCGCTTACTCC	1740
DB	1681	CCCTACCTGGATATACACAGCTGAGATCTCTCAATGATATAGTGGCGCTTACTCC	1740
QY	1741	ATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCGGCGACGGGCTCTTTCGAAAC	1800
DB	1741	ATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCGGCGACGGGCTCTTTCGAAAC	1800
QY	1801	GGATCTTGTGAGATTTAAAGTTGAGGCTGCGAGCTCTCAACCATCTGCTGCAT	1860
DB	1801	GGATCTTGTGAGATTTAAAGTTGAGGCTGCGAGCTCTCAACCATCTGCTGCAT	1860
QY	1861	CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGAGGATCAAGGTGACCTCAAG	1920
DB	1861	CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGAGGATCAAGGTGACCTCAAG	1920
QY	1921	GGAAATACACCATTAACCTGCGAGCTCTCGCAGAGGATGAATCGGTGTTGTTCCAT	1980
DB	1921	GGAAATACACCATTAACCTGCGAGCTCTCGCAGAGGATGAATCGGTGTTGTTCCAT	1980
QY	1981	GAGTGGGCAATACCAACCGCTACGCTAAGCCCGAGTGCAGCTCAACATCAACGAAAG	2040
DB	1981	GAGTGGGCAATACCAACCGCTACGCTAAGCCCGAGTGCAGCTCAACATCAACGAAAG	2040
QY	2041	AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTCTCAACCTGAGTGCAGCTGT	2100
DB	2041	AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTCTCAACCTGAGTGCAGCTGT	2100

[illegible]

RESULT 4
US-09-687-372-17
; Sequence 17, Application US/09687372
; Patent No. 6481379
; GENERAL INFORMATION:
; APPLICANT: Aquabio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Neuring, Jacqueline
;

DECEMBER 4

```

; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; FILE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT APPLICATION NUMBER: US/09/687,372
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-09-687-372-17

```

```

Query Match      100.0%; Score 4134; DB 4; Length 4134;
Best Local Similarity 100.0%; Pred No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy	1	AATTCGGTTGCTGCGGTTCAAGTCCAGTCTCTCCAGTGCAAAATGAGAAATGTTGTC	60
Db	1	AATTCGGTTGCTGCGGTTCAAGTCCAGTCTCTCCAGTGCAAAATGAGAAATGTTGTC	60
Qy	61	GCCATTACAGGACATGCACTACATCTGTTAATGAATATGTCAGTTATCTGAAGT	120
Db	61	GCCATTACAGGACATGCACTACATCTGTTAATGAATATGTCAGTTATCTGAAGT	120
Qy	121	TATTAATAATGTTTCTGCAAGGATGGCTTCCAGAGAAATCAATCTGCGAGTTTCCCAT	180
Db	121	TATTAATAATGTTTCTGCAAGGATGGCTTCCAGAGAAATCAATCTGCGAGTTTCCCAT	180
Qy	181	GTCAATTGATGAATACTACCAAGAGGATGTAAACAAATGGAACAAAGCTGAGACAC	240
Db	181	GTCAATTGATGAATACTACCAAGAGGATGTAAACAAATGGAACAAAGCTGAGACAC	240
Qy	241	GTTCACCCCTTTCTTGAGCATACGATCAACCTGGAAGAGATGGAAGCTTGAGAGAA	300
Db	241	GTTCACCCCTTTCTTGAGCATACGATCAACCTGGAAGAGATGGAAGCTTGAGAGAA	300
Qy	301	ATGGGAAATGATCTTCCAGGATTCGTGTGTAAGGATCCCTCAACCAATTAACAAAGATA	360
Db	301	ATGGGAAATGATCTTCCAGGATTCGTGTGTAAGGATCCCTCAACCAATTAACAAAGATA	360
Qy	361	GCAGAAATCCTCCAGGATCTCTGTAAACGGCTGGGCTAGTGGTTCAGGAA	420
Db	361	GCAGAAATCCTCCAGGATCTCTGTAAACGGCTGGGCTAGTGGTTCAGGAA	420
Qy	421	CAGACAGGGCTGCACATGCTCAGCTTCACTGCCAACTTATTTCTGGGATTTACA	480
Db	421	CAGACAGGGCTGCACATGCTCAGCTTCACTGCCAACTTATTTCTGGGATTTACA	480
Qy	481	CTCCTACAGTCTACATGCTCAGGGATGTGTCCAAACCAAGGCTCCAGAGAAAGGA	540
Db	481	CTCCTACAGTCTACATGCTCAGGGATGTGTCCAAACCAAGGCTCCAGAGAAAGGA	540
Qy	541	GACATCATACTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600
Db	541	GACATCATACTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600
Qy	601	TTAAATCAGAGACCGAGGCGCAAAATGTATTCGGTACAAATTTTCAGAGGCTTCGATGG	660
Db	601	TTAAATCAGAGACCGAGGCGCAAAATGTATTCGGTACAAATTTTCAGAGGCTTCGATGG	660
Qy	661	CTCCAGGCGATGATATTCGCAATTCAGAGATTAACACAGTATGACCTTCTGCGCCAAAT	720
Db	661	CTCCAGGCGATGATATTCGCAATTCAGAGATTAACACAGTATGACCTTCTGCGCCAAAT	720
Qy	721	ATCACCCCTGGGATATCGCATATTTGACACGTTGTAACACCGTGTCCAAAGCGCTAGAGCA	780
Db	721	ATCACCCCTGGGATATCGCATATTTGACACGTTGTAACACCGTGTCCAAAGCGCTAGAGCA	780
Qy	781	ACACTCAGCTTTGCGCCAGACAAATTCGCTCGCTGAACTAGATGAGTCTGTAAAC	840
Db	781	ACACTCAGCTTTGCGCCAGACAAATTCGCTCGCTGAACTAGATGAGTCTGTAAAC	840

Qy	841	TGCTCTGACCATATCCATCCACATAGCAGTGGTGGGGCAACCCGGTTCAGGAATCTCC	900
Db	841	TGCTCTGACCATATCCATCCACATAGCAGTGGTGGGGCAACCCGGTTCAGGAATCTCC	900
Qy	901	ACGGCTGTGGCCAAATCTATTGGGATTTATTATTCACATCCACAGGTTCAGTATGCTCTCG	960
Db	901	ACGGCTGTGGCCAAATCTATTGGGATTTATTATTCACATCCACAGGTTCAGTATGCTCTCG	960
Qy	961	AGCAGGCTGTCTCAGCAACAAGATGATCAAGGCTTCTGAGGACCATCCCAATGAT	1020
Db	961	AGCAGGCTGTCTCAGCAACAAGATGATCAAGGCTTCTGAGGACCATCCCAATGAT	1020
Qy	1021	GAGCAACAGGCGCACGGCATGGCGAGATCATCGAGCACTTCCAGTGGAACTGGTGGGA	1080
Db	1021	GAGCAACAGGCGCACGGCATGGCGAGATCATCGAGCACTTCCAGTGGAACTGGTGGGA	1080
Qy	1081	ACCCTGGCAGCCGACGATGACTATGGCCGCCAGGCAATTCACAAAGTTCCGGGAGGAGGC	1140
Db	1081	ACCCTGGCAGCCGACGATGACTATGGCCGCCAGGCAATTCACAAAGTTCCGGGAGGAGGC	1140
Qy	1141	GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG	1200
Db	1141	GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG	1200
Qy	1201	CAGTTGAGTTTCATCGCCGACGTTCATCCAGAACTCTCTCGGCCAAGGTTCATCGTGTCTTC	1260
Db	1201	CAGTTGAGTTTCATCGCCGACGTTCATCCAGAACTCTCTCGGCCAAGGTTCATCGTGTCTTC	1260
Qy	1261	TCCAAATGGCCCGACCTGGAGCCGCTCATCCAGAGATAGTTCCGGAACAATCAACCGAT	1320
Db	1261	TCCAAATGGCCCGACCTGGAGCCGCTCATCCAGAGATAGTTCCGGAACAATCAACCGAT	1320
Qy	1321	CGGATCTGGCTGGCCAGCGAGGCTTGGCCGAGCTCTTCGCTCATTTCCCAAGCCAGAGTAC	1380
Db	1321	CGGATCTGGCTGGCCAGCGAGGCTTGGCCGAGCTCTTCGCTCATTTCCCAAGCCAGAGTAC	1380
Qy	1381	TTCCACGTGTCTGGCGGCGCACCATCGCTCTCAGGCGCGGGCTATCCCGAGGTTTC	1440
Db	1381	TTCCACGTGTCTGGCGGCGCACCATCGCTCTCAGGCGCGGGCTATCCCGAGGTTTC	1440
Qy	1441	AACAAGTTCTGAAGAGAGTCCACCCAGCAGGTCTCTCGCAAAATGGGTTTGTCAAGGAG	1500
Db	1441	AACAAGTTCTGAAGAGAGTCCACCCAGCAGGTCTCTCGCAAAATGGGTTTGTCAAGGAG	1500
Qy	1501	TTCTGGAGGAGACCTTCAACTGCTACTTCCACGAGAGACCTTGACGAGCTGGAAGAT	1560
Db	1501	TTCTGGAGGAGACCTTCAACTGCTACTTCCACGAGAGACCTTGACGAGCTGGAAGAT	1560
Qy	1561	TCCAAAGTGGCTTCGACGAGCGGCTCAGAGGAGCGGCTCCAGAGCGGGGACTCC	1620
Db	1561	TCCAAAGTGGCTTCGACGAGCGGCTCAGAGGAGCGGCTCCAGAGCGGGGACTCC	1620
Qy	1621	AGACGAGACGCGCTTACGCCACCTTGCATCGGAGGAGAGAAATCAACAGCGTGGAGACC	1680
Db	1621	AGACGAGACGCGCTTACGCCACCTTGCATCGGAGGAGAGAAATCAACAGCGTGGAGACC	1680
Qy	1681	CCCTACCTGGATATACACCTGAGGATCTCCTACAATGTATACGTGGCGCTCTACTCC	1740
Db	1681	CCCTACCTGGATATACACCTGAGGATCTCCTACAATGTATACGTGGCGCTCTACTCC	1740
Qy	1741	ATTGCTCACGCCCTGCAAGACATCCACTCTTGCAAAACCCGGGACCGGCATCTTTGCAAA	1800
Db	1741	ATTGCTCACGCCCTGCAAGACATCCACTCTTGCAAAACCCGGGACCGGCATCTTTGCAAA	1800
Qy	1801	GGATCTTTGTCAGATATTAATAAAGTTGAGGCTGCGAGTCTCTCAACCATCTGTGTCAT	1860
Db	1801	GGATCTTTGTCAGATATTAATAAAGTTGAGGCTGCGAGTCTCTCAACCATCTGTGTCAT	1860
Qy	1861	CTCAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGTCACTCAAG	1920
Db	1861	CTCAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGTCACTCAAG	1920

Qy	1921	GGGAAC	TACACCA	TATTA	CAACTG	CAGCTCTCCG	CAGGATGA	ATCGTGT	TTCAT	1981
Db	1921	GGGAAC	TACACCA	TATTA	CAACTG	CAGCTCTCCG	CAGGATGA	ATCGTGT	TTCAT	1980
Qy	1981	GAGGTG	GGCAACTA	CAAGCCTA	CGCTAAG	CCAGTCAC	CGACTCA	ACATCA	CAAGAAAG	2040
Db	1981	GAGGTG	GGCAACTA	CAAGCCTA	CGCTAAG	CCAGTCAC	CGACTCA	ACATCA	CAAGAAAG	2040
Qy	2041	AAAA	TCCTG	AGTGGCTT	CTCAAA	GTGGTTCT	CTTCTT	CCAACTCG	AGTGTGT	2100
Db	2041	AAAA	TCCTG	AGTGGCTT	CTCAAA	GTGGTTCT	CTTCTT	CCAACTCG	AGTGTGT	2100
Qy	2101	GTGCGG	GCACAG	GAAGGAT	CATCGA	GGGAGCC	ACCTGCT	TTGAA	TGCATG	2160
Db	2101	GTGCGG	GCACAG	GAAGGAT	CATCGA	GGGAGCC	ACCTGCT	TTGAA	TGCATG	2160
Qy	2161	GCATG	TCAGAGG	GAGATT	CAGTGA	TGAAAAC	GATCAAG	TGCGTGT	CAAAAGTGC	2220
Db	2161	GCATG	TCAGAGG	GAGATT	CAGTGA	TGAAAAC	GATCAAG	TGCGTGT	CAAAAGTGC	2220
Qy	2221	AATGAT	TTCTG	TGATGA	AGAAC	CAACGTC	GTGCATCG	CCAAAGG	ATCGAGTAC	2280
Db	2221	AATGAT	TTCTG	TGATGA	AGAAC	CAACGTC	GTGCATCG	CCAAAGG	ATCGAGTAC	2280
Qy	2281	TCGTG	GACG	AGCCCTT	CGGATCG	CTGAC	CACTTT	CGCGTACT	TGGGCATC	2340
Db	2281	TCGTG	GACG	AGCCCTT	CGGATCG	CTGAC	CACTTT	CGCGTACT	TGGGCATC	2340
Qy	2341	ACCTC	TTCTG	TGCTGG	GGCTTTC	ATCAAG	TTAGAAC	TCTCC	ATCTGTAAG	2400
Db	2341	ACCTC	TTCTG	TGCTGG	GGGTCTT	ATCAAG	TTAGAAC	TCTCC	ATCTGTAAG	2400
Qy	2401	AACG	GGA	TTGTCT	ACTCTG	CTTCTT	CCCTCAT	CTGCTG	CTTCCAGT	2460
Db	2401	AACG	GGA	TTGTCT	ACTCTG	CTTCTT	CCCTCAT	CTGCTG	CTTCCAGT	2460
Qy	2461	ATCTT	CA	TCG	CAGCC	AGGACTG	TCGGTTC	CGCCAA	CCGGCTTT	2520
Db	2461	ATCTT	CA	TCG	CAGCC	AGGACTG	TCGGTTC	CGCCAA	CCGGCTTT	2520
Qy	2521	AGCTT	CGTCT	GTGCAT	CTCTG	ATCCTG	TGAGAC	CAACCG	GTCTGCTTC	2580
Db	2521	AGCTT	CGTCT	GTGCAT	CTCTG	ATCCTG	TGAGAC	CAACCG	GTCTGCTTC	2580
Qy	2581	GAGG	CCAA	AGATCCC	ACCAG	CTCC	ACGCAAG	TGGGTGG	GCCTCA	2640
Db	2581	GAGG	CCAA	AGATCCC	ACCAG	CTCC	ACGCAAG	TGGGTGG	GCCTCA	2640
Qy	2641	CTG	GTCTT	CTCTG	ATCTG	TGTAAT	CGTCA	CTG	CACTAC	2700
Db	2641	CTG	GTCTT	CTCTG	ATCTG	TGTAAT	CGTCA	CTG	CACTAC	2700
Qy	2701	CCTC	CTC	AGCTAC	GAA	CCATG	AGCTG	GAGGAC	AGGTCAT	2760
Db	2701	CCTC	CTC	AGCTAC	GAA	CCATG	AGCTG	GAGGAC	AGGTCAT	2760
Qy	2761	GAGG	GT	CGTCA	TGGGCTT	TCTT	CA	TGGGCT	TACCTG	2820
Db	2761	GAGG	GT	CGCT	CATGGG	CTTCT	CA	TGGGCT	TACCTG	2820
Qy	2821	TGCTT	CTT	TCG	CTTCAAG	TCCG	TAA	GTGCG	GAGAACTT	2880
Db	2821	TGCTT	CTT	TCG	CTTCAAG	TCCG	TAA	GTGCG	GAGAACTT	2880
Qy	2881	ATCA	CTT	TG	CA	TGTTG	ATCTT	TC	TGATCT	2940
Db	2881	ATCA	CTT	TG	CA	TGTTG	ATCTT	TC	TGATCT	2940
Qy	2941	AGCA	CT	AC	GCA	AGTTT	GTG	CGG	CGTGG	3000
Db	2941	AGCA	CT	AC	GCA	AGTTT	GTG	CGG	CGTGG	3000
Qy	3001	GGGT	GTCT	GGG	CTG	CA	TTTACTT	CA	AAAGTGT	3060

[illegible]

Db 4081 AAGCGCGCCGACAGCAACGG 4134

RESULT 5

US-09-975-553-17

; Sequence 17, Application US/09975553

; Patent No. 6564747

; GENERAL INFORMATION:

; APPLICANT: Harris, H. William, Jr.

; APPLICANT: Russell, David R.

; APPLICANT: Nearing, Jacqueline

; APPLICANT: Betka, Marlies

; TITLE OF INVENTION: Fish

; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous

; FILE REFERENCE: 2213.1004-001

; CURRENT APPLICATION NUMBER: US/09/975,553

; CURRENT FILING DATE: 2001-10-11

; PRIOR APPLICATION NUMBER: 09/687,477

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 09/687,476

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 09/687,372

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 4134

; TYPE: DNA

; ORGANISM: Dogfish Shark

US-09-975-553-17

Query Match 100.0%; Score 4134; DB 4; Length 4134;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGGTGTCTGCGTTCAGTCCAAAGTCTCTCCAGTGCAGAAATGAGAAATGCTGTC 60

DB 1 AATTCGGTGTCTGCGTTCAGTCCAAAGTCTCTCCAGTGCAGAAATGAGAAATGCTGTC 60

QY 61 GCATTACAGGAACATGCACTACATCTGTGTTAAATGAATATGTGAGTTATCTGAAGT 120

DB 61 GCATTACAGGAACATGCACTACATCTGTGTTAAATGAATATGTGAGTTATCTGAAGT 120

QY 121 TATTAATGTTTCTGCAAGGATGGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 180

DB 121 TATTAATGTTTCTGCAAGGATGGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 180

QY 181 GTCAATGTATGAATACTGACCAAGGATGTAACAAATGGAATGGAACAAAGCTGAGGAC 240

DB 181 GTCAATGTATGAATACTGACCAAGGATGTAACAAATGGAATGGAACAAAGCTGAGGAC 240

QY 241 GTTACCCCTTCTGAGGATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 300

DB 241 GTTACCCCTTCTGAGGATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 300

QY 301 ATGGGATTTGATCTTCCAGGATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAG 360

DB 301 ATGGGATTTGATCTTCCAGGATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAG 360

QY 361 GCAGAAATCTTCCAGGATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 420

DB 361 GCAGAAATCTTCCAGGATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 420

QY 421 CAGAGACAGGCTGCAATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 480

DB 421 CAGAGACAGGCTGCAATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 480

QY 481 CTCCTACAGTGTGTAATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 540

DB 481 CTCCTACAGTGTGTAATGCTTCAAGAGGATGCTTCAAGAGGATGCTTCAAGAGG 540

QY 541 GACATCACTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600

Db 541 GACATCACTGGAGGCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600

QY 601 TTAATAATCGAGACCGGAGGCGCAAAATGATTCGGTACAAATTTTCAGGCTTCCGATGG 660

DB 601 TTAATAATCGAGACCGGAGGCGCAAAATGATTCGGTACAAATTTTCAGGCTTCCGATGG 660

QY 661 CTCAGGCGATGATTTTCGCAATTTGAAGAGATTAACAACAGTAGTATCTTCTGCGCAAT 720

DB 661 CTCAGGCGATGATTTTCGCAATTTGAAGAGATTAACAACAGTAGTATCTTCTGCGCAAT 720

QY 721 ATCACCTGGGATATCGCATATTTGACAGTGTAAACCGTGTCCAGGCGCTAGAGGCA 780

DB 721 ATCACCTGGGATATCGCATATTTGACAGTGTAAACCGTGTCCAGGCGCTAGAGGCA 780

QY 781 ACCTCAGCTTTGTGGCCCGAGAAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAA 840

DB 781 ACCTCAGCTTTGTGGCCCGAGAAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAA 840

QY 841 TGCTCTGACCATATCCCATCCAAATAGCAGTGGTGGGCGCAACCGGTCAGGAATCTCC 900

DB 841 TGCTCTGACCATATCCCATCCAAATAGCAGTGGTGGGCGCAACCGGTCAGGAATCTCC 900

QY 901 ACGGCTGTGGCCCAATCTATTGGGATTTATTTTCAATTTCCACAGGTCAGCTATGCTCTCG 960

DB 901 ACGGCTGTGGCCCAATCTATTGGGATTTATTTTCAATTTCCACAGGTCAGCTATGCTCTCG 960

QY 961 AGCAGGCTGTCTCAGCAACAAAGATGAGTCAAGGCGCTTCCCTGAGGACCAATCCCAATGAT 1020

DB 961 AGCAGGCTGTCTCAGCAACAAAGATGAGTCAAGGCGCTTCCCTGAGGACCAATCCCAATGAT 1020

QY 1021 GAGCAACAGGCGCAGGCGCATGCGCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080

DB 1021 GAGCAACAGGCGCAGGCGCATGCGCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080

QY 1081 ACCCTGCGAGCGAGATGATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140

DB 1081 ACCCTGCGAGCGAGATGATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140

QY 1141 GTTAAGAGGAGACATCTGATTTGAGTTCAGTGAGATGATCTCTCAGTACTACACCCAGAG 1200

DB 1141 GTTAAGAGGAGACATCTGATTTGAGTTCAGTGAGATGATCTCTCAGTACTACACCCAGAG 1200

QY 1201 CAGTTGAGTTTCATCGCGCGAGCTCATCCAGAACTCCTCGCGCGCGCGCGCGCGCGCGCG 1260

DB 1201 CAGTTGAGTTTCATCGCGCGAGCTCATCCAGAACTCCTCGCGCGCGCGCGCGCGCGCG 1260

QY 1261 TCCATGCG 1320

DB 1261 TCCATGCG 1320

QY 1321 CGGATCTGGGCG 1380

DB 1321 CGGATCTGGGCG 1380

QY 1381 TTCCAGTGTGCG 1440

DB 1381 TTCCAGTGTGCG 1440

QY 1441 AACAGTCTGCG 1500

DB 1441 AACAGTCTGCG 1500

QY 1501 TTCTGGGAGGAGACCTTTCAACTGCTACTTCCACGAGAGGACCCCTGACGAGCTGAAGAAT 1560

DB 1501 TTCTGGGAGGAGACCTTTCAACTGCTACTTCCACGAGAGGACCCCTGACGAGCTGAAGAAT 1560

QY 1561 TCCAGTGTGCG 1620

DB 1561 TCCAGTGTGCG 1620

QY 1621 AGACGAGACGCGCTTACG 1680

DB 1621 AGACGAGACGCGCTTACG 1680

Qy	1681	CCCTACTGTGATTATACACACTGTAGGATCTCTCAATGTATACGTGGCCGTCTACTCC	1740
Db	1681	CCCTACTGTGATTATACACACTGTAGGATCTCTCAATGTATACGTGGCCGTCTACTCC	1740
Qy	1741	ATTGCTCACGCCCTGCAAGACATCCACTCTTTGCAAAACCGGSCACGGGCATCTTTTGAAAC	1800
Db	1741	ATTGCTCACGCCCTGCAAGACATCCACTCTTTGCAAAACCGGSCACGGGCATCTTTTGAAAC	1800
Qy	1801	GGATCTTTGTGCAGATATATAAAAGTTGAGCCTGCGAGGTCTCTCAACCATCTGCTGCAT	1860
Db	1801	GGATCTTTGTGCAGATATATAAAAGTTGAGCCTGCGAGGTCTCTCAACCATCTGCTGCAT	1860
Qy	1861	CTGAGTTTACCAACAGCATGGGTGAGCAGTTTGACTTTGACCATCAAGGTGACCTCAAG	1920
Db	1861	CTGAGTTTACCAACAGCATGGGTGAGCAGTTTGACTTTGACCATCAAGGTGACCTCAAG	1920
Qy	1921	GGAACTTACACCATTTAACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTGTTCCAT	1980
Db	1921	GGAACTTACACCATTTAACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTGTTCCAT	1980
Qy	1981	GAGTGGGCAACTACAAAGCCTAGCTAAGCCAGATGACCGACTCAACATCAACGAAAAG	2040
Db	1981	GAGTGGGCAACTACAAAGCCTAGCTAAGCCAGATGACCGACTCAACATCAACGAAAAG	2040
Qy	2041	AAATCTCTCGGAGTGCGTTCTCAAAGTGTTCTTTCTCCAACTGCAGTCGAGACTGT	2100
Db	2041	AAATCTCTCGGAGTGCGTTCTCAAAGTGTTCTTTCTCCAACTGCAGTCGAGACTGT	2100
Qy	2101	GTGCGGCGCACAGGAAGGGATCATCGAGGGGAGCCCACTGCTGCTTTGAATGCATG	2160
Db	2101	GTGCGGCGCACAGGAAGGGATCATCGAGGGGAGCCCACTGCTGCTTTGAATGCATG	2160
Qy	2161	GCATGTGCAGGGAGGTTTCAGTGATGAAAAAGATGCGGTGTAACAAAGTGCCCG	2220
Db	2161	GCATGTGCAGGGAGGTTTCAGTGATGAAAAAGATGCGGTGTAACAAAGTGCCCG	2220
Qy	2221	AATGATTTCTGTGCGAATGAGAACCAACGCTGTGCATCGCCAAGGAGATCGAGTACCTG	2280
Db	2221	AATGATTTCTGTGCGAATGAGAACCAACGCTGTGCATCGCCAAGGAGATCGAGTACCTG	2280
Qy	2281	TGTTGACGAGCGCTTCGGGATCGCTGACCATCTTGGCGTACTGGGCATCTTGATC	2340
Db	2281	TGTTGACGAGCGCTTCGGGATCGCTGACCATCTTGGCGTACTGGGCATCTTGATC	2340
Qy	2341	ACCTCCTTCGTGTGGGGTCTTCATCAAGTTCAGGAACACTCCCATCGTGAAGGCCACC	2400
Db	2341	ACCTCCTTCGTGTGGGGTCTTCATCAAGTTCAGGAACACTCCCATCGTGAAGGCCACC	2400
Qy	2401	AAACGGAGTTGCTCACTGCTGCTTCTCCTCATCTGCTGCTTCCAGTCCGCTC	2460
Db	2401	AAACGGAGTTGCTCACTGCTGCTTCTCCTCATCTGCTGCTTCCAGTCCGCTC	2460
Qy	2461	ATCTTCATCGGCGAGCCAGGACTGACCTGTGGCTCGCCAAACCGGCTTTGGCATC	2520
Db	2461	ATCTTCATCGGCGAGCCAGGACTGACCTGTGGCTCGCCAAACCGGCTTTGGCATC	2520
Qy	2521	AGCTTCGCTCTGTGCATCTCCTGCATCCTGGTGAAGAACCAACGGGTGCTGTGCTTTC	2580
Db	2521	AGCTTCGCTCTGTGCATCTCCTGCATCCTGGTGAAGAACCAACGGGTGCTGTGCTTTC	2580
Qy	2581	GAGGCCAGATCCACACAGCTCCACCGCAAGTGGTGGGCTCAACCTGAGTTCTCTC	2640
Db	2581	GAGGCCAGATCCACACAGCTCCACCGCAAGTGGTGGGCTCAACCTGAGTTCTCTC	2640
Qy	2641	CTGCTCTCTCTGTGCATCTCTGGTGCAATCGTCACTGTCATCATCTGGGTCTACACGGG	2700
Db	2641	CTGGTCTTCTCTGTGCATCTCTGGTGCAATCGTCACTGTCATCATCTGGGTCTACACGGG	2700
Qy	2701	CTCTCCTTCCAGCTACAGGAACCATGAGCTGGAGCGAGGTGCATCTTCACTCGCTCGAC	2760
Db	2701	CTCTCCTTCCAGCTACAGGAACCATGAGCTGGAGCGAGGTGCATCTTCACTCGCTCGAC	2760

Qy	2761	GAGGGCTCGCTCATGGCGCTTGGGCTTCCTCATCGGCTACACCTGCGCTCTCTCGCGCGCATC	2820
Db	2761	GAGGGCTCGCTCATGGCGCTTGGGCTTCCTCATCGGCTACACCTGCGCTCTCTCGCGCGCATC	2820
Qy	2821	TGCTTCTTCTTCCGCTTCAAGTCCCGTAAAGCTCCGCGAGAACTTCAACGAGGCTAAGTTC	2880
Db	2821	TGCTTCTTCTTCCGCTTCAAGTCCCGTAAAGCTCCGCGAGAACTTCAACGAGGCTAAGTTC	2880
Qy	2881	ATCACCTTCAGCAATGTGTATCTTTCATCTGCTCTGGATCTCTCATCCCGGCTATGTC	2940
Db	2881	ATCACCTTCAGCAATGTGTATCTTTCATCTGCTCTGGATCTCTCATCCCGGCTATGTC	2940
Qy	2941	AGCACCTACGGCAAGTTTGTGTGGCGGTGAGGTGATTGGCCATCTCTGSCCTCCAGCTTC	3000
Db	2941	AGCACCTACGGCAAGTTTGTGTGGCGGTGAGGTGATTGGCCATCTCTGSCCTCCAGCTTC	3000
Qy	3001	GGGCTGCTGGCTGCAATTACTTCAACAAAGTGTATACATCATCTGTTCAAGCGTGCCTG	3060
Db	3001	GGGCTGCTGGCTGCAATTACTTCAACAAAGTGTATACATCATCTGTTCAAGCGTGCCTG	3060
Qy	3061	AACACCATCGAGAGTGGCTGCACACGGGGCGGCCACGCTTCAAGTGTGGCGGCGCGG	3120
Db	3061	AACACCATCGAGAGTGGCTGCACACGGGGCGGCCACGCTTCAAGTGTGGCGGCGCGG	3120
Qy	3121	GCCACCTCTCGGCGCAGCGCGCTCTCCAAAGCGTCCAGCAGGCTGTGCGGCTCCACC	3180
Db	3121	GCCACCTCTCGGCGCAGCGCGCTCTCCAAAGCGTCCAGCAGGCTGTGCGGCTCCACC	3180
Qy	3181	ATCTCTCGCGCGCTCTGTCACCTCGGGCGCGGCTCACCATGGAGATGACAGCGCTGC	3240
Db	3181	ATCTCTCGCGCGCTCTGTCACCTCGGGCGCGGCTCACCATGGAGATGACAGCGCTGC	3240
Qy	3241	AGCAGCAGAAGTTCAGCTTCGGCAGCGCACCGTCAACCTGTGCTCAGCTTCGAGGAG	3300
Db	3241	AGCAGCAGAAGTTCAGCTTCGGCAGCGCACCGTCAACCTGTGCTCAGCTTCGAGGAG	3300
Qy	3301	ACAGGCGGATACGCCACCTTAGCCGCACGGCCCGCAGCAGAACTTCGGCGGATGCGCGC	3360
Db	3301	ACAGGCGGATACGCCACCTTAGCCGCACGGCCCGCAGCAGAACTTCGGCGGATGCGCGC	3360
Qy	3361	AGCGGCGAGACTCGCCATCTAGACACACGACCGACGGGCCCGCTCAGAAATCGCAGCCC	3420
Db	3361	AGCGGCGAGACTCGCCATCTAGACACACGACCGACGGGCCCGCTCAGAAATCGCAGCCC	3420
Qy	3421	CAGCCCGCAACGATGCCCGATACAAAGGGGGGGCCGACCAAGGGGACCCCTAGAGTCCCG	3480
Db	3421	CAGCCCGCAACGATGCCCGATACAAAGGGGGGGCCGACCAAGGGGACCCCTAGAGTCCCG	3480
Qy	3481	GGCGGCGAGAGAGCGGCCCACTATGAGAGGAAACCTATTCMACTCCTCCTCATCAAC	3540
Db	3481	GGCGGCGAGAGAGCGGCCCACTATGAGAGGAAACCTATTCMACTCCTCCTCATCAAC	3540
Qy	3541	CCCAAGAACTCCTCCACGGCAGCACCGTCGACAACTGACATCAACTCCTTAACCGGTGCG	3600
Db	3541	CCCAAGAACTCCTCCACGGCAGCACCGTCGACAACTGACATCAACTCCTTAACCGGTGCG	3600
Qy	3601	TGCCCAACCTCTCCCTCTCGCGCACTTTCGCTTTGTCTGGAAGATGTCAGCATCTGCACT	3660
Db	3601	TGCCCAACCTCTCCCTCTCGCGCACTTTCGCTTTTGTCTGGAAGATGTCAGCATCTGCACT	3660
Qy	3661	TCCTTTTATCCCTGATTTTCTGCACTTGGATATTTTACTAGTGTGCGATGGAATATCACAC	3720
Db	3661	TCCTTTTATCCCTGATTTTCTGCACTTGGATATTTTACTAGTGTGCGATGGAATATCACAC	3720
Qy	3721	ATAATGAGTTGCAATAATAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACCTATCTGAAGT	3780
Db	3721	ATAATGAGTTGCAATAATAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACCTATCTGAAGT	3780
Qy	3781	ATCTGAACCTATTTATCTCTCGAATGTATACAAACATTTGAAGTATTTTTAGTGACA	3840
Db	3781	ATCTGAACCTATTTATCTCTCGAATGTATACAAACATTTGAAGTATTTTTAGTGACA	3840
Qy	3841	TTATGTTCTAACATTCGCAAGATAATTTGCTTACACATATAAGGTACACCTCGAAGCAGT	3900

```
Db      3841  TTATGTTCTAAACATTTGTCAGATAATTTGTTACAACATATAGTACCACCTGAAGCAGT 3900
Qy      3901  GACTGAGATTGCCACTGTGATGACAGAACTGTTTATTAACATTTATTAACCTGGA 3960
Db      3901  GACTGAGATTGCCACTGTGATGACAGAACTGTTTATTAACATTTATTAACCTGGA 3960
Qy      3961  TTGCAACAGGAATATAATCACTGTAAACAAAAAATTTGTTATTTCTTAAAAATGCAAA 4020
Db      3961  TTGCAACAGGAATATAATCACTGTAAACAAAAAATTTGTTATTTCTTAAAAATGCAAA 4020
Qy      4021  TGTAAATCAGATGTGTAATAATTTGGTAAATTTCTGTACATTAATGCAATTTCTTGATA 4080
Db      4021  TGTAAATCAGATGTGTAATAATTTGGTAAATTTCTGTACATTAATGCAATTTCTTGATA 4080
Qy      4081  AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 4134
Db      4081  AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 4134

RESULT 6
US-10-270-795-17
; Sequence 17, Application US/10270795
; Patent No. 6637371
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT APPLICATION NUMBER: US/10/270,795
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,372
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-795-17

Query Match      100.0%; Score 4134; DB 4; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AATTCGGTTGCTGCTCGGTTTCAGTCCAAAGTCTCTCCAGTGCAAAATGAGAAATGTTGTC 60
Db      1  AATTCGGTTGCTGCTCGGTTTCAGTCCAAAGTCTCTCCAGTGCAAAATGAGAAATGTTGTC 60
Qy      61  GCATTACAGGAACATGCATCTGTTGTTAAATGAATATGTCAGTTATCTGAAGT 120
Db      61  GCATTACAGGAACATGCATCTGTTGTTAAATGAATATGTCAGTTATCTGAAGT 120
Qy      121  TATTAATAATGTTCTGCAAGGATGGCTTCCAGAGAAATCAATCTGCAGCTTTTCCCAAT 180
Db      121  TATTAATAATGTTCTGCAAGGATGGCTTCCAGAGAAATCAATCTGCAGCTTTTCCCAAT 180
Qy      181  GTCATTGTATGAATACCTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGACCAAC 240
Db      181  GTCATTGTATGAATACCTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGACCAAC 240
Qy      241  GTTCACCTTTCTTGGAGATACGATCAACCTGAGGAGATGGAAGCTTGAAGAGGAA 300
Db      241  GTTCACCTTTCTTGGAGATACGATCAACCTGAGGAGATGGAAGCTTGAAGAGGAA 300
Qy      301  ATGGGATTTGATCTTCCAGGAGTTCTGCTGTTAAAGCGATCCCTCACCATTACAAAGATAA 360
Db      301  ATGGGATTTGATCTTCCAGGAGTTCTGCTGTTAAAGCGATCCCTCACCATTACAAAGATAA 360
```

```
Qy      361  GCAGAAATCCTCAGGCATCCTCTGTAAACGGGCTGGCTAGTGTGGCTTGGTCAAGGAA 420
Db      361  GCAGAAATCCTCAGGCATCCTCTGTAAACGGGCTGGCTAGTGTGGCTTGGTCAAGGAA 420
Qy      421  CAGAGCAGGGCTGCACAAATGGCTCAGCTTCACTGCCAACTCTTATTTCTTGGGATTTACA 480
Db      421  CAGAGCAGGGCTGCACAAATGGCTCAGCTTCACTGCCAACTCTTATTTCTTGGGATTTACA 480
Qy      481  CTCTCAGTCGTACAAATGTCTCAGGGTATGTTCCAAACCAAGGCCCCAGAGAAGA 540
Db      481  CTCTCAGTCGTACAAATGTCTCAGGGTATGTTCCAAACCAAGGCCCCAGAGAAGA 540
Qy      541  GACATCATCTGGAGGCTCTCTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
Db      541  GACATCATCTGGAGGCTCTCTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
Qy      601  TTAATAATCGAGACCGGAGCGCAAAAATGTTATTCGGTACAAATTTTCGAGGCTTCCGATG 660
Db      601  TTAATAATCGAGACCGGAGCGCAAAAATGTTATTCGGTACAAATTTTCGAGGCTTCCGATG 660
Qy      661  CTCAGGCGATGATATTCGCAATTTGAAGATTAACAAACAGTATGACTTTCTTCCCAAT 720
Db      661  CTCAGGCGATGATATTCGCAATTTGAAGATTAACAAACAGTATGACTTTCTTCCCAAT 720
Qy      721  ATCACCCTGGGATATCGCATATTTGACAGCTGTAACACCGTGTCCAAAGCGGTAGAGGCA 780
Db      721  ATCACCCTGGGATATCGCATATTTGACAGCTGTAACACCGTGTCCAAAGCGGTAGAGGCA 780
Qy      781  ACACCTCAGCTTTGTCGCCCAAGAAACAAAATCGACTCTGCTGAACTTAGATGAGTTCTTAAC 840
Db      781  ACACCTCAGCTTTGTCGCCCAAGAAACAAAATCGACTCTGCTGAACTTAGATGAGTTCTTAAC 840
Qy      841  TGCTCTGACCATATCCATCCCAATAGCAGTGTGCGGGGCAACCGGGTCAGAAATCTCC 900
Db      841  TGCTCTGACCATATCCATCCCAATAGCAGTGTGCGGGGCAACCGGGTCAGAAATCTCC 900
Qy      901  ACGGCTGTGGCCAAATCTATTGGGATTTATTACATTCACAGGTGAGTATGCTCTCTCG 960
Db      901  ACGGCTGTGGCCAAATCTATTGGGATTTATTACATTCACAGGTGAGTATGCTCTCTCG 960
Qy      961  AGCAGGCTGTGACCAACAAAGATGATGACAGGCTTCTGAGGACCAATCCCAATGAT 1020
Db      961  AGCAGGCTGTGACCAACAAAGATGATGACAGGCTTCTGAGGACCAATCCCAATGAT 1020
Qy      1021  GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Db      1021  GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Qy      1081  ACCCTGCAAGCCAGCATGATATGCGCCGCCAGGCAATGACAAAGTTCCGGGAGGAGGCC 1140
Db      1081  ACCCTGCAAGCCAGCATGATATGCGCCGCCAGGCAATGACAAAGTTCCGGGAGGAGGCC 1140
Qy      1141  GTTAAGAGGACATCTGTTGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Db      1141  GTTAAGAGGACATCTGTTGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Qy      1201  CAGTTGAGTTATCGCCGACGTCATCCAGAACTCTCGGCCCAAGGTCTATCGTGTCTTC 1260
Db      1201  CAGTTGAGTTATCGCCGACGTCATCCAGAACTCTCGGCCCAAGGTCTATCGTGTCTTC 1260
Qy      1261  TCCAAATGGCCCACTGGAGCGCTCATCCAGAGATAGTTCCGAGAAACATCAACCGAT 1320
Db      1261  TCCAAATGGCCCACTGGAGCGCTCATCCAGAGATAGTTCCGAGAAACATCAACCGAT 1320
Qy      1321  CGGATCTGGGTGCGCAGCGAGGCTTGGGCGAGCTTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Db      1321  CGGATCTGGGTGCGCAGCGAGGCTTGGGCGAGCTTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Qy      1381  TTCCACGTGTGCGGCGCACCATCGGCTTCTCAGGGCGGGGCTATCCAGGGTTTC 1440
Db      1381  TTCCACGTGTGCGGCGCACCATCGGCTTCTCAGGGCGGGGCTATCCAGGGTTTC 1440
Qy      1441  AACCAAGTTCTCTGAAGAGGAGGTCCACCCCGAGGCTCTCGGCAAAATGGGTTTGTCAAGGAG 1500
```


Db 1441 AACAGTTTCTTGAAGAGGTCACCCACGAGGTCCTCGCAATGGGTGTGTCAAGGAG 1500
Qy 1501 TTCTGGAGGAGACCTTCAACTGCTACTTACCGAGAGAGACCTGACGACGCTGAAGAAT 1560
Db 1501 TTCTGGAGGAGACCTTCAACTGCTACTTACCGAGAGAGACCTGACGACGCTGAAGAAT 1560
Qy 1561 TCCAAAGTTCCTTCGCAAGGACCGGCGCTCAAGGGAGCGGCTCAAGGGCGGGGAATCC 1620
Db 1561 TCCAAAGTTCCTTCGCAAGGACCGGCGCTCAAGGGAGCGGCTCAAGGGCGGGGAATCC 1620
Qy 1621 AGACGGACAGCCCTACGCAAGCACCCTTCGCACTGGGAGGAGAAATCAACAGAGGTGGAGACC 1680
Db 1621 AGACGGACAGCCCTACGCAAGCACCCTTCGCACTGGGAGGAGAAATCAACAGAGGTGGAGACC 1680
Qy 1681 CCCTACCTGGATTAACACACTGAGGATCTCTACAAATGATAGTGGCGGCTTACTTCC 1740
Db 1681 CCCTACCTGGATTAACACACTGAGGATCTCTACAAATGATAGTGGCGGCTTACTTCC 1740
Qy 1741 ATTGCTCAGCCCTCAGAGATCACTCTTGCAAACCCGACCGGCGATCTTGCRAAC 1800
Db 1741 ATTGCTCAGCCCTCAGAGATCACTCTTGCAAACCCGACCGGCGATCTTGCRAAC 1800
Qy 1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTGGCAGGTCCTCAACATCTGCTGCAT 1860
Db 1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTGGCAGGTCCTCAACATCTGCTGCAT 1860
Qy 1861 CTGAAGTTTACACAGCATGGTGAGCAGGTTGACTTTGAGGATCAAGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACACAGCATGGTGAGCAGGTTGACTTTGAGGATCAAGTGACCTCAAG 1920
Qy 1921 GGGAACTACACCATATCAATGGCAGCTCTCCGAGAGGATGAATCGGTCTGTTCAT 1980
Db 1921 GGGAACTACACCATATCAATGGCAGCTCTCCGAGAGGATGAATCGGTCTGTTCAT 1980
Qy 1981 GAGTGGGCAACTACAAAGCTTACGTAAGCCAGTGAACGACTCAACATCAACGAAAG 2040
Db 1981 GAGTGGGCAACTACAAAGCTTACGTAAGCCAGTGAACGACTCAACATCAACGAAAG 2040
Qy 2041 AAAATCCTCTGGAGTGGCTTCTCAAAGTGTCTTCTTCAACTGCGAGTGTG 2100
Db 2041 AAAATCCTCTGGAGTGGCTTCTCAAAGTGTCTTCTTCAACTGCGAGTGTG 2100
Qy 2101 GTCCGGGACACAGGAAGGGATCATCGAGGGGAGCCACCTGCTTGTGAATGCATG 2160
Db 2101 GTCCGGGACACAGGAAGGGATCATCGAGGGGAGCCACCTGCTTGTGAATGCATG 2160
Qy 2161 GCATGTGAGAGGAGAGTTCAAGTGAATAAAGATGCAAGTGGTGTAAGAGTGGCG 2220
Db 2161 GCATGTGAGAGGAGAGTTCAAGTGAATAAAGATGCAAGTGGTGTAAGAGTGGCG 2220
Qy 2221 AATGATTTCTGGTGAATGAGAACACACGCTCGTGCATCGGCAAGGAGATCGAGTACCTG 2280
Db 2221 AATGATTTCTGGTGAATGAGAACACACGCTCGTGCATCGGCAAGGAGATCGAGTACCTG 2280
Qy 2281 TCGTGGACGAGCCCTTCGGGATCGCTGTACCAATCTTCGCGTACTGGGCATCCTGATC 2340
Db 2281 TCGTGGACGAGCCCTTCGGGATCGCTGTACCAATCTTCGCGTACTGGGCATCCTGATC 2340
Qy 2341 ACCTCCTTCTGCTGGGGTCTTTCATCAAGTTTCAGGAACACTCCCATCTGTAAGGCCACC 2400
Db 2341 ACCTCCTTCTGCTGGGGTCTTTCATCAAGTTTCAGGAACACTCCCATCTGTAAGGCCACC 2400
Qy 2401 AACCGGAGTTGTCTTACTGCTGTCTTCTCCCTCATCTGCTCTTCTCAGCTCGCTC 2460
Db 2401 AACCGGAGTTGTCTTACTGCTGTCTTCTCCCTCATCTGCTCTTCTCAGCTCGCTC 2460
Qy 2461 ATCTTCATCGGGAGCCAGGACCTGACCTGTGGCTCCGCAACCGGCTTTGGCATC 2520
Db 2461 ATCTTCATCGGGAGCCAGGACCTGACCTGTGGCTCCGCAACCGGCTTTGGCATC 2520
Qy 2521 AGCTTCGCTGTGATCTCTGATCTCTGATCTGCTGTAAGACCAACCGGCTGCTGCTCTC 2580
Db 2521 AGCTTCGCTGTGATCTCTGATCTCTGATCTGCTGTAAGATTTGCTGAGATCTGCACT 2580

Db 2521 AGCTTCGCTGTGATCTCTGATCTCTGATCTCTGTAAGACCAACCGGCTGCTGCTCTTC 2580
Qy 2581 GAGGCAAGATCCCAACCAAGCTTCCACCAAGTGGTGGCTCAACCTGCAATCTCTTC 2640
Db 2581 GAGGCAAGATCCCAACCAAGCTTCCACCAAGTGGTGGCTCAACCTGCAATCTCTTC 2640
Qy 2641 CTGGTCTTCTCTGATCTCTGATCTCTGTAAGTCACTGATCATCTGCTCTACACGGG 2700
Db 2641 CTGGTCTTCTCTGATCTCTGATCTCTGTAAGTCACTGATCATCTGCTCTACACGGG 2700
Qy 2701 CCTCCCTTCAGCTTACAGGAACCATGAGCTGGAGGAGAGGTGATCTTCTATCACTCCGAC 2760
Db 2701 CCTCCCTTCAGCTTACAGGAACCATGAGCTGGAGGAGAGGTGATCTTCTATCACTCCGAC 2760
Qy 2761 GAGGCTTCGCTCATGCGCTGGGCTCTCATCGGTACACCTGCTCTCGCGGCATC 2820
Db 2761 GAGGCTTCGCTCATGCGCTGGGCTCTCATCGGTACACCTGCTCTCGCGGCATC 2820
Qy 2821 TGTCTTCTTTCGCTTCAAGTCCCGTAAGTCCCGGAGAACTTCAACGAGGCTAAGTTC 2880
Db 2821 TGTCTTCTTTCGCTTCAAGTCCCGTAAGTCCCGGAGAACTTCAACGAGGCTAAGTTC 2880
Qy 2881 ATCACTTCAGCATGTTGATCTTCTTCTCATGCTGATCTCTTCTATCCCGCTATGTC 2940
Db 2881 ATCACTTCAGCATGTTGATCTTCTTCTCATGCTGATCTCTTCTATCCCGCTATGTC 2940
Qy 2941 AGCACCTACGGCAAGTTGTGTCGCGCTGGAGGTGATGGCCATCTGCGCTCCAGTTC 3000
Db 2941 AGCACCTACGGCAAGTTGTGTCGCGCTGGAGGTGATGGCCATCTGCGCTCCAGTTC 3000
Qy 3001 GGCTCTGGCTGCTATTTACTTCAACAAAGTGTATCATCATCTGTTCAAGCGCTGCCGT 3060
Db 3001 GGCTCTGGCTGCTATTTACTTCAACAAAGTGTATCATCATCTGTTCAAGCGCTGCCGT 3060
Qy 3061 AACACATCGAGAGGTGCGCTGACAGCGGCGGCCACGCTTCAAGTGGCGGCCGG 3120
Db 3061 AACACATCGAGAGGTGCGCTGACAGCGGCGGCCACGCTTCAAGTGGCGGCCGG 3120
Qy 3121 GCCACCTTCGCGGCGAGCGCGCTCTCGAAGCGCTCCAGAGCTTCCAGAGCTTCCAGC 3180
Db 3121 GCCACCTTCGCGGCGAGCGCGCTCTCGAAGCGCTCCAGAGCTTCCAGAGCTTCCAGC 3180
Qy 3181 ATCTCTCGCCCTCTGCTTCACTTCGCGCGCGGCTTCAACATGAGATGAGAGCTGC 3240
Db 3181 ATCTCTCGCCCTCTGCTTCACTTCGCGCGCGGCTTCAACATGAGATGAGAGCTGC 3240
Qy 3241 AGCACGAGAGGTGAGCTTCGCGAGCGGCAAGTCACTCTGCTGCTGAGTTCGAGAG 3300
Db 3241 AGCACGAGAGGTGAGCTTCGCGAGCGGCAAGTCACTCTGCTGCTGAGTTCGAGAG 3300
Qy 3301 ACAGGCGGATACGCCACCTTCAGCCCGCAGCGCGCGGAGAACTTCGCGGATGGCGG 3360
Db 3301 ACAGGCGGATACGCCACCTTCAGCCCGCAGCGCGCGGAGAACTTCGCGGATGGCGG 3360
Qy 3361 AGCGGCGAGAGCTTCGCTTACAGACAGGAGCGGCGGCTCAGAAATGCGAGGCC 3420
Db 3361 AGCGGCGAGAGCTTCGCTTACAGACAGGAGCGGCGGCTCAGAAATGCGAGGCC 3420
Qy 3421 CAGCCGCGCAACGATGCCGATACAGGCGGCGCGGAGGCACTTAGAGTGGCGG 3480
Db 3421 CAGCCGCGCAACGATGCCGATACAGGCGGCGCGGAGGCACTTAGAGTGGCGG 3480
Qy 3481 GGCGGAGCAAGGAGCGGCGGCAACTATGAGGAGAACTTATCCAACTCTCTCCATCAAC 3540
Db 3481 GGCGGAGCAAGGAGCGGCGGCAACTATGAGGAGAACTTATCCAACTCTCTCCATCAAC 3540
Qy 3541 CCCAAGAACTCTCCAGCGGAGCGGCTGACATCACTCACTTACCGGTGGC 3600
Db 3541 CCCAAGAACTCTCCAGCGGAGCGGCTGACATCACTCACTTACCGGTGGC 3600
Qy 3601 TGCCCAACTCTCTCCCGGCTTTCGCTTTTGTGTAAGATTTGAGATCTGCACTTGCAGT 3660
Db 3601 TGCCCAACTCTCTCCCGGCTTTCGCTTTTGTGTAAGATTTGAGATCTGCACTTGCAGT 3660


```

Db 3421 CAGCCGCGCAACGATGCGCGGATACAAAGCGCGCGCGCAAGGCGCACCTAGATGCGCG 3480
Qy 3481 GCGGCGAGCAAGGCGCGCGCAACTATGGAGGAACTTAATCCAACTCTCTCCATCAAC 3540
Db 3481 GCGGCGAGCAAGGCGCGCGCAACTATGGAGGAACTTAATCCAACTCTCTCCATCAAC 3540
Qy 3541 CCCAAGAACATCTCCACGCGAGCGCGCGCGCAACTATGGAGGAACTTAATCCAACTCTCTCCATCAAC 3600
Db 3541 CCCAAGAACATCTCCACGCGAGCGCGCGCGCAACTATGGAGGAACTTAATCCAACTCTCTCCATCAAC 3600
Qy 3601 TCGCCMACTCTCCCTCTCCGCGACTTTGGGTTTGGTGAAGATTCGAGCATCTGCACT 3660
Db 3601 TCGCCMACTCTCCCTCTCCGCGACTTTGGGTTTGGTGAAGATTCGAGCATCTGCACT 3660
Qy 3661 TCGTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCACAA 3720
Db 3661 TCGTTTATCCCTGATTTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCACAA 3720
Qy 3721 ATAAGAGTTGCAATTAAGTTGAGGAGAGTTGTCTCAAGTATCTGAACTATCTGAAGT 3780
Db 3721 ATAAGAGTTGCAATTAAGTTGAGGAGAGTTGTCTCAAGTATCTGAACTATCTGAAGT 3780
Qy 3781 ATCTGAAGTACTTTATCTCTGCAATTTGTTATTAACAACATTTGAAGTATTTTGTAGTACA 3840
Db 3781 ATCTGAAGTACTTTATCTCTGCAATTTGTTATTAACAACATTTGAAGTATTTTGTAGTACA 3840
Qy 3841 TTATGTTCTTAACATTTCTCAAGTATTTTGTATTAACAACATTTGAAGTATTTTGTAGTACA 3900
Db 3841 TTATGTTCTTAACATTTCTCAAGTATTTTGTATTAACAACATTTGAAGTATTTTGTAGTACA 3900
Qy 3901 GACTGAGTTGCCACTGTGATGACAACTGTTTATTAACAACATTTGAAGTATTTTGTAGTACA 3960
Db 3901 GACTGAGTTGCCACTGTGATGACAACTGTTTATTAACAACATTTGAAGTATTTTGTAGTACA 3960
Qy 3961 TTGCAACAGGAAATAATGACTGTAAACAAATAATTTGTTATTAACAACATTTGAAGTATTTTGTAGTACA 4020
Db 3961 TTGCAACAGGAAATAATGACTGTAAACAAATAATTTGTTATTAACAACATTTGAAGTATTTTGTAGTACA 4020
Qy 4021 TGTATTCAGATGTGAAATTTGGTAAATTTGTTATTAACAACATTTGAAGTATTTTGTAGTACA 4080
Db 4021 TGTATTCAGATGTGAAATTTGGTAAATTTGTTATTAACAACATTTGAAGTATTTTGTAGTACA 4080
Qy 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4134
Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4134

```

```

RESULT 8
US-10-268-051-7
; Sequence 7, Application US/10268051
; Patent No. 6748900
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jury, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A
; APPLICANT: Betka, Marlies
; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213.2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-268-051-7

```

```

Query Match
Best Local Similarity 100.0%; Score 4134; DB 4; Length 4134;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTCGGTGTCTGTCGGTTCAGTCCAGTCTCTCCAGTGCAGAAATGAGAAATGGTGGC 60
Db 1 AATTCGGTGTCTGTCGGTTCAGTCCAGTCTCTCCAGTGCAGAAATGAGAAATGGTGGC 60
Qy 61 GCCATTACAGGAATATGCACTACATCTGTGTAAATGAAATATTTGTCAAGT 120
Db 61 GCCATTACAGGAATATGCACTACATCTGTGTAAATGAAATATTTGTCAAGT 120
Qy 121 TATTAATAATTTCTGCAAGGATGGTTCACAGGAAATCAATTCCTCAGTTCCTCAT 180
Db 121 TATTAATAATTTCTGCAAGGATGGTTCACAGGAAATCAATTCCTCAGTTCCTCAT 180
Qy 181 GTCAATTTGATGAATAACTGACCAAGGATGTAAACAAATGAAACAAAGCTGAGGAC 240
Db 181 GTCAATTTGATGAATAACTGACCAAGGATGTAAACAAATGAAACAAAGCTGAGGAC 240
Qy 241 GTTCACCCCTTTCTGAGGATACGATCAACCCCTGAGGAGATGGAAGACTTGAAGG 300
Db 241 GTTCACCCCTTTCTGAGGATACGATCAACCCCTGAGGAGATGGAAGACTTGAAGG 300
Qy 301 ATGGGAGTTCATCTCCAGGATTTCTGCTGTAAGCGATCCCTCACCATTACAAAGTAA 360
Db 301 ATGGGAGTTCATCTCCAGGATTTCTGCTGTAAGCGATCCCTCACCATTACAAAGTAA 360
Qy 361 GCAGAAATCTCTCAGGATCTCTGTAAGCGGCTGCGTGTAGTGGCTTTGTCAGGAA 420
Db 361 GCAGAAATCTCTCAGGATCTCTGTAAGCGGCTGCGTGTAGTGGCTTTGTCAGGAA 420
Qy 421 CAGAGACAGGCTGCAATTTGCTGCTGTAAGCGGCTGCGTGTAGTGGCTTTGTCAGG 480
Db 421 CAGAGACAGGCTGCAATTTGCTGCTGTAAGCGGCTGCGTGTAGTGGCTTTGTCAGG 480
Qy 481 CTCTCAGTTCGATCAATTTGCTGCTGTAAGCGGCTGCGTGTAGTGGCTTTGTCAGG 540
Db 481 CTCTCAGTTCGATCAATTTGCTGCTGTAAGCGGCTGCGTGTAGTGGCTTTGTCAGG 540
Qy 541 GACATCATCTGCGAGGCTCTCTCCAAATACATTTTGGAGTAGCGCCCAAGGATCAGG 600
Db 541 GACATCATCTGCGAGGCTCTCTCCAAATACATTTTGGAGTAGCGCCCAAGGATCAGG 600
Qy 601 TTAATAATCGAGCCGAGGCGCAAAATGATTCGGTACAAATTTTCGAGGCTTTCCGAT 660
Db 601 TTAATAATCGAGCCGAGGCGCAAAATGATTCGGTACAAATTTTCGAGGCTTTCCGAT 660
Qy 661 CTCAGGCGATGATTTTCGAAATTTGAAGATTTAAACAGATGATGATTTCTTCCGCAAT 720
Db 661 CTCAGGCGATGATTTTCGAAATTTGAAGATTTAAACAGATGATGATTTCTTCCGCAAT 720
Qy 721 ATCACTCGGATATGCGATATTTGACAGTGTAAACCGTGTCCAGGCGCTAGAGGCA 780
Db 721 ATCACTCGGATATGCGATATTTGACAGTGTAAACCGTGTCCAGGCGCTAGAGGCA 780
Qy 781 ACACTCAGCTTTTGTGGCCCGAGCAAAATCGACTCGCTGAACTTAGATGATTTCTGTA 840
Db 781 ACACTCAGCTTTTGTGGCCCGAGCAAAATCGACTCGCTGAACTTAGATGATTTCTGTA 840
Qy 841 TGCTCTGACAAATTCCTCAATATGAGTGTTCGGGCGCAACCGGCTCAGGAATCTCC 900
Db 841 TGCTCTGACAAATTCCTCAATATGAGTGTTCGGGCGCAACCGGCTCAGGAATCTCC 900
Qy 901 ACCTGCTGCGCAATCTTATTTGGATTTTATTAATTCACAGTGTAGTATGCTCTCG 960
Db 901 ACCTGCTGCGCAATCTTATTTGGATTTTATTAATTCACAGTGTAGTATGCTCTCG 960
Qy 961 AGCAGGCTGCTCAGCAACAAAGATAGTACAAGGCTTCTCAGGAGGACCTCCCAATG 1020
Db 961 AGCAGGCTGCTCAGCAACAAAGATAGTACAAGGCTTCTCAGGAGGACCTCCCAATG 1020

```

Qy	1021	GAGCAACAGGCCACGGCCGATGCGAGATCATCGAGCACTTCCAGTGAACTGGGTGGGA	1080	Db	2101	GTCCGGGACACAGGAAGGGGATCATCGAGGGGAGCCACCTGCTGCTTTGAATGCATG	2160
Db	1021	GAGCAACAGGCCACGGCCGATGCGAGATCATCGAGCACTTCCAGTGAACTGGGTGGGA	1080	Qy	2161	GCATGTGCAGAGGAGAGTTCACTGATGAAAACGATGCAAGTGGTGTACAAAGTGGCG	2220
Qy	1081	ACCCTGGCAGCCGACGATGATATGGCCGCCAGGCAATGCAAGTTCCGGGAGAGGCC	1140	Db	2161	GCATGTGCAGAGGAGAGTTCACTGATGAAAACGATGCAAGTGGTGTACAAAGTGGCG	2220
Db	1081	ACCCTGGCAGCCGACGATGATATGGCCGCCAGGCAATGCAAGTTCCGGGAGAGGCC	1140	Qy	2221	AATGATTTCTGGTTCGAATGAGAACACACGCTCGTGCATGCCAAGAGAGATCGAGTACCTG	2280
Qy	1141	GTTAAGAGGAGCATCTGTATTGACATTCACTGATGAGATGATCTCTCAGTACTACACCCAGAAG	1200	Db	2221	AATGATTTCTGGTTCGAATGAGAACACACGCTCGTGCATGCCAAGAGAGATCGAGTACCTG	2280
Db	1141	GTTAAGAGGAGCATCTGTATTGACATTCACTGATGAGATGATCTCTCAGTACTACACCCAGAAG	1200	Qy	2281	TCGTGAGCGAGAGCCCTTCGGGATCGCTCTGACCATCTTGCCCGTACTGGGCATCTTGATC	2340
Qy	1201	CAGTTGGAGTTTCATGCCGACGTCATCCAGAACTCCTCGGCCAAGGTTCATCGTGGTCTTC	1260	Db	2281	TCGTGAGCGAGAGCCCTTCGGGATCGCTCTGACCATCTTGCCCGTACTGGGCATCTTGATC	2340
Db	1201	CAGTTGGAGTTTCATGCCGACGTCATCCAGAACTCCTCGGCCAAGGTTCATCGTGGTCTTC	1260	Qy	2341	ACCTTCCTTCGTGTGGGGTCTTTCACTCAAGTTCCAGAACTCCCATCGTGAAGGCCACC	2400
Qy	1261	TCCAAATGCCCGGACCTCGAGCGGCTCATCCAGGAGATAGTTCGAGAAACATCACCGAT	1320	Db	2341	ACCTTCCTTCGTGTGGGGTCTTTCACTCAAGTTCCAGAACTCCCATCGTGAAGGCCACC	2400
Db	1261	TCCAAATGCCCGGACCTCGAGCGGCTCATCCAGGAGATAGTTCGAGAAACATCACCGAT	1320	Qy	2401	AACGGGAGTTGTCCTACCTGCTGCTTCTCCCTCATCTGCTGCTTCTCCAGCTGGCTC	2460
Qy	1321	CGGATCTGGCTGGCCAGGAGAGCTTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380	Db	2401	AACGGGAGTTGTCCTACCTGCTGCTTCTCCCTCATCTGCTGCTTCTCCAGCTGGCTC	2460
Db	1321	CGGATCTGGCTGGCCAGGAGAGCTTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380	Qy	2461	ATCTTCATCGGCGAGCCAGGACTGGACCTGTCGCTCGCCAAACCGGCTTTTGGCATC	2520
Qy	1381	TTCCACGTGGTGGCGGACACATCGGCTTCGCTCTCAGGGGGGGCGGTATCCAGGGTTC	1440	Db	2461	ATCTTCATCGGCGAGCCAGGACTGGACCTGTCGCTCGCCAAACCGGCTTTTGGCATC	2520
Db	1381	TTCCACGTGGTGGCGGACACATCGGCTTCGCTCTCAGGGGGGGCGGTATCCAGGGTTC	1440	Qy	2521	AGTTTCCTCTGTGCATCTCTCTGCATCTCTGCATCTCTGCATCTCTGCATCTCTGCATCT	2580
Qy	1441	AACAAAGTTCTTGAAGAGGTCCACCCAGCAGGTCTCTCGCAATGGGTTTGTCAAGGAG	1500	Db	2521	AGTTTCCTCTGTGCATCTCTCTGCATCTCTGCATCTCTGCATCTCTGCATCTCTGCATCT	2580
Db	1441	AACAAAGTTCTTGAAGAGGTCCACCCAGCAGGTCTCTCGCAATGGGTTTGTCAAGGAG	1500	Qy	2581	GAGGCCAAGATCCCCACAGCCTCCACCGAAGTGGGTGGGCTCAACCTGCGATTCCTC	2640
Qy	1501	TTCTCGGAGGAGACCTTCACTGTACTTACCGAGAGACCTTGACCGACGTGAAGAAT	1560	Db	2581	GAGGCCAAGATCCCCACAGCCTCCACCGAAGTGGGTGGGCTCAACCTGCGATTCCTC	2640
Db	1501	TTCTCGGAGGAGACCTTCACTGTACTTACCGAGAGACCTTGACCGACGTGAAGAAT	1560	Qy	2641	CTGTGCTTCTCTGCACTCTGCTGGTGAATCGTCACTGCACTCATCTGGCTCTACACCGCG	2700
Qy	1561	TCCAAAGTCCCTGCAAGGAGTCCACCCAGCAGGTCTCTCGCAATGGGTTTGTCAAGGAG	1620	Db	2641	CTGTGCTTCTCTGCACTCTGCTGGTGAATCGTCACTGCACTCATCTGGCTCTACACCGCG	2700
Db	1561	TCCAAAGTCCCTGCAAGGAGTCCACCCAGCAGGTCTCTCGCAATGGGTTTGTCAAGGAG	1620	Qy	2701	CCTTCCTCTCAGCTACAGAAACCATAGCTGGAGAGAGGTCACTTTCATCACTCGGAC	2760
Qy	1621	AGACGACAGCCCTACGCCACCCCTGCACTGGGGAGGAGAAACATCACAGAGGTGGAGACC	1680	Db	2701	CCTTCCTCTCAGCTACAGAAACCATAGCTGGAGAGAGGTCACTTTCATCACTCGGAC	2760
Db	1621	AGACGACAGCCCTACGCCACCCCTGCACTGGGGAGGAGAAACATCACAGAGGTGGAGACC	1680	Qy	2761	GAGGGCTCGCTACGGGCTGGGCTTCTCATCGGTACACCTGCTTCTCGGCGCCATC	2820
Qy	1681	CCTTACCTGGATATACACCTGAGGATCTCTCAATGATATAGTGGCGGTCTACTCC	1740	Db	2761	GAGGGCTCGCTACGGGCTGGGCTTCTCATCGGTACACCTGCTTCTCGGCGCCATC	2820
Db	1681	CCTTACCTGGATATACACCTGAGGATCTCTCAATGATATAGTGGCGGTCTACTCC	1740	Qy	2821	TGCTTCTTCTTCGCTTCAAGTCCCGTAAGCTGCGGAGAACTTCAAACGAGGCTAAGTTC	2880
Qy	1741	ATTGCTCAGCCCTGCAAGACATCCACTCTTCAAAACCGGACCGGCACTTTTGCAAAC	1800	Db	2821	TGCTTCTTCTTCGCTTCAAGTCCCGTAAGCTGCGGAGAACTTCAAACGAGGCTAAGTTC	2880
Db	1741	ATTGCTCAGCCCTGCAAGACATCCACTCTTCAAAACCGGACCGGCACTTTTGCAAAC	1800	Qy	2881	ATCACTTCAGATGTTGATCTTCTTCATCGTCTGATCTCTTCTCATCCCGGCTATGTC	2940
Qy	1801	GGATCTTGTGCAGATATTAATAAAGTTGAGGCTCGCAGGTCTTCAACCATCTGCTGCAT	1860	Db	2881	ATCACTTCAGATGTTGATCTTCTTCATCGTCTGATCTCTTCTCATCCCGGCTATGTC	2940
Db	1801	GGATCTTGTGCAGATATTAATAAAGTTGAGGCTCGCAGGTCTTCAACCATCTGCTGCAT	1860	Qy	2941	AGCACTTACGGCAAGTTTGTTCGGCGTGAGGTGATTCCTCATCTGGGCTCCAGCTTC	3000
Qy	1861	CTGAGTTTACCAACAGCATGGTGAGCGGTTGATTTGAGATCAAGGTGACCTCAAG	1920	Db	2941	AGCACTTACGGCAAGTTTGTTCGGCGTGAGGTGATTCCTCATCTGGGCTCCAGCTTC	3000
Db	1861	CTGAGTTTACCAACAGCATGGTGAGCGGTTGATTTGAGATCAAGGTGACCTCAAG	1920	Qy	3001	GGGCTGTGGGCTGATTTACTTCAACAAAGTGTTCATCATCTGTTTCAAGCGCTGCGGT	3060
Qy	1921	GGGAACTACACCATATCAACTGGAGCTCTCGCAGAGGATGAATCGGTGTGTTCCAT	1980	Db	3001	GGGCTGTGGGCTGATTTACTTCAACAAAGTGTTCATCATCTGTTTCAAGCGCTGCGGT	3060
Db	1921	GGGAACTACACCATATCAACTGGAGCTCTCGCAGAGGATGAATCGGTGTGTTCCAT	1980	Qy	3061	AACACCATCGAGGAGTGGCTCGACACGGCGCCACGCCCTTCAAGTGGCGGCCGG	3120
Qy	1981	GAGGTGGGCAACTACAAACCCCTACGCTAAGCCAGTACCGGACTCAACATCAACAAAAG	2040	Db	3061	AACACCATCGAGGAGTGGCTCGACACGGCGCCACGCCCTTCAAGTGGCGGCCGG	3120
Db	1981	GAGGTGGGCAACTACAAACCCCTACGCTAAGCCAGTACCGGACTCAACATCAACAAAAG	2040	Qy	3121	GCACCCCTCGGGGAGCGGCTCTCGCAAGCGTTCAGACAGCTTGTGCGCTCCACC	3180
Qy	2041	AAAACTCTCGAGTGGCTTCTCCAAAGTGGTTCTTTCTCCAACTGAGTGGAGCTGT	2100	Db	3121	GCACCCCTCGGGGAGCGGCTCTCGCAAGCGTTCAGACAGCTTGTGCGCTCCACC	3180
Db	2041	AAAACTCTCGAGTGGCTTCTCCAAAGTGGTTCTTTCTCCAACTGAGTGGAGCTGT	2100	Qy	3181	ATCTCTCGCGGCTCTGCTCCACTGCGGCGCGGCTCACCATGAGATGCGAGCTGC	3240
Qy	2101	GTCCGGGACACAGGAAGGGGATCATCGAGGGGAGCCACCTGCTGCTTTGAATGCATG	2160				

```

Db 3181 ATCTCTCGCGCCCTCGTCCACCTGCGGGCGGGCCCTCACCATGAGATGACGCGTGC 3240
QY 3241 AGACGCGAGAGTTCAGCTTCGGGAGCGCACCGTCAACCTGTCGCTGAGCTTCGAGGAG 3300
Db 3241 AGCAGCGAGAGTTCAGCTTCGGGAGCGCACCGTCAACCTGTCGCTGAGCTTCGAGGAG 3300
QY 3301 ACAGGCGGATACGCGCACCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3360
Db 3301 ACAGGCGGATACGCGCACCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3360
QY 3361 AGCGCGAGCGCTGCGCATCTAGACACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3420
Db 3361 AGCGCGAGCGCTGCGCATCTAGACACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3420
QY 3421 CAGCGCGCAAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3480
Db 3421 CAGCGCGCAAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3480
QY 3481 GCGCGCAGCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3540
Db 3481 GCGCGCAGCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3540
QY 3541 CCGAAGAACTCTCCAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3600
Db 3541 CCGAAGAACTCTCCAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3600
QY 3601 TGCGCAACTCTCCCGCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3660
Db 3601 TGCGCAACTCTCCCGCTCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3660
QY 3661 TCGTTTATCCCTGATTTCTGACCTGGGATATTTACTAGTGTGCGATGCAATCATCAAC 3720
Db 3661 TCGTTTATCCCTGATTTCTGACCTGGGATATTTACTAGTGTGCGATGCAATCATCAAC 3720
QY 3721 ATATGAGTTCGCAATAGGTGAGCGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3780
Db 3721 ATATGAGTTCGCAATAGGTGAGCGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3780
QY 3781 ATCTGAACACTTTTATCTCTGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3840
Db 3781 ATCTGAACACTTTTATCTCTGCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3840
QY 3841 TTATGTTCTAACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3900
Db 3841 TTATGTTCTAACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3900
QY 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATGCAATTTATGCAATTTATGCA 3960
Db 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATGCAATTTATGCAATTTATGCA 3960
QY 3961 TTGCAACAGGATATTAATGACTGTACAAAAAATTTGTTGTTGTTGTTGTTGTTGTTG 4020
Db 3961 TTGCAACAGGATATTAATGACTGTACAAAAAATTTGTTGTTGTTGTTGTTGTTGTTG 4020
QY 4021 TGTAAATCAGATGTGTAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4080
Db 4021 TGTAAATCAGATGTGTAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4080
QY 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCGCG 4134
Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCGCGCG 4134

```

RESULT 9

```

US-08-485-588-3
; Sequence 3, Application US/08485588
; Patent No. 5688938
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE

```

```

; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; SUITE: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,588
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/355,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3809 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 373..3606
; OTHER INFORMATION:
; US-08-485-588-3

```

```

Query Match 42.2% Score 1745.2; DB 1; Length 3809;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;

QY 501 CTCAGGGTATGGTCCAAACCAAGAGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560
Db 423 CTCGCTACGGGCGCAGACCCAGCGAGGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 482
QY 561 CTTCCCAATACACTTTGGAGTAGCCCGAGGATCAGGACTTAAATCGAGACCGGAGGC 620
Db 483 CTTTCCTATTCAATTTGGAGTAGCAGTAAAGATCAAGATCTCAATCAAGCCGAGGC 542

```

QY 621 GACAAATGATTCGGTACAAATTTTCGAGGTTCCGATGGTCCAGGCGATGATATTCGC 680
Db 543 TGTGGAATGATCAGGTATATTTCCGCTGGGTTTCGCTGGTTACAGGCTATGATATTCG 602
QY 681 AATTGAAGAGATTAAACACAGTATGACATTTCTGCGCAATATACACCTGGGATATCGCAT 740
Db 603 CATAGAGAGATAAACACAGCCGACCCGCTTTCTCCCAACTTGACGCTGGGATACAGGAT 662
QY 741 ATTTGACAGTGTAAACACCGTGTCAAGCGCTAGAGCAACACTCAGCTTTGTGGCCCA 800
Db 663 AATTGACACTTGCACACCGTTCTAAGCCTTGAAGCCACCTGAGTTTGTGCTCA 722
QY 801 GAACAAATTCGACTCGCTGAATAGATGAGTTCTGTAACCTGCTGACCATATCCCATC 860
Db 723 AAACAAATTTGATTTCTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACATTCCTC 782
QY 861 CACATACAGTGTGCGGCAACCGGTGAGGATCTCCAGGCTGCGGCTGCGCAATCTATT 920
Db 783 TACGATTTGCTGGTGGGAGCAACTGGCTCAGGCTCTCCAGGCGAGTGGCAATCTGCT 842
QY 921 GGGATATTTTACATTCACAGGTGAGTATGCTCTCCGAGGAGGTGCTCAGCAACAA 980
Db 843 GGGGCTCTTACATTTCCAGGTGAGTTATGCTCTCTCCAGGACTCTCAGCAACAA 902
QY 981 GAATGAGTACAGGCTTCTGAGGACCATCCCAATGATGAGCAACAGGCCACGGCCAT 1040
Db 903 GAATCAATTCAGTCTTCTCTCCGAACCATCCCAATGATGAGCAACAGGCCACTGCCAT 962
QY 1041 GCGCAGATCATCGAGCACTTCCAGTGAACCTGGGTGGGAACCTGGCAGCGCAGCATGA 1100
Db 963 GGCAGACATCATCGAGTATTTCCGCTGGAACTGGTGGCAATTTGCGCTGATGAGA 1022
QY 1101 CTATGGCGCCAGGATGACAAAGTTCGGGAGGAGGCGGTTAAGAGGACATCTGAT 1160
Db 1023 CTATGGCGCGCGGATTTGAAATTCGAGAGGAAGTCTGAGGAAGGATATCTGAT 1082
QY 1161 TGACTTCAGTGAATCTCTCAGTACTACACCAAGAGAGTGGAGTTTCATCGCGGA 1220
Db 1083 CGACTTCAGTGAATCTCTCCAGTACTCTGATGAGGAAGATCCAGCATGTGTAGA 1142
QY 1221 CGTATCCAGAACTCTCGGCAAGGTATCTGTGTTCTTCCAAATGCCCGGACCTTGA 1280
Db 1143 GGTGATTCAAATTCACGGCCAAAGTCACTGTGTTTCTCCAGTGGCCAGATCTTGA 1202
QY 1281 GCGCTCATCAGGAGATGATTCGAGAAACATACCCGATCGGATCTGGCTGGCCAGGA 1340
Db 1203 GCGCTCATCAGGAGATGATTCGCGCGCAATATCACGGGCAAGATCTGGCTGGCCAGGA 1262
QY 1341 GCGTTGGGCGAGTCTTCTGCTCATTCGCAAGCCAGAGTACTTCCACGTGGTTCGGCGGAC 1400
Db 1263 GCGCTGGGCGAGTCTCTCTGATGCGCATGCTCAGTACTTCCAGTGGTGGCGGAC 1322
QY 1401 CATCGGCTTCTCAGGCGGGGCTATCCAGGGTTCAACAAAGTTCTCTGAAGAGGT 1460
Db 1323 CATTCGATTCGCTGAAGGCTGGGAGATCCAGGCTTCCGGGAATTCCTGAAGAGGT 1382
QY 1461 CCACCCGAGAGTCTCGCAAAATGGTTCTCAAGGAGTTCTGGGAGGAGACCTTCAA 1520
Db 1383 CCATCCGAGAGTCTGTCCCAAAATGGTTTCCCAAGGAGTTTGGGAAGAAACATTTAA 1442
QY 1521 CTGCTACTTCACCGAAGACCTTGACGAGTGAAGATTCGAAGGTGCCCTCCGACGG 1580
Db 1443 CTGCGACCTTCAAGA-----AGGTGCAAAAGGACCTTTTACCTGTGGACACCTTTCTG 1494
QY 1581 ACGGCGGCTCAAGGGAGGCTCCAGCGGGGAACTCCAGCGGAGAGCCCTACGCA 1640
Db 1495 AGAGG----TCACGAAGAAGTGGGACAGGTTTACCAACAGCTCGACAGCCCTCCGACC 1550
QY 1641 CCCCTGACTGGGAGGAGAAACATCACAGCGTGGAGACCCCTACCTGGATTATACACA 1700
Db 1551 CCTCTGTACAGGAGTGAACATCAGCAGTGTGCGAGACCCCTTACATAGATTACGCA 1610

QY 1701 CTTGAGATCTCTCAAAATGTATATCTGGCGGTCTACTCAATGTCTCAGCCCTGCAAGA 1760
Db 1611 TTTACGGATATCTCAAAATGTGTACTTAGCAGTCTACTCAATGTCCACCGCTTGAAGA 1670
QY 1761 CATCCACTCTTGCACAAACCCGCGACGGCATCTTTGCAAAACGATCTTGTGCAGATTTAA 1820
Db 1671 TATATATCTCTTACTTGGGAGAGGCTCTTCAACATGGCTCTGTGCAGACATCAA 1730
QY 1821 AAAAGTTGAGGCTGCGCAGGTCTCAACCATCTGCTGCATCTGAAGTTTACCAACAGCAT 1880
Db 1731 GAAAGTTGAGGCTGCGCAGGTCTGAAGCACCTTACGCGCATCTAAACTTTACAAACAATAT 1790
QY 1881 GGTGAGCAGTTGACTTTGACGATCAAGGTGACCTCAAGGGGAACTACACCATTTATCAA 1940
Db 1791 GGGGAGCAGGTGACCTTTTATGAGTGTGGTGAACCTTGGTGGGAACTATTTCCATCATCAA 1950
QY 1941 CTGCGACTCTCCGCGAGAGATGAATCGGTGTTTGTTCATGAGTGGGCAACTTACAACGC 2000
Db 1851 CTGCGACTCTCCGCGAGAGATGGCTCCATCGTGTTTAAGGAAGTCCGGTATTACAACGT 1910
QY 2001 CTAGCTAAGCCAGTGAACGACTCAACATCAACGAAGAAATAATCTCTGAGTGGCTT 2060
Db 1911 CTATGCCAAGAGGAGAAAGACTTCTCATCAACGAGGAGAAATCTCTGAGTGGGTT 1970
QY 2061 CTCAAAAGTGTCTCTTCTCCAACTGCACTCGAGACTGTGTGCCGGGACACAGGAAGG 2120
Db 1971 CTCCAGGAGTGGCTTCTTCCAACTGCACTCGAGCGAGTCTCTGCGAGGACACAGGAAG 2030
QY 2121 GATCATCAGGGGAGCCCACTGCTGTTTGAATGATGAGTGTGAGTGTGAGTGTCTGATGGGAGTA 2180
Db 2031 GATCATGAGGGGAGCCCACTGCTGTTTGAATGATGAGTGTGAGTGTGAGTGTCTGATGGGAGTA 2090
QY 2181 CAGTGATGAACGATCAAGTGGCTGACAAAGTCCCGAAATGATTTCTGTCGAATGA 2240
Db 2091 TAGTGATGAGACAGTGCAGTGCCTGTAAACAGTCCCGAGATGACTTCTGTTCCATGA 2150
QY 2241 GAACCAACACTCTGTCATCGCCAAAGGAGATCGAGTACTGTCTGTGAGCGAGCCCTTCGG 2300
Db 2151 GAACCAACACTCTGTCATTCGCAAGGAGATCGAGTGTCTGTCTGAGCGAGCCCTTCGG 2210
QY 2301 GATGCTCTGACCATCTTCCGCGTACTGGGCATCTGATCACCTCTCTGCTGCTGGGGT 2360
Db 2211 GATGCACTCACCTCTTCTGCGCTGCTGGGCAATTTTCTGACAGCCCTTGTGCTGGGTGT 2270
QY 2361 CTTTCATCAAGTTGAGGAACACTCCCATGTAAGGCGCACCAACCGGAGTTGTCTTACCT 2420
Db 2271 GTTTATCAAGTTCCGCAACACACCCATTGTCAAGGCCACCAACCGAGAGCTCTCTTACCT 2330
QY 2421 GCTGCTCTTCTGCTCATCTGCTGCTTCTCCAGTCTGCTCATCTTATCGGCGAGCCAG 2480
Db 2331 CCTGCTCTTCTGCTGCTGCTTCTCCAGTCTGCTTCTTCTTATCGGGGAGGCCCA 2390
QY 2481 GGACTGACCTGTGCGCTCGCCAAACCGGCTTTTGGCATCAGCTTCTGCTGTCATCTC 2540
Db 2391 GGACTGACCTGTGCGCTCGCCAGCGGCTTTTGGCATCAGCTTCTGCTGTCATCTC 2450
QY 2541 CTGCACTCTGTTGAAGACCAACCGGCTGCTGTTTTCGAGGCCAAGATCCCAACAG 2600
Db 2451 ATGCACTCTGTTGAAGACCAACCGGCTGCTTCTGTTTGTGAGGCCAAGATCCCAACAG 2510
QY 2601 CTTCCACCGAAGTGGTGGGCTCAACCTGAGTCTTCTGCTGCTTCTGCTGCTGCT 2660
Db 2511 CTTCCACCGAAGTGGTGGGCTCAACCTGAGTCTTCTGCTGCTTCTGCTGCTGCT 2570
QY 2661 GGTGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2720
Db 2571 CATGCAATTTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2630
QY 2721 CCATGCTGAGGAGCAAGGCTCATCTTTCATCACTGCGAGAGGCTCGCTCATGGGCT 2780
Db 2631 CCAGGAGTGGAGGATGAGATCATCTTTCATCAGTGGCAGAGGCTCCCTCATGGGCT 2690
QY 2781 GGGCTTCTCATCGGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTCAA 2840

QY	981	GAATGAGTACAGGCTTCTCTGAGACCATCCCAATGATGAGCAACAGGCCACCGCCAT	1040
Db	903	GAATCAATCAAGTCTTTCTCCGAACCATCCCAATGATGAGCAACAGGCCACCGCCAT	962
QY	1041	GGCCGAGATCATCGAGCACTTCCAGTGAACCTGGGTGGGAAACCTGGCAGCGCAGATGA	1100
Db	963	GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCACAAATTCAGCTGATGACGA	1022
QY	1101	CTATGGCCGCCAGSACATGACAACTTCGGGAGGAGGCCGTTAGAGGGACATCTGTAT	1160
Db	1023	CTATGGCGGGCGGGGATTTGAAATTCGGAGAGAAGCTGAGGAAAGGATATCTGCAT	1082
QY	1161	TGACATTCACTGAGATGATCTCTCACTACTACACCCAGAGAGAGTTGGAGTTTCATCGCCGA	1220
Db	1083	CGACTTCAGTGAACTCACTCCAGTACTCTGATGAGGAGAGATCCAGCATGTGTAGA	1142
QY	1221	CGTCATCCAGAACTCTCTGGCCAAAGGTGATCTGTGTCTTCTCAATGACCCGACCTGGA	1280
Db	1143	GGTGTATCAAAATTCGACGGCCAAAGTATCTGTGTCTTCTCCAGTGGCCAGATCTTGA	1202
QY	1281	GGCGTCTATCCAGGAGATGATTCGAGAGAAATACCCGATCGATCTGGCTGGCCAGGA	1340
Db	1203	GGCCCTCATCAAGAGATTTCCGGCGGAAATACAGGGCAAGATCTGGCTGGCCAGGA	1262
QY	1341	GGCTTGGGCCAGCTCTCTCGCTCATTTGCCAAGCCAGAGTACTTCCACGTGGTGGCGGAC	1400
Db	1263	GGCCTGGGCCAGCTCTCTCGCTCATTTGCCAAGCCAGTACTTCCACGTGGTGGCGGAC	1322
QY	1401	GATCGCTTCGCTCTCAGGGCGGGGGTATCCAGGGTTCACAGTTCCTTGAAGAGGT	1460
Db	1323	CATTGGATTCTGCTGAAGGCTGGGAGATCCAGGCTTCGGGAAATTCCTGAAGAAGGT	1382
QY	1461	CCACCCCGCAGAGTCTCTGGCAATGGGTTTCTCAAGGAGTTCTCGGAGGAGACCTTCAA	1520
Db	1383	CCATCCCGAGAGTCTGTCCCAATGGTTTTCGCAAGGAGTTTGGGAGAAACATTTAA	1442
QY	1521	CTGCTACTTACCGAGAGACCCCTGACGAGCTGAGAAATTCGAAGTGGCCCTCCGACGG	1580
Db	1443	CTGCCACCTTCCAAGA-----AGGTGCAAAAGGACCTTTACCTGTGGACACCTTTCTG	1494
QY	1581	ACCGCGGCTCAAGGGAGCGCTCAAGSGGGGAATCCAGCGGACAGCCCTACGCGCA	1640
Db	1495	AGAGG-----TCAGAGAAAGTGGCGACAGGTTTAGACACAGCTCGACAGCCTCCGACC	1550
QY	1641	CCCTCGACTGGGAGGAGAAATCACAGCGTGGAGACCCCTACCTGGATTTATACACA	1700
Db	1551	CCTCTGTACAGGGGATGAACATCAGCAGTGTGAGACCCCTTACATAGATTACACGCA	1610
QY	1701	CCTGAGGATCTCTACATGATATAGTGGCGGCTTACTCCATTGCTCAGCCCTGCAGA	1760
Db	1611	TTTACGGATATCTTAAATGTGTACTTAGCAGTCTACTCCATTGCCCCAGCCTTCAAGA	1670
QY	1761	CATCCACTCTTGCAAACCCGGCAGCGGATCTTTGCAAACGGATCTTTGTGAGATATTAA	1820
Db	1671	TATATATACCTGTTACCTGGGAGAGGGCTCTTACCAATGCTCTCTGTGAGACATCAA	1730
QY	1821	AAAAGTTAGGCTTGGCAGGCTCTCAACATCTGTGTGATCTGAAGTTTACCAAGCAT	1880
Db	1731	GAAAGTTGAGGGCTGGCAGGCTCTGAAGCAGCTACGGCATCTTAAACCTTTTACAAACAATAT	1790
QY	1881	GGGTGAGCAGGTTGACTTTTGCAGATCAAGTCACTCAAGGGAACTACACCATATCAA	1940
Db	1791	GGGGAGCAGGTTGACCTTTGATGAGTGTGGTGAACCTGTGGGGAATATTCCATCATCAA	1850
QY	1941	CTGGCAGCTCTCCGAGAGGATGAATCGGTGTTGTTCCATGAGGTGGGCAACTACAAAGC	2000
Db	1851	CTGGCACCTCTCCCCAGAGGATGGGTCCATCTGTGTTAAGGAAGTCGGGTATTACAAAGT	1910
QY	2001	CTACCTAGCCGAGTGCAGCTCAACATCAACGAAAGAAATCTCTGGAGTGGCTT	2060
Db	1911	CTATGCCAAGAGGGGAGAAAGACTCTTCAATCAACGAGGAGAAATCTCTGTGGAGTGGGT	1970
QY	2061	CTCCAAAGTGGTTCTTTCTCCAACTGCAGTCGAGACTGTGTGCCGGCCACAGGAGGG	2120
Db	1971	CTCCAGGAGGTGGCTTCTCCAACTGCAGCCGAGACTGCTCGCAGGACACAGGAAAG	2030
QY	2121	GATCATCGAGGGGAGGCCACCTGTGCTTTTGAATGCAATGGCATGTGCAGAGGAGAGTT	2180
Db	2031	GATCATTTAGGGGAGGCCACCTGTGCTTTTGAATGCAATGGAGTGTCTCTGATGGGAGTA	2090
QY	2181	CAGTGATGAAACGATGCAAGTGCGTGTACAAAGTGCCTGAAATGATTTCTGGTCTGAATGA	2240
Db	2091	TAGTGATGAGACAGATGCCAGTGCCTGTAAAGTGCCTGAGATGACTTCTGGTCCAAATGA	2150
QY	2241	GAACCAACACCTCTGTCATCGCCAAAGAGATFCGAGTACCTGTCTGTGAACGAGGCCCTTCGG	2300
Db	2151	GAACCAACACCTCTGTCATCGCCAAAGAGATFCGAGTACCTGTCTGTGAACGAGGCCCTTCGG	2210
QY	2301	GATCGCTCTGACCATCTTTCGCGTACTGGGCACTCTGATCACCTCTTCTGTCTGGGGT	2360
Db	2211	GATCGCACTCACCTCTTTCGCGTACTGGGCACTTTCCTGACAGCCTTCTGTCTGGGTGT	2270
QY	2361	CTTCATCAAGTTTCAGGAACACTCCCATCTGTGAAGGGCCACCAACCGGGAGTTGTCTTACCT	2420
Db	2271	GTTCATCAAGTTTCGGAACACACCCATTTGTAAGGCCACCAACCGAGAGCTCTCTTACCT	2330
QY	2421	GCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTGCTCATCTTCTATCGGCGAGGCCAG	2480
Db	2331	CCTCTCTTCTCCCTGCTGCTGCTTCTCCAGCTGCTTCTTCTTCTATCGGGAGGCCCA	2390
QY	2481	GGATGACCTGTGCGCTCGCCAAACCGGCTTTTGGCATCAGTTCGTCTCTGTGCATCTC	2540
Db	2391	GGATGACCTGTGCGCTCGCCAAACCGGCTTTTGGCATCAGTTCGTCTCTGTGCATCTC	2450
QY	2541	CTGCATCTCTGGTGAAGACCAACCGGGTGTGCTGCTTTCGAGGCCAAAGATCCCCACCAG	2600
Db	2451	ATGCATCTCTGGTGAAGACCAACCGGTGTCTCTCTGGTGTTCGAGGCCAAAGATCCCCACCAG	2510
QY	2601	CTTCCACCGCAAGTGGTGGGCTCACCTGCACTTCTCTCTGCTTCTCTCTGCTGCTCT	2660
Db	2511	CTTCCACCGCAAGTGGTGGGCTCACCTGCACTTCTCTCTGCTTCTCTCTGCTGCTCT	2570
QY	2661	GGTGCAATCTGTCACCTGCTATCTGCTCTACACCGCGCTCTCTCTCTCTCTCTCTCTCT	2720
Db	2571	CATGCAGATTGTCTCTGCTGCTGCTCTACACCGCGCTCTCTCTCTCTCTCTCTCTCTCT	2630
QY	2721	CCATGAGCTGGAGACAGAGTCACTTTCATCACCTGCGGAGAGGGCTCGTCTATGGGCT	2780
Db	2631	CCAGGAGCTGGAGATGAGATCATCTTCATCACCTGCGGAGGGCTCCCTCATGCGCCT	2690
QY	2781	GGGCTTCTCTCATCGGCTTACACCTGCTCTCGCGGCTCTCTCTCTCTCTCTCTCTCTCT	2840
Db	2691	GGGCTTCTCTCATCGGCTTACACCTGCTCTCGCGGCTCTCTCTCTCTCTCTCTCTCTCT	2750
QY	2841	GTCCCGTAACTGCCGAGAACTTCAACGAGGTAAAGTTTCATCACCTTCAGCATGTTGAT	2900
Db	2751	GTCCCGTAACTGCCGAGAACTTCAATGAAGCCAAAGTTTCATCACCTTCAGCATGTTGAT	2810
QY	2901	CTTCTTCATCTGCTGATCT	2960
Db	2811	CTTCTTCATCTGCTGATCT	2870
QY	2961	GTCCGGCTGGAGGTGATTTGCCATCTCTGCTCTCAGCTTCTGGGCTGCTGGGCTGCTATTA	3020
Db	2871	CTCTGCCGTAGAGTGTATTTGCCATCTCTGCTCAGCAGCAGCTTCTGGGCTGCTGCTCTT	2930
QY	3021	CTTCAACAAAGTGTATCATCT	3080
Db	2931	CTTCAACAAAGTGTATCATCT	2990
QY	3081	CTGCAGCACGGGCCCCACCGCTTCAAGGTGGGGCCCGGGCCACCCCTCTCGGGGCGAGCGC	3140
Db	2991	TTGCAGCACCGGAGCTCACCGCTTCAAGGTGGCTGCTGGGGCCCGCCGCTGCGCGCAGCAA	3050
QY	3141	CGGCTCTCGCAAGCGCTCCAGAGCCTGTGGGCTCCACCATCTCTCTCTCGCCCGGCTCGTC	3200

Db 3051 CGTCTCCGCAAGCGTCCAGAGCCTTGAGGCTCCAGGGATCCACCCCTCTCTCTC 3110
QY 3201 CACCTCGGGCGGGGCTCCACCATGAGATGAGCGCTGACGCGGAGAGGTCAGCTT 3260
Db 3111 CATCAGCAGAGAGCAACA----GCGAAGACCCATTCCACAGCCCGAGAGGAGAG 3165
QY 3261 CGGCAGCGCAGCGTCACCTGTCGCTGAGCTTCGAGGAGAGCAGCGCATGCCACCT 3320
Db 3166 CAGCAGCAGCGCTGCGCCCTAACCCAGCAAGCAGCAGCAGCGCCCTGACCTCCCA 3225
QY 3321 CAGCCGCAAGCGCGGCGGAGAGCAACTCGGCGGATGGCCGCGAG 3362
Db 3226 CAGCAGCAAGCATCTCAGCAGCAGCCAGATGCAAGCAGAG 3267

RESULT 11

US-08-480-751-3
; Sequence 3, Application US/08480751
; Patent No. 5858684
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,751
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/004
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3809 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 373..3606
; OTHER INFORMATION:
US-08-480-751-3
Query Match 42.2%; Score 1745.2; DB 2; Length 3809;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;
QY 501 CTCAGGGTATGTTCCAAACCAAGGGCCCAAGAGAGAGACATCATCTGGAGGTCT 560
Db 423 CTGCGCTACGGCCAGACCCAGCGAGCCCAAGAGAGGGGACATTATCTTTGGGGGCT 482
QY 561 CTTCCTCAATACATTGGAGTAGCGGCCAAGGATCAGGACTTAAATTCAGAGCCGAGGC 620
Db 483 CTTTCTCTATTCTTTGGAGTAGCAGCTAAAGATCAAGATCTCAAATCAAGGCCGAGTC 542
QY 621 GACAAATGATTTCGGTACAAATTTTCAGGCTTCCGATGCTCCAGGCGATGATATTCG 680
Db 543 TGTGGAATGATCAGGATTAATTTCCGTGGTTTCCTGTGTACAGGCTATGATATTGC 602
QY 681 AATTGAAGAGATTAAACAACAGTATGACTTTTCCTGCCCAATATCACCTGGGATATCCAT 740
Db 603 CATAGAGGAGATAAACAAGAGCCAGCCCTTCTTCCCACTTTCAGCGTGGGATACAGAT 662
QY 741 ATTGACACGTGTAAACCGGTGTCAGAGGGCTAGAGGCAACACTCAGTTTGTGCCCCA 800
Db 663 ATTGACACTTGCAACACCGTTTCTAAGGCTTTGGAAGCCACCTGAGTTTGTGCTCA 722
QY 801 GAACAAATCGACTCGCTGAACCTTAGATGAGTTCTGTAACTGCTGTGACCAATATCCATC 860
Db 723 AACAAATTTGATCTTTGACCTTGTGATGTTCTGCACTGCTCAGAGCACATTCCTC 782
QY 861 CACAATAGCAGTGTGCGGGCAACCGGGTCAGAAATCTCCAGCGCTGTGCCCAATCTAT 920
Db 783 TAGCAATTGCTGTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAATCTGT 842
QY 921 GGGATTTATTTACATTCACAGGTGAGTATGCTCTCGAGCAGGCTGCTCAGCAACAA 980
Db 843 GGGGCTCTTCTCATTTCCCGAGTATGATGCTCTCTCCAGCAGACTCTCTCAGCAACAA 902
QY 981 GAATGAGTACAAGGCTTCTCTGAGGACCAATCCCAATGATGAGCAACAGGCCACGCGCAT 1040
Db 903 GAATCAATTTCAAGTCTTTCTCCGAAACCAATCCCAATGATGAGCAGCAGGCCACTGCCAT 962
QY 1041 GGCGGAGATCATGAGCAGCTTCCAGTGGAACTGGGTGGGAACCTGGCGAGCCGACCATGA 1100
Db 963 GGCAGACATCATGAGTATTTCCGCTGGAACTGGGTGGGACAAATTCAGGAGGATATCTGCAT 1022
QY 1101 CTATGGCCGCCAGGCAATTCACAAGTTCCGGGAGGAGGCCGTTTAAAGAGGACATCTGTAT 1160
Db 1023 CTATGGCCGCCGCGGATTCAGAAATTCAGAGAGGAGCTGAGGAAAGGATATCTGCAT 1082
QY 1161 TGATTCAGTGAAGATGATCTCTCAGTACTACCCAGAGCAGTTGGAGTTCTATCGCGCA 1220
Db 1083 CGACTTCAGTGAATCTATCTCCAGTACTCTGTATGAGGAGAGATCCAGCATGTGTAGA 1142
QY 1221 CGTCATCCAGAACTCTCTCGGCCCAAGGTGATCGTGGTCTTCTCCAATGGCCCCGACCTGA 1280
Db 1143 GGTGATTCAAAATTCACGGCCAAAGTATCTGTGGTTTCTCCAGTGGCCGACATCTTGA 1202
QY 1281 CGCGCTCATCCAGAGATAGTTTCGGAGAAACATCAAGGATCGGATCTGGCTGGCCAGCGA 1340

Db 1203 GGCCTCATCAAGAGAGTTGTCGGGCGCAATATCAAGGCAAGATCTGCTGGCCAGCGA 1262
Qy 1341 GCTTGGGCGCAGCTCTTCTGCTCATTTCCAGGCGAGAGTACTTCCACGTGGTGGCGGCAC 1400
Db 1263 GGCCTGGGCGCAGCTCTGCTGCTGATCGCATGCTCAGTACTTCCACGTGGTGGCGGCAC 1322
Qy 1401 CATCGCTTCGCTCTCAGGCGGGGCGGTATCCAGGTTTCAACAAGTTCTCTGAAGAGGT 1460
Db 1323 CATTGATTCGCTCTGAAGGCTGGGCGAGATCCAGGCTTCCGGGAATTCCTGAAGAAGGT 1382
Qy 1461 CCACCCCGCAGAGTCTCGGCAAAATGGGTTTCTCAAGGAGTTCTGGGAGGAGACCTTCAA 1520
Db 1383 CCATCCGAGAGTCTGTCCCAATGGTTTCCCAAGGAGTTTGGGAAGAAACATTTAA 1442
Qy 1521 CTGCTACTTACCGAGAGACCCCTGACGAGCTGAAGAATTCGAAGTGGCCCTCCGACGG 1580
Db 1443 CTGCCACCTCCAGA-----AGTGCAAAAGGACCTTTACCTGTGGACACCTTTCTG 1494
Qy 1581 ACCGGGGCTCAAGGGGCGGCTCAAGGGCGGGAACTCCAGACGAGCAGCCCTACGCCA 1640
Db 1495 AGAGG-----TCAGGAAGAAGTGGGCAAGGTTTAGCAACAGCTCGACAGCCTCCGACC 1550
Qy 1641 CCCCTGCACTGGGAGGAGAAATCACCAAGCTGGAGACCCCTACCTGGATTTACACAA 1700
Db 1551 CCTCTGTACAGGGGATGAACAATCAGCAGTGTGAGACCCCTTACATAGATTACACGCA 1610
Qy 1701 CTGAGGATCTCCTACATGATATAGTGGCCCTCTACTCCATTTGCTCAGCCCTCAGGA 1760
Db 1611 TTACGGATATCCTACATGTGTACTTAGCAGTCTACTCCATTTGCTCCAGCCCTTCAAGA 1670
Qy 1761 CATCACTCTTCAAAACCGGACCGGCTCTTTGCAACGAGATCTTTGTCAGATATTAA 1820
Db 1671 TATATATACCTGTTACCTGGGAGAGGCTCTTACCAATGGCTCTGTGAGACATCAA 1730
Qy 1821 AAAAGTTAGGCTGGCAGTCTCAACATCTGCTGATCTGAAGTTTACCAAGCAT 1880
Db 1731 GAAAGTTAGGCTGGCAGTCTTGAAGCACCCTACGGCATTTAAACCTTTTCAAAACAATAT 1790
Qy 1881 GGTGAGCAGGTGTACTTTAGCATCAAGGTCACTCAAGGGGAACCTACACCATTTCAA 1940
Db 1791 GGGGAGCAGGTGACCTTTGATGAGTGTGTGACCTGTGGGGAACCTATTCATCATCAA 1850
Qy 1941 CTGGCAGCTCTCCGAGAGATGAATCGGTGTTTTCATGAGTGGGCAACTACAAAGC 2000
Db 1851 CTGGCAGCTCTCCGAGAGATGGTCCATCTGTTTAAAGGAAGTCGGGTATTACAAAGT 1910
Qy 2001 CTACCTAAGCCAGTACCGGACTCAACATCAACGAAGAAGAACTCTCGAGTGGCTT 2060
Db 1911 CTATGCCAAGAAGGAGAAAGACTCTTCAACAGGAGAAATTCCTGTGGAGTGGGT 1970
Qy 2061 CTCCAAAGTGGTTTCCTTTCTCCAACTGCAGTCEGAGCTGTGTCGGGCGACCCAGGAAGG 2120
Db 1971 CTCCAGGAGGTGCCCTTCTCCAACTGCAGCCGAGACTCCCTGGCAGGAGCCAGGAAGG 2030
Qy 2121 GATCATCGAGGGGAGCCACCTGCTGTTGAATGCAATGGCATGTGAGAGGAGAGTT 2180
Db 2031 GATCATCGAGGGGAGCCACCTGCTGTTGAGTGTGGAGTGTCTGATGGGGAGTA 2090
Qy 2181 CAGTGATGAAAACGATGCAAGTGCCTGATCAAGTGCCTGGAATGATTTCTGTGCAATGA 2240
Db 2091 TAGTGATGACAGATGCCAGTGCCTGTGAACAGTGGCCAGATGACTTCTGTGCAATGA 2150
Qy 2241 GAACCAACAGTGTGATGCCCAAGAGATCGAGTACCTGTGTCGAGCGAGCCCTTCGG 2300
Db 2151 GAACCAACAGTGTGATGCCCAAGAGATCGAGTTCCTGTGTGGAGCGGAGCCCTTTGG 2210
Qy 2301 GATCGCTGACCATCTTCCCGTACTGGGCTACTGATCACTCTCTGCTGGGGGT 2360
Db 2211 GATCGACTCACCTCTTTGGCGTGTGGGCAATTTCTGACAGCCTTTGCTGGGGT 2270
Qy 2361 CTTTCATCAAGTTTCAAGAACATCTCCATCGTGAAGGCCACCAACCGGAGTTGTCTACCT 2420

Db 2271 GTTTATCAAGTTCCGAAACACACCCATTGTCAAGGCCACCAACGAGAGCTCTCTACCT 2330
Qy 2421 GCTGCTTTTTCCTCATCTGCTGCTTTCAGCTGCTGCTCATTTTATTCGGGAGGCCAG 2480
Db 2331 CCTCCTTTCTCCTGCTGCTGCTTCTCAGCTCCTGTTCTTTCATCGGGAGGCCCA 2390
Qy 2481 GGACTGACCTGTGCGCTCGCAACCGGCTTTTGGCATCAGCTTGTCTCTGTGCTCTC 2540
Db 2391 GGACTGACGTGCGCTGCGCAGCGGCTTTTGGCATCAGCTTGTGCTGTGCTCTC 2450
Qy 2541 CTGCATCCTGTGAAGACCAACCGGCTGTGCTGCTTTCGAGGCCAAGATCCCAACAG 2600
Db 2451 ATGCATCCTGGTGAACCAACCGTGTCTCTGCTGCTTTCGAGGCCAAGATCCCAACAG 2510
Qy 2601 CCTCCACGGAAGTGGTGGGCTCAACCTGCAAGTTCCTGCTCTCTGCTCTGCTCT 2660
Db 2511 CTTCCACGGAAGTGGTGGGCTCAACCTGCAAGTTCCTGCTGCTTTCCTCTGCACTT 2570
Qy 2661 GGTCAAAATCGTCACTGTCATCTGCTCTACACCGGCTTCCCTCCAGCTACAGGAA 2720
Db 2571 CATGCAGATTGTCTGCTGCTGCTCTACACCGGCTTCCCTCCAGCTACAGGAA 2630
Qy 2721 CCATGAGCTGAGGACGAGGTCTCTTTCATCTCCTGGAGCAGGGCTCGCTCATGGGCT 2780
Db 2631 CCAGAGCTGGAGATGAGATCTTTCATCAGTGCACGAGGCTCCCTCATGGGCT 2690
Qy 2781 GGGCTTCTCATCGGCTACACCTGCTCTCGCGCATCTGCTTCTTCTTCTGCTTCAA 2840
Db 2691 GGGCTTCTCATCGGCTACACCTGCTGCTGCTGCTGCTGCTGCTTCTTCTTCTGCTTCAA 2750
Qy 2841 GTCCGCTGAGTCCGAGAACTTCAACGAGGTAAAGTTCATCACTTTCAGCATGTTGAT 2900
Db 2751 GTCCGGAAGTCCGAGAACTTCAATGAAGCAAGTTCATCACTTTCAGCATGCTCAT 2810
Qy 2901 CTTCTTCATGCTGATCTCTCTTTCATCCCGCTATGTCAGCAGCTTACGCAAGTTGT 2960
Db 2811 CTTCTTCATGCTGATCTCTCTTTCATTCAGGCTATGTCAGCAGCTTATGGCAAGTTGT 2870
Qy 2961 GTCCGCTGAGGATGATTCCTCTCTGCTCTCAGCTTCCGGCTGCTGGGCTGCAATTA 3020
Db 2871 CTCTGCCGTAGAGTGTATTCCTCTCTGTCAGCAGCTTTCGCTTCTGCTGCTGCTCT 2930
Qy 3021 CTTCAACAGTGTATCATCTCTTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3080
Db 2931 CTTCAACAGATCTACATCTCTTTCAGGCTATCCGCAACCACTTCAGGAGTGG 2990
Qy 3081 CTGCAGCAGCGGCGCCACGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCG 3140
Db 2991 TTGCAGCAGCGGAGCTCACGCTTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3050
Qy 3141 CGGCTCTGCAAGGCTTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3200
Db 3051 CGTCTCCGCAAGCGGCTCCAGAGCTTGGAGGCTCCAGGGATCCACCCCTCTCTCTC 3110
Qy 3201 CACTGCGGCGGCTCTACCATGAGATGAGGCTGTCAGCAGCAGCAGCAGCAGCAGCAG 3260
Db 3111 CATCAGCAGCAGGCAACCA-----GCAAGACCCATTCCACAGCCCGAGGAGAG 3165
Qy 3261 CGGAGCGGCGGCTCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3320
Db 3166 CAGCAGCAGCGCTGGGCTTAAACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3225
Qy 3321 CAGCGCAGCGGCGGAGGAGGAGTCTGGGCGGATGGCGGAG 3362
Db 3226 CAGCAGCAACGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3267

RESULT 12
US-08-943-986-3
; Sequence 3, Application US/08943986
; Patent No. 5962314
; GENERAL INFORMATION:
APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert
 APPLICANT: James E. Garrett, Jr.
 TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
 TITLE OF INVENTION: MOLECULES
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: First Interstate World Center
 STREET: Suite 4700
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: FASTSEQ
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/943,986
 FILING DATE: 03-OCT-1997
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/484,565
 FILING DATE: 7-June-1995
 APPLICATION NUMBER: 08/353,784
 FILING DATE: 9 December, 1994
 APPLICATION NUMBER: PCT/US/94/12117
 FILING DATE: 21 October, 1994
 APPLICATION NUMBER: U.S. 08/292,827
 FILING DATE: 23 August, 1994
 APPLICATION NUMBER: U.S. 08/141,248
 FILING DATE: 22 October, 1993
 APPLICATION NUMBER: U.S. 08/009,389
 FILING DATE: 23 February, 1993
 APPLICATION NUMBER: U.S. 08/017,127
 FILING DATE: 12 February, 1993
 APPLICATION NUMBER: U.S. 07/934,161
 FILING DATE: 21 August, 1992
 APPLICATION NUMBER: U.S. 07/834,044
 FILING DATE: 11 February, 1992
 APPLICATION NUMBER: U.S. 07/749,451
 FILING DATE: 23 August, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Heber, Sheldon O.
 REGISTRATION NUMBER: 38,179
 REFERENCE/DOCKET NUMBER: 213/006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3809 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 373..3606
 OTHER INFORMATION:
 US-08-943-986-3

Query Match 42.2%; Score 1745.2; DB 2; Length 3809;
 Best Local Similarity 76.4%; Pred. No. 0;
 Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;
 501 CTCAGGGTATGGTCCAAACCAAGGCGCCAGAGAAAGGAGACATCATACTCGGAGGTCT 560
 423 CTCTGCTACGGCCAGACGAGCCCAAGAGAGGGGACATTAATCTTGGGGGGCT 482

QY	561	CTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGACTTTAAATTCAGACCGGAGGC	620
DB	483	CTTTCTCTATTTCATTTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGGCGGAGTC	542
QY	621	GACAAATGATTCGGGTACAAATTTTCGAGGCTTCGATGGCTCCAGGCGGATGATATCCG	680
DB	543	TGTGGAATGATCAGGTATAATTTTCGGTGGTTCGCTGGTTACAGGCTATGATATTCG	602
QY	681	AATTTGAAGAGATTAAACAACAGATATGACTTTCTCTGCCCAATATCACCTGGGATATCCGAT	740
DB	503	CATAGAGGAGATAAACAGACGCCAGCCCTCTTCCCACTTGACGCTGGGATACAGGAT	662
QY	741	ATTTGACACGTGTAAACACCGTGTCCAGGGCGGTAGAGGCAACACTCAGCTTTGTGGCCCA	800
DB	663	ATTTGACACTTGCAACACCGTTCCTAAGGCTTTGGAAGCCACCTCAGTTTGTGCTCA	722
QY	801	GAACAAATCGACTCGCTGAACCTAGATGATGTTCTGTAACTGCTCTGACCATATCCCATC	860
DB	723	AAACAAATTTGATTTTGAACCTTGTGATGTTCTGCTGCTCAGAGCACATTTCCCTC	782
QY	861	CACAAATAGCAGTGTGCGGGCAACCGGGTCAGAAATCTCCACGGCTGTGGCCCAATCTAT	920
DB	783	TAGGATTCGTGTGGTGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAATCTGCT	842
QY	921	GGGATTTATTTTACATTCACAGCTCAGCTATGCTCTCTCGAGCAGGCTGCTCAGCAACAA	980
DB	843	GGGGCTCTTCTCATTTCCCGAGGTGAGTTTANGCTCTCTCAGCAGACTCTCTCAGCAACAA	902
QY	981	GATAGATCAACAGGCTTCTCTGAGGACCATCCCAATGATAGCAACAGGCCACCGCCAT	1040
DB	903	GATCATTTCAAGTCTTCTCTCGAACCCTCCCAATGATGACACACGCGCACTGCCAT	962
QY	1041	GGCGAGATCATCAGACACTTCCAGTGGAACTGGGTGGGAACCTGGCGCCGACCATCA	1100
DB	963	GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCAAAATTCAGCTGATGACGA	1022
QY	1101	CTATGGCGGCCAGGCAATTCACAAGTTCCGGGAGGAGGCGGTAAAGAGGACATCTGTAT	1160
DB	1023	CTATGGCGGCCGGGATTTGAGAAATTCGAGAGGAGAGCTGAGGAAAGGATATCTGCAT	1082
QY	1161	TGACTTCAGTGAATGATCTCTCAGTACTACACCCAGAGACAGTGGAGTTATCTCCCGCA	1220
DB	1083	CGACTTCAGTGAATCTCATCTCCAGTACTCTGATGAGGAGAGATCCAGCATGTGTAGA	1142
QY	1221	CGTCATCCAGAACTCTCTGGGCCAAGGTCTCGTGGTCTTCTCCAAATGGGCCCCGACCTGA	1280
DB	1143	GGTGATTCAAATTCACGGCCAAAGTATCTCGTGGTCTTCTCCAGTGGGCCAGATCTTGA	1202
QY	1281	GCCTCTCATCCAGGAGATAGTTCCGAGAAACATCAACGATCGGATCTGGTGGCCAGCGA	1340
DB	1203	GCCCTCATCAAGGAGATTTCCGGGCAATATCACGGGCAAGATCTGGTGGCCAGCGA	1262
QY	1341	GGCTTGGCCAGCTCTTCGCTCATTCCTCCAGCAGAGTACTTCCAGCTGGTGGCGGCGAC	1400
DB	1263	GGCTTGGCCAGCTCTTCGCTCATTCCTCCAGCAGAGTACTTCCAGCTGGTGGCGGCGAC	1322
QY	1401	CATCGGCTTCGCTCTCAGGGCGGGCGGTATCCCAAGGTTTCAACAAGTTCTCTGAAGAGGT	1460
DB	1323	CATTGGATTCGCTCTGAAGCTGGCAGATCCCAAGGCTTCGGGAAATTCCTGAAGAAGGT	1382
QY	1461	CCACCCAGCAGGTCTCTCGGACAAATGGGTTGTCAAGGAGTTCTGGAGAGAGACCTTCA	1520
DB	1383	CCATCCCAAGGAAGTCTGTCCACAATGGTTTTCGCAAGGAGTTTGGGAGAAACATTTAA	1442
QY	1521	CTGCTACTTCCCGAGAGAGACCTCTGACGAGCTGAAGAATTCGAAGGTGCGCTCGCACCG	1580
DB	1443	CTGCCACTCTCAAGA-----AGTGTCAAAGGACCTTTTACTGTGGACACCTTTCTG	1494
QY	1581	ACCGCGGCTCAAGGGGACCGCTCCAAAGGCGGGGAATCCAGAGCGGACAGCCCTTAGCCCA	1640
DB	1495	AGAGG----TCAACGAAGAAAGTGGCGACAGGTTTAGCAACAGCTCGACAGCTTCCGACC	1550
QY	1641	CCCCTGCACTGGGAGGAGGAGACATCACCGGTGAGACCCCTTACTCTGGATTATACACA	1700

1551 DB CTTCTGTACAGGGATGAGACATCAGCAGTGTGAGAGCCCTTACATAGATTACAGCA 1610
1701 QY CTTGAGGATCTCTCAATATATACGTCGCGCTTACTCCATGCTACGCGCTTGCAGA 1760
1611 DB TTACGGGATATCTCAATATGTTACTTTAGCAGTCTACTCCATGTCGCGCTTGCAGA 1670
1761 QY CATCACTCTTCAAAACCGGACGCGCATCTTTGCAAAACGATCTTTGTCAGATATTAA 1820
1671 DB TATATATACCTCTTACTCTGGGAGAGGCTCTTACCAATGCTCTGTGAGACATCAA 1730
1821 QY AAAAGTGAAGGCTGGGAGGCTCTCAACATCTGTCATCTGATGAAAGTTTACACAGCAT 1880
1731 DB GAAAGTGAAGGCTGGGAGGCTCTCAACATCTGTCATCTGTCATCTGTCATCTGTCAT 1790
1881 QY GGGTGAAGGCTGGGAGGCTCTCAACATCTGTCATCTGTCATCTGTCATCTGTCATCTG 1940
1791 DB GGGGAGGAGGTCATCTTGTAGTGTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCT 1850
1941 QY CTTGAGGATCTCTCGGAGAGGATGAAATCGTGTGTTTCCATGAGTGGGCACTTACAAGC 2000
1851 DB CTTGACACCTCTCCGAGAGGATGCTCATCTGTGTTTAAAGGAAGTCGGGTATTACAAGT 1910
2001 QY CTTACCTTAAGCCAGTGAACGCTCAACATCAACGAAAGAAATCTCTGAGTGGCTT 2060
1911 DB CTTATCCAAAGAGGAGGAGGATCTCTTCAACAGGAGGAAATCTCTGAGTGGGTT 1970
2061 QY CTTCAAAGTGTCTCTTCTCAACAGTGTGTCAGTGTGTCGCGGACACAGGAAGG 2120
1971 DB CTTCAAGGAGGTCCTCTCTCAACAGTGTGTCAGTGTGTCGCGGACACAGGAAGG 2030
2121 QY GATCATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2180
2031 DB GATCATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2090
2181 QY CAGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2240
2091 DB TAGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2150
2241 QY GAACACACAGTGTGTCATCTGTCGCAAGGAGATCGAGTGTGTCGTCGTCGTCGTCGTCG 2300
2151 DB GAACACACCTCTCTGATTTGCCAAGGAGATCGAGTGTGTCGTCGTCGTCGTCGTCGTCG 2210
2301 QY GATCGCTGTGACATCTTCCGCGTACTGGGATCTGATCACTCTCTGTCGTCGTCGTCGTCG 2360
2211 DB GATCGACTACCTCTTTCGCGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2270
2361 QY CTTTCAAGTTCAGGAGACACTCCCATCTGTGAAGGCCACCAACCGGAGTGTCTCTACT 2420
2271 DB GTTATCAAGTTCAGGAGACACTCCCATCTGTGAAGGCCACCAACCGGAGTGTCTCTACT 2330
2421 QY GTGCT 2480
2331 DB CTTCT 2390
2481 QY GAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2540
2391 DB GAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2450
2541 QY CTTGATCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2600
2451 DB ATGATCTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2510
2601 QY CTTCAACCGCAGTGGTGGGCTCAACCTGAGTGTCTCTGTCGTCGTCGTCGTCGTCGTCGTC 2660
2511 DB CTTCAACCGCAGTGGTGGGCTCAACCTGAGTGTCTCTGTCGTCGTCGTCGTCGTCGTCGTC 2570
2661 QY GGTGCAAAATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCT 2720
2571 DB CATGAGATGTCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCATCT 2630
2721 QY CCAATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2780

2631 DB CCAGGAGTGGAGGATGAGATCATCTTATCATGCTCCAGGAGGCTCCCTCATGCGCT 2690
2781 QY GGGCTTCTCATCGGCTACACCTCTCTCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2840
2691 DB GGGCTTCTCATCGGCTACACCTCTCTCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2750
2841 QY GTCCGTAAGCTCCGCGAGAACTTCAACGAGGTAAGTTTATCACCTTTCAGCATGTGAT 2900
2751 DB GTCCGTAAGCTCCGCGAGAACTTCAATGAAGCAAGTTTATCACCTTTCAGCATGTGAT 2810
2901 QY CTTCTTCATCTGTGATCT 2960
2811 DB CTTCTTCATCTGTGATCT 2870
2961 QY GTGGCGCTGAGTGTGATCT 3020
2871 DB CTCTGCGTAGAGTGTGATCT 2930
3021 QY CTTCAACAAAGTGTATCATCT 3080
2931 DB CTTCAACAAAGTGTATCATCT 2990
3081 QY CTTGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3140
2991 DB TTGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3050
3141 QY CGGCTCTCGCAAGCGCTTCCAGCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3200
3051 DB CGTCTCCGCAAGCGGCTTCCAGCAGCGCTTCCAGCAGCGCTTCCAGCAGCGCTTCCAGCAGCG 3110
3201 QY CACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3260
3111 DB CATCAGCAGCAAGAGCAACA-----CGAAGAGCCCATTTCCACAGCGCGGAGAGGAGGAG 3165
3261 QY CGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3320
3166 DB CAGCAGCAGCGGCTGGCGCTTAAACCAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3225
3321 QY CAGCGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3362
3226 DB CAGCAGCAAGCATCTCAGCAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3267

RESULT 13
US-08-353-784-3
; Sequence 3, Application US/08353784
; Patent No. 6011068
GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Forrest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December, 1994

CLASSIFICATION: 514
 PRIOR APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below: 8
 PRIOR APPLICATION DATA: described below: 8
 APPLICATION NUMBER: PCT/US/94/12117
 FILING DATE: 21 October, 1994
 APPLICATION NUMBER: 1994
 FILING DATE: 23 August, 1994
 APPLICATION NUMBER: U.S. 08/292,827
 FILING DATE: 23 August, 1994
 APPLICATION NUMBER: U.S. 08/141,248
 FILING DATE: 22 October, 1993
 APPLICATION NUMBER: U.S. 08/009,389
 FILING DATE: 23 February, 1993
 APPLICATION NUMBER: U.S. 08/017,127
 FILING DATE: 12 February, 1993
 APPLICATION NUMBER: U.S. 07/934,161
 FILING DATE: 21 August, 1992
 APPLICATION NUMBER: U.S. 07/834,044
 FILING DATE: 11 February, 1992
 APPLICATION NUMBER: U.S. 07/749,451
 FILING DATE: 23 August, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Heber, Sheldon O.
 REGISTRATION NUMBER: 38,179
 REFERENCE/DOCKET NUMBER: 209/069
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3

SEQUENCE CHARACTERISTICS:
 LENGTH: 3809 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 373..3606
 OTHER INFORMATION:
 US-08-353-784-3

Query Match 42.2%; Score 1745.2; DB 3; Length 3809;

Best Local Similarity 76.4%; Pred. No. 0; Mismatches 658; Indels 17; Gaps 3;
Matches 2187; Conservative 0;

Qy	501	CTCAGGGTATGGTCCAAACCAAGGCCCCAGAGAAAGGAGACATCATCTGGAGGTCT	560
Db	423	CTCTGCTACGGCCAGACCCAGCGAGCCCAAGAGGGGACATTTCTTGGGGGCT	482
Qy	561	CTTCCCAATACATTGGAGTAGCCGCCAAGGATCAGGACTTAAATCGAGACCGGAGGC	620
Db	483	CTTTCTTATTCATTTGGAGTAGCAGCTAAAGATCTCAATCAAGCCCGGAGTC	542
Qy	621	GACAAATATGTCGTGACAAATTTCCAGGCTTCGATGGCTCCAGGGGATGATATTCGC	680
Db	543	TGTGGAATGTATCAGGTATTAATTTCCGTGGGTTTCTGCTGTACAGGCTATGATTTTCG	602
Qy	681	AATTGAAGAGATTAAACACAGTATGATCTTCTGCCCAATATCACCTGGGATATCGCAT	740
Db	603	CATAGAGGAGATAAACAGCAGCCAGCCCTCTTCCCACTTTCAGCTGGGATACAGGAT	662
Qy	741	ATTGACAGTGTAAACACCGTGTCCAGCGGTAGAGCAACACTCAGCTTTGTGGCCCA	800
Db	663	ATTGACACTTGAACACCGCTTTCTAAGGCCCTTGAAGCCCACTTGTGCTCA	722
Qy	801	GAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAACTGCTCTGACCATATCCCATC	860
Db	723	AAACAAATGATCTTTTGAACCTTGATGAGTTCTGCAACTGCTCAGAGCACATTTCCCTC	782
Qy	861	CACATAGCAGTGTGGCGGCAACCGGTTCAGGATCTCCAGGCTGTGGCCAAATCTATT	920
Db	783	TACGATTGCTGTGGTGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAATCTGCT	842

Qy	921	GGGATATTTTACATTCACAGGTACGCTATGCTCTCGAGCAGGCTGCTCAGCAACA	980
Db	843	GGGGCTCTTCTATATTCCTCCAGGTAGTTATGCTCTCTCCAGCAGACTCTCTCAGCAACA	902
Qy	981	GAATGAGTACAAGGCTTCTCTGAGGACCATCCCAATGATGAGCAACAGGCCACGCGCAT	1040
Db	903	GAATCAATTCAAGTCTTTCTCCGAAACCATCCCAATGATGAGCAACAGGCCACTGCCAT	962
Qy	1041	GGCCGAGATCATGAGCAGCTTCCAGTGGAACTGGGTGGGAACTCCCTGGCAGCCAGCATGA	1100
Db	963	GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCAAAATTCGAGCTGATGACGA	1022
Qy	1101	CTATGGCCGCCAGGCAATTCACAAGTTCCGGGAGGAGGCCGTTAAGAGGAGACATCTGTAT	1160
Db	1023	CTATGGGGCCCGGGATTTGAGAAATTCGAGAGGAGCTGAGGAAAGGATATCTGCAT	1082
Qy	1161	TGACTTCAGTGAAGATGATCTCTCAGTACTACACCCAGAGCAGTTGGAGTTTATCGCCGA	1220
Db	1083	CGACTTCAGTGAATCTATCTCCAGTACTCTGATGAGGAAGATCCAGCATCTGTAGA	1142
Qy	1221	CGTCATCCAGAACTCTCTGGCCCAAGGTATCGTGGTCTTCTCCAATGGCCCCACCTGGA	1280
Db	1143	GGTGATTCAAAATTCACGGCCAAAGTATCTGTTGTTTCTCCAGTGGCCAGATCTTGA	1202
Qy	1281	GGCGCTCATCCAGGAGATAGTTCCGAGAAACATCAACCGATCGGATCTGGCTGGCCAGGA	1340
Db	1203	GGCCCTCATCAAGGAGATTTCCGGGCCAATATCAAGGGCAAGATCTGGGTGGCCAGCGA	1262
Qy	1341	GGCTTGGCCAGCTCTTCGCTCATTCGCCAGCCAGAGTACTTCCAGTGGTGGCGGCAC	1400
Db	1263	GGCTTGGCCAGCTCTTCGCTCATTCGCCAGCCAGAGTACTTCCAGTGGTGGCGGCAC	1322
Qy	1401	CATCGGCTTCGCTCTCAGGGCGGGGCTATCCAGGGTTCAACAAGTTCTTGAGGAGGT	1460
Db	1323	CATTGGATTCGCTCTGAGGCTGGCCAGATCCAGGCTTCCGGGAATTCCTGAAGAGGT	1382
Qy	1461	CCACCCAGCAGGTCTCGGACAAATGGTTTGTCAAGAGTCTTGGAGAGACCTTCAA	1520
Db	1383	CCATCCAGGAAGTCTTCCACAATGGTTTTCACAAGGAGTCTTGGGAAAGAAATTTAA	1442
Qy	1521	CTGCTACTTCCAGGAGAGACCCTCGACAGCTGAAGAAATTCCAAGTGCCTTCGACCG	1580
Db	1443	CTGCCACTTCAAGA-----AGGTGCAAAAGACCTTACTCTGGACACTTCTG	1494
Qy	1581	ACCGCGGCTCAAGGGGAGCGCTCCAAAGCGGGAACTCCAGAGGAGACGCCCTAGCCCA	1640
Db	1495	AGAGG-----TCAGGAAGAAAGTGGCGACAGGTTTAGCAACAGCTCGACAGCTTCGACC	1550
Qy	1641	CCCTCGACTGGGGAGGAGAACATCACCGGTGGAGACCCCTACTCTGATTTATACACA	1700
Db	1551	CCTCTGTACAGGGGATGAGAAACATCAGAGTTCGAGACCCCTTACATGATTACAGCA	1610
Qy	1701	CCTGAGGATCTCTACAATGTATACGTGGCGCTTACTCCATTCCTCAGCCCTGCAAGA	1760
Db	1611	TTTACGGATATCTACAAATGTATCTAGCAGTCTACTCCATTCGCGCAAGCTTGAAGA	1670
Qy	1761	CATCCACTCTTGAACCCCGGACGGGCATCTTTGCAAGCGATCTTGTGCATATTAA	1820
Db	1671	TATATATACCTGTCTACCTGGGAGAGGCTCTTCAACAATGGCTCTGTGACAGATCAA	1730
Qy	1821	AAAAGTTGAGGCTTGGCAGGTCTCAACCATCTGCTGCATCTGAAGTTTACCAACAGCAT	1880
Db	1731	GAAAGTTGAGGCTGTCAGGTCTTGAAGCACTTACGGCATCTAACTTTTACAAACAATAT	1790
Qy	1881	GGGTGAGCAGGTGACTTTGACGATCAAGTACCTCAGGGGAACTACACCAATTTCAA	1940
Db	1791	GGGGGAGCAGGTGACCTTTGATGAGTGTGTGACCTCGTGGGGAATATTTCCATCATCA	1850
Qy	1941	CTGCGACTCTCGCAGAGGATGAATCGGTGTTGTTTCCATGAGTGGGAACTTACAAACGC	2000
Db	1851	CTGCGACTCTCTCCAGAGGATGGCTCCATCGTGTGTTTACGAGTGGGTATTACACGT	1910
Qy	2001	CTACGCTAAGCCCGCAGTGAACCGACTCAACATCAACAGAAAGAAATCTCTGTGAGTGGCTT	2060

1911 CTATGCCAAGAGGAGAGAACTCTTCATCAACGAGGAGAAATCTCTGTGGAGTGGGTT 1970
2061 CTCCTAAAGTGTCTCTCTCAACTGAGTGCAGTGCAGTGTGCGGCGCACACGAGAGGG 2120
1971 CTCCTAGGAGTGGCCCTCTCTCAACTGAGCGGAGACTGCGTGGCAGGAGACAGAAAGG 2030
2121 GATCATCAGGAGGAGGAGCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2180
2031 GATCATCAGGAGGAGGAGCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2090
2181 GATCATCAGGAGGAGGAGCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2240
2091 TAGTATGAGACAGATGCGAGTGCCTGTAAACAGTGCAGTGCCTCTCTCTCTCTCTCT 2150
2241 GAAACACACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2300
2151 GAAACACACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2210
2301 GATCGCTGAGCACTCTGCGCGTACTGGGCACTCTGATCACTCTCTCTCTCTCTCTCTCT 2360
2211 GATCGCACTCTGCGCGTACTGGGCACTCTGATCACTCTCTCTCTCTCTCTCTCTCTCT 2270
2361 CTTCATCAAGTTCAGGAACTCCATCTGTAAGGCGCCACCAACCGGAGTGTCTCTACT 2420
2271 GTTATCAAGTTCAGGAACTCCATCTGTAAGGCGCCACCAACCGGAGTGTCTCTACT 2330
2421 GCTGCT 2480
2331 CTTCT 2390
2481 GSACTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2540
2391 GSACTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2450
2541 CTGCACTCTGTAAGAGCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2600
2451 ATGCACTCTGTAAGAGCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2510
2601 CTTCAACGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2660
2511 CTTCAACGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2570
2661 GGTGCAATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2720
2571 CATGAGATGTCATCTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2630
2721 CCATGAGTGGAGGAGGTCATCTCTCATCTGCGACGAGGCTGCTGCTGCTGCTGCTG 2780
2631 CCAGAGTGGAGGATGATCATCTCTCATCTGCGACGAGGCTGCTGCTGCTGCTGCTG 2690
2781 GGGCTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2840
2691 GGGCTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2750
2841 GTCCGCTAAGTGGCGGAGAACTTCAACGAGGCTAAGTTCATCACTCTGAGCATCTT 2900
2751 GTCCGAGAGTGGCGGAGAACTTCAATGAGGCTAAGTTCATCACTCTGAGCATCTT 2810
2901 CTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2960
2811 CTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2870
2961 GTCCGCTGAGGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3020
2871 CTTCTGCTGAGGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2930
3021 CTTCAACAGTGTATCATCTCTCTCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3080
2931 CTTCAACAGATCTACATCTCTCTCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2990
3081 CTTGAGGAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3140

2991 TTGACGACCGCAGCTCAGCTTTCAAGTGGTGTGCGCGGCGCACGCTGCGCGCAGCAA 3050
3141 CGGCTCTCGCAAGCGCTTCCAGCAGCGCTGCGGCTCCACCATCTCTCTGCGCGCGCTCGTC 3200
3051 CGTCTCCGCAAGCGTCCAGCAGCGCTTGGAGGCTCCACGGATCCACCGCTCTCTCCIC 3110
3201 CACTGCGGCGCGGCTTACCATGAGATGAGCGCTGAGCAGCAGCAGAGTCTGCTT 3260
3111 CATCAGCAGCAAGAGCAACA-----GCGAAGACCCATTCCACAGCCCGAGGAGGAG 3165
3261 CGCAGCGGCGCAGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3320
3166 CAGCAGCGCGCTGCGCTTACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3225
3321 CAGCGCAGCGCGCGCAGCAGGAACTCGGCGGATGCGCGCAG 3362
3226 CAGCAGCAACGATCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3267

RESULT 14
US-08-484-719B-3
; Sequence 3, Application US/08484719B
; Patent No. 6031003
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth, Edward M.
; APPLICANT: Brown, Steven C. Hebert,
; APPLICANT: Bradford C. Van Wagenen,
; APPLICANT: Manuel F. Balandrin,
; APPLICANT: Forrest H. Fuller, Eric G.
; APPLICANT: Delmar, Scott T. Moe
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Word
; SOFTWARE: FastSeq for Windows Version 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,719B
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Douglas C. Murdock
; REGISTRATION NUMBER: 37,549

/ REFERENCE/DOCKET NUMBER: 213/007
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3809 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 373..3606
/ US-08-484-719B-3

Query Match 42.2%; Score 1745.2; DB 3; Length 3809;
Best Local Similarity 76.4%; Pred No. 0;
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;

QY	501	CTCAGGGTATGTCCAAACCAAGAGGCGCCAGAGAAAGAGACATCATCTACTGGAGGTCT	560
DB	423	CTCTGCTACCGGCGCAGACGAGAGCCCAAGAGGGGACATTATCTTGGGGGCT	482
QY	561	CTTCCCAATACACTTGGAGTAGCCGCGCAAGGATCAGGACTTAAATCAGACCGGAGGC	620
DB	483	CTTTCCTATTCATTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGGCCGAGTC	542
QY	621	GACAAATATATTCGGTACAAATTTTCGAGGCTTCGGATGGCTCCAGGGGATCATATTCG	680
DB	543	TGTGGAATGATCAGGTATAATTTCCGUGGTTTCGCTGGTTTACAGGCTATGATATTGC	602
QY	681	AATTGAGAGATTAACACAGTATGACTTTCCTGCCCAATATACCTTGGGATATCGAT	740
DB	603	CATAGAGGAGATAAACAGACGCGCCAGCCCTTCTCCCAATGACCTGGGATACAGAT	662
QY	741	ATTTGACAGTGTAAACACCGTGTCCAAGCGGTAGAGGCAACACTCAGCTTTGTGGCCCA	800
DB	663	ATTGACACTTGCACACCGCTTCTAAGCCTTGAAGCCACCTGAGTTTGTGTCTCA	722
QY	801	GAACAAATTCGACTCGCTGAACTTAGATGAGTTCTGTAACTGCTTGACCATATCCCATC	860
DB	723	AAACAAATTTGATTTCTTTGAACCTTGTAGTGTCTGCAACTGCTCAGAGCAATTCCTC	782
QY	861	CACATAGCAGTGTGGGGCAACCGGTCAGGAATCTCCACGGCTGTGGCCAACTATT	920
DB	783	TACGATTGCTGTGGGAGCAACTGGCTCAGCGCTCTCCACGGCAGTGGCAATCTGCT	842
QY	921	GGGATTTATTTTCACTTCCACAGGTACGCTATGCTCTCTCGAGCAGCGTCTCAGCAAA	980
DB	843	GGGGCTCTTCTACATTTCCCGAGGTCACTTATGCTCTCTCCAGCAGACTCTCAGCAAA	902
QY	981	GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1040
DB	903	GATCAATTTCAAGTCTTTCTCCGACCACTCCCAATGATGAGCACCAGGCGCTGCGCAT	962
QY	1041	GGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGAACTCCCTGGCAGCGCAGATGA	1100
DB	963	GGCAGACATCATGAGTATTTCCGCTGGAACCTGGGTGGGCAATTTGACGCTGATGAGA	1022
QY	1101	CTATGGCCGCCAGGATTTGACAGTTCCGGGAGAGAGCGGCTTAAGAGGCACTCTGAT	1160
DB	1023	CTATGGCGCGCGGGGATTTGAGAAATTCGAGAGGAGCTGAGGAAGGAGATATCTGCAT	1082
QY	1161	TGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAGAGAGTGGAGTTTCATCGCCGA	1220
DB	1083	CGACTTCAGTGAATCATCTCCAGTACTCTGATGAGGAAGATTCAGCATGTGGTAGA	1142
QY	1221	CGTATCCAGAACTCCTCGGCGCAAGGTATGATGATGATGATGATGATGATGATGATGATG	1280
DB	1143	GGTGATTTCAAAATTCACGCGCAAAAGTATCATGTGTTTCTCCAGTGGGCCAGATCTTGA	1202

QY	1281	GCCGCTCATCCAGGAGATAGTTCCGAGAAACATCACCGATCGATCTGCTGCGCCAGCA	1340
DB	1203	GCCGCTCATCAAGGAGATTTGTCGGGCGCAATATCACGGGCAAGATCTGCTGCGCCAGCA	1262
QY	1341	GGTTGGGCCAGCTCTTGGCTCATTTCCCAAGCCAGAGTACTTCCAGTGGTGGGGGAC	1400
DB	1263	GGCTGGGCCAGCTCTCTCTGATCGCATGCTCAGTACTTCCAGTGGTGGGGGAC	1322
QY	1401	CATCGCTTCTCTCAGGCGGGGCGTATCCAGGGTTCAACAGTTCCTCAGAGAGT	1460
DB	1323	CATTGGATTGCTCTGAAAGCTGGGAGATCCAGGCTTCCGGAATTCCTGAAGAGT	1382
QY	1461	CCACCCAGCAGTCTCGGACAAATGGTTTGTCAAGGAGTTCTGGAGAGACCTTCAA	1520
DB	1383	CCATCCAGGAAGTCTGTCCCAATGTTTGGCAAGGAGTTTGGGAAGAACATTTAA	1442
QY	1521	CTGCTACTTCCCGAGAAGACCTGACGAGCTGGAAGAAATCCAGGTGCCCTCGCACG	1580
DB	1443	CTGCCACTTCCAAGA-----AGGTGCAAAAGGACCTTTACCTTGGACACCTTTCTG	1494
QY	1581	ACGGGGCTCAAGGGGACGGCTCCAGGGGGGAACTCCAGACGAGACGCGCTAGCCCA	1640
DB	1495	AGAGG----TCAGAAAGAAAGTGGCGACAGTTTAGCAACAGCTCAGACGCTTCCGACC	1550
QY	1641	CCCTGCACTGGGGAGAGAAACATCACAGCGTGGAGACCCCTACTCGATTTATACACA	1700
DB	1551	CTCTGTACAGGGGATGAGNACATCAGCAGTGTGAGAGCCCTTACATAGATTACAGCA	1610
QY	1701	CTGAGGATCTCTCAATGTATACGTGGCGGTCTACTCATGCTCAGCGCTGCAAGA	1760
DB	1611	TTTACGGATATCTACAAATGTGTACTTAGCAGTCTACTCCATTTGCCACGCGCTGCAAGA	1670
QY	1761	CATCCACTCTTGCACAAACCGGCAACGGGCTCTTTGCAAAACGGATCTTGTGAGATTTAA	1820
DB	1671	TATATATCTGTCTTACTTGGGAGAGGCTCTTTCACCAATGCTCTCTGTGAGACATCAA	1730
QY	1821	AAAAGTTGAGGCTGTCAGGTCTCAACCATCTGTGTCATCTGAAGTTTACAAACAGCAT	1880
DB	1731	GAAAGTTGAGGCTGTCAGGTCTCTGAAGCACCTTACGGCATCTAAACTTTACAAACATAT	1790
QY	1881	GGGTGAGCAGTTGACTTTGACGATCAAGTGACCTCAAGGGGAACTACACCATATCAA	1940
DB	1791	GGGGAGCAGGTGACCTTTGATGAGTGTGACCTTGTGGGAACTATTCATCATCAA	1850
QY	1941	CTGGCAGCTCTCCGAGAGAGTGAATCGGTGTTGTTTCCATGAGTGGGCAACTACACGC	2000
DB	1851	CTGGCAGCTCTCCGAGAGAGTGGCTCCATCGTGTTTAAGGAAGTCGGGTATTACACGT	1910
QY	2001	CTAGCTTAAGCCAGTGAACGACTCAACATCAAGCAAGAAAGAAATCTCTGGAGTGGCTT	2060
DB	1911	CTATGCCAAGAGGAGAAAGACTCTTTCATCAACAGGAGAAATCTCTGGAGTGGGT	1970
QY	2061	CTCAAAGTGGTTCCTTTCTCCAACTGCACTCGAGTGTGTGCCGGGACACAGGAAGG	2120
DB	1971	CTCAAGGAGTGGCTTTCTCCAACTGCACTCGAGTGTGTGCCGGGACACAGGAAGG	2030
QY	2121	GATCATCGAGGGGAGCCCACTGCTGCTTGAATGATGAGCATGTGAGAGGAGAT	2180
DB	2031	GATCATTTGAGGGGAGCCCACTGCTGCTTGAATGATGAGCATGTGAGAGGAGAT	2090
QY	2181	CAGTGATGAAACGATGCAAGTGCCTGTAACAAAGTCCCGAATGATTTCTGTCGATCA	2240
DB	2091	TAGTATGAGACAGATGCCAGTCTGTAAACAGTCCAGATGACTTTGTGTCATCA	2150
QY	2241	GAACCCACAGTCTGTCATCGCCAAAGGAGATCGAGTACTGTCTGTGACGAGCCCTTCG	2300
DB	2151	GAACCCACAGTCTGTCATCGCCAAAGGAGATCGAGTACTGTCTGTGACGAGCCCTTCG	2210
QY	2301	GATCGCTCTGACCATCTTGGCGTACTGGGCACTCTGATCAGCTCTCTGCTGCTGGGT	2360
DB	2211	GATCGCACTCACCTCTTGGCGGTGCTGGGCACTTCTCTGACAGCCCTTTGTCTGGGT	2270
QY	2361	CTTTCATCAAGTTGAGGAACACTCCCATCTGTAAGGCGCACCAACCGGAGTTGTCTTACT	2420

Db 2271 GTTATCAAGTTCCGCAACACACCACTTGTCAAGGCCACCAACGAGAGCTCTCTACCT 2330
Qy 2421 GGTGCTCTTCCTCCCTCATCTGCTGCTTCTCCAGCTCGCTCACTTCTATCGGCGAGCCGAG 2480
Db 2331 CCTCCTCTCTCCCTGCTCTGCTGCTTCTCCAGCTCCCTGTTCTTCTATCGGCGAGCCCA 2390
Qy 2481 GGACTGGACCTGTGCGCTCGGCAACCGGCTTTGGCATCAGCTTCGTCGTGTCATCTC 2540
Db 2391 GGACTGGACCTGTGCGCTCGGCAACCGGCTTTGGCATCAGCTTCGTCGTGTCATCTC 2450
Qy 2541 CTGCACTCTGTTGAAGACCAACCGGCTGTGCTGCTTCTCGAGGCCAAGATCCCAACGAG 2600
Db 2451 ATGCATCTGTTGAAGACCAACCGGCTGTGCTGCTTCTCGAGGCCAAGATCCCAACGAG 2510
Qy 2601 CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTTCCTGCTGCTGCTTCTGACCTT 2660
Db 2511 CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTTCCTGCTGCTGCTTCTGACCTT 2570
Qy 2661 GGTGCAAAATCGTCACTGCTGCTGCTGCTTACACCGGCTCCCTCCAGTACAGGAA 2720
Db 2571 CATGAGATGTCTGCTGCTGCTGCTTACACCGGCTCCCTCCAGTACAGGAA 2630
Qy 2721 CCATGAGTGGAGGACGAGTCACTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2780
Db 2631 CCAGGAGTGGAGGATGAGTCACTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2690
Qy 2781 GGGCTTCCTCATCGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2840
Db 2691 GGGCTTCCTCATCGGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2750
Qy 2841 GTCCGCTGAAGTCCGCGAATCTCAACGAGGCTAAGTTTCACTTCACTTCACTTCACTT 2900
Db 2751 GTCCGCGAAGTCCGCGAATCTCAATGAAGCCAAAGTTTCACTTCACTTCACTTCACT 2810
Qy 2901 CTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2960
Db 2811 CTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2870
Qy 2961 GTCCGCTGAAGTCCGCGAATCTCAACGAGGCTAAGTTTCACTTCACTTCACTTCACT 3020
Db 2871 CTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2930
Qy 3021 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3080
Db 2931 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2990
Qy 3081 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3140
Db 2991 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3050
Qy 3141 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3200
Db 3051 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3110
Qy 3201 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3260
Db 3111 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3165
Qy 3261 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3320
Db 3165 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3225
Qy 3321 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3380
Db 3225 CTTCAACAGTGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3280

RESULT 15
US-08-546-998-2
; Sequence 2, Application US/08546998
; Patent No. 6211244
; GENERAL INFORMATION:

APPLICANT: Van Wagenen, Bradford C.
APPLICANT: Moe, Scott T.
APPLICANT: Balandrin, Manuel F.
APPLICANT: DelMar, Eric G.
APPLICANT: Nemeth, Edward F.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,998
FILING DATE: October 23, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 215/304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 499-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3809 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 373...3606
OTHER INFORMATION:
US-08-546-998-2
Query Match 42.2%; Score 1745.2; DB 3; Length 3809;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;
Qy 501 CTCAGGCTATGTTCCAAACCAAGGCGCCAGAGAGGAGATCATATCTGCGAGGTCT 560
Db 423 CTCGCTCTAGCGGCGACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 482
Qy 561 CTTCCCAATACATCTTTCGAGTAGCGCCAAAGGATCAGGACTTAAATTCGAGACCGGAGGC 620
Db 483 CTTTCTCTATTTCATTTTGGAGTAGCAGCTAAAGATCAAGATCTCAAAATCAAGGCGGAGTC 542
Qy 621 GACAAATGTATTCGGTACAAATTTTCGAGCTTCGAGCTTCGAGCTTCGAGCTTCGAGCT 680
Db 543 TGTGAAATGTATCAGGTATTAATTTTCGCTGGGTTTCGCTGGGTTTCGCTGGGTTTCGCT 602
Qy 681 AATTGAAGAGATTAAACACAGATGATGACTTTTCCTGCCCAATATCACCTCGGATATCGCAT 740
Db 603 CATAGAGAGATTAACACAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 662
Qy 741 ATTTGACAGCTGTAAACACCGGTGTCCTCAAGGCGCTAGAGGCAACACTCAGCTTTTGGCCCA 800

Db 663 ATTGACACTGCAACACCGTTTCTAAGGCTTGAAGCCACCTGAGTTTGTGCTCA 722
QY 801 GAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAACTGCTCTGACCATATCCCATC 860
Db 723 AAACAAAATTTGATTTTGAACCTTGTATGAGTTCTGCAACTCTGAGAGCAATTCCTC 782
QY 861 CACAATAGCAGTGGTGGGGCAACCGGTGAGAAATCTCCAGGTGTGGCCAAATCTATT 920
Db 783 TAGGATTTGCTGGTGGAGCACTGGCTCAGGCTCTCCAGCGAGTGGCAATCTGCT 842
QY 921 GGATTTATTTTACATTTCCAGCTAGCTATGCTCTCTGAGCAGGCTGCTCAGAAACAA 980
Db 843 GGGGCTCTTCTACATTTCCACAGTCACTGATGATGATGATGATGATGATGATGATGAT 902
QY 981 GAATGAGTACAGGCTCTCTGAGGACCATCCCAATGATGATGATGATGATGATGATGAT 1040
Db 903 GAATCAATTTCAAGTCTTTCTCCGAACCATCCCAATGATGATGATGATGATGATGATGAT 962
QY 1041 GGCAGATCATCGAGCACTTCCAGTGAACCTGGGTGGAACTCCGAGCGACGATGA 1100
Db 963 GGCAGACATCATCGAGTATTCCGCTGGAATGGGTGGGCAAAATTCAGCTGATGAGA 1022
QY 1101 CTATGCGCCCGCAGGATTTGACAAAGTTCGGGAGAGGCGGTAAAGAGGACATCTGAT 1160
Db 1023 CTATGGGCGCGGGGATTTGAGAAATTCGAGAGAACTGAGGAAAGGATATCTGAT 1082
QY 1161 TGACTTCACTGAGATGATCTCTCAGTACTACACCGAGAGAGTGGAGTTTCATCGCCGA 1220
Db 1083 CGACTTCACTGAGTACTCTCCAGTACTCTGATGAGGAGAGATCCAGCATGTGTAGA 1142
QY 1221 CGTATCCAGAACTCTCTCGGCAAGGTATCTGTGTCTTCTCAATGGCCCGACCTGGA 1280
Db 1143 GGTGATTTCAAAATTCACGCGCAAGTATCTGTGGTTTCTCAGTGGCCCGAGATCTTGA 1202
QY 1281 GCGCTCATCCAGGAGATAGTTTCGGAGAAATCATCCAGTCTGGCTGGCCAGGGA 1340
Db 1203 GCGCTCATCAAGGAGATTTGCGGCGCAATATACGGGCAAGATCTGGCTGGCCAGGGA 1262
QY 1341 GCGTTGGCCAGCTCTCTGCTCATTTCCAGGAGAGTACTTCCAGTGGTGGCGGAC 1400
Db 1263 GCGCTGGGCGAGCTCTCTGCTGATCGCATGCTCAGTACTTCCAGTGGTGGCGGAC 1322
QY 1401 CATCGCTTCGCTCAGGCGGGGCGGTATCCAGGTTCAACAGTTCTGAGGAGGT 1460
Db 1323 CATGGAATTCGCTCAGAGCTGGGCGAGATCCAGGCTTCGGGGAATTCCTGAAGAGGT 1382
QY 1461 CCACCCAGCAGGCTCTCGAACAATGGGTTTGTCAAGGAGTTCTGGGAGGAGCTTCAA 1520
Db 1383 CCATCCAGGAGTCTGTCCAATGGTTTGTCCAAAGGAGTTTGGGAAGAAACATTAA 1442
QY 1521 CTGCTACTTCCAGGAGAGACCTCAGCAGCTGAAGAAATCCAGAGTGGCTCGCAGCG 1580
Db 1443 CTGCGACCTTCCAGA-----AGGTGCAAAAGACCTTTACCTGTGGACACCTTTCTG 1494
QY 1581 ACCGGCGGCTCAAGGGAGCGGTCCAAAGCGGGGAATCCAGACGAGCGCTACGCCA 1640
Db 1495 AGAGG-----TCAGGAAGAAAGTGGCGCAGGTATTAGCAACAGCTCGACAGCTTCCGACC 1550
QY 1641 CCCCTGCACTGGGAGGAGAAACATCAGCAGGCTGGAGACCCCTTACCTGGATTTACACA 1700
Db 1551 CCTCTGTACAGGGGATGAGAAACATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1610
QY 1701 CCGTAGGATCTCTCAATGATAGTGGCGCTTACTCTTCTGCTCAGCGCTTGCAGA 1760
Db 1611 TTTACGGATATCTCAATGATGATTTAGAGTCTACTCTTCTGCTTCTGCTTCTGAGAGA 1670
QY 1761 CATCCACTTTGCAACCGGACCGGATCTTTGCAAAAGGATCTTTGTGAGATATTAA 1820
Db 1671 TATATATACCTTCTTACCTGGGAGAGGCTTTTACCAATGGCTCTGTGAGAGATCA 1730
QY 1821 ABAAGTTAGGCTCGCAGGCTCTCAACCATCTGCTGATCTGAGTTTACCAAGCAT 1880

Db 1731 GAAAGTTAGGCTGGCAGGTCTGAAGCAGCTACGGCATCTAACTTTTCAAAACAATAT 1790
QY 1881 GGGTGAAGCAGTTGACTTTTGAACGATCAAGGTGACCTCAAGGGAACTACACCATTTCAA 1940
Db 1791 GGGGAGCAGGTGACCTTTGATGAGTGGTGACCTGGTGGGAACTATTTCACATCAA 1850
QY 1941 CTGCGACTCTCGCGAGAGATGAATCGGTGTTGTTCCATGAGTGGGCAACTACAAACG 2000
Db 1851 CTGSCACTCTCCCGAGAGATGCTCCATCGTGTAAAGGAAGTGGGTATTACAACT 1910
QY 2001 CTAGCTTAAGCCAGTGAACGACTCAACATCAAGAAAGAAATCTCTGAGTGGCTT 2060
Db 1911 CTATGCCAAGAGGAGAAAGACTCTTCATCAAGAGGAGAAATCTCTGAGTGGCTT 1970
QY 2061 CTCCAAAGTGGTTCTTTCTCCAACTGCAGTGCAGACTGTGTCCGGGACCAAGGAGG 2120
Db 1971 CTCAGGAGGTGCTCTTCTCAACTGCAGCGAGACTGCTGGCAGGAGCCAGGAAG 2030
QY 2121 GATCATCGAGGAGGACCCACCTGCTGCTGTTGAATGCAATGGCATGTGCAGAGGAGT 2180
Db 2031 GATCATTTAGGGGAGGACCCACCTGCTGCTGAGTGTGGAGTGTCTGATGGGAGTA 2090
QY 2181 CAGTGATGAAGACGATGCGAGTGTCAAGAGTCCCGAATGATTTCTGTGCGATCA 2240
Db 2091 TAGTGATGACAGATGCCAGTGCCTGTAAAGTCCAGATGACTTCTGTCCAAATGA 2150
QY 2241 GAACCAACATCTGCTGATCGCCAGGAGATCGAGTACTGTCTGTGAGCGAGCCCTCG 2300
Db 2151 GAACCAACATCTGCTGATTTGCCAAGGAGATCGAGTTTCTGTCTGTGAGCGAGCCCTCG 2210
QY 2301 GATCGCTGACCATCTTCCCGTACTGGGCATCTGATCACTCTCTGCTGCTGGGGT 2360
Db 2211 GATCGCACTCACCTCTTTCGCGTGTGGGCAATTTCTCGAGAGCCCTTGTGCTGGTGT 2270
QY 2361 CTTTCATCAAGTTTCAGAAACACTCCCATCGTGAAGGACCAACCGGAGTTGTCTACTCT 2420
Db 2271 GTTTATCAAGTTTCGCAACACACCATTTGTCAAGGCCACCAACCGAGACTCTCTACTCT 2330
QY 2421 GCTGCTCTTCTCCTCATCTGCTGCTTCTCAGCTCGCTCATCTTCATCGGAGGCCAG 2480
Db 2331 CTTCTCTTCTCCTGCTGCTGCTTCTCCAGTCCCTGTTCTTCATCGGAGGCCCA 2390
QY 2481 GGACTGACCTGCTGCTCGCCAAACCGGCTTTGGCATCAGCTGCTGCTGTGATCTC 2540
Db 2391 GGACTGAGCTGCTGCTGGCCAGCGGCTTTGGCATCAGCTGCTGCTGTGATCTC 2450
QY 2541 CTGCATCTCTGTGAAGCAACCGGCTGCTGCTGCTTTGAGGCAAGATCCCCACAG 2600
Db 2451 ATGCATCTCTGGTGAAGCAACCGGCTGCTGCTGCTTTGAGGCAAGATCCCCACAG 2510
QY 2601 CCTCCACCGCAGTGGTGGGCTCAACCTGAGTCTCTCTGCTGCTTCTCTGATCTCT 2660
Db 2511 CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTCTCTGCTGCTTCTCTGACCTT 2570
QY 2661 GGTGCAAAATCTGCTCAGCTGATCATCTGGCTCTACACCGGCGCTCCCTCCAGCTACAGGAA 2720
Db 2571 CATGCAGATTGTCATCTGTGTGATCTGGCTCTACACCGGCGCTCCCTCAAGCTACCGCAA 2630
QY 2721 CCATGAGCTGGAGGACGAGTCTTCTGATCACTGCGAGGAGGCTGCTCATGGCGT 2780
Db 2631 CCAGGAGCTGGAGGATGAGTCTTCTGATCACTGCTGCTGCTGCTGCTGCTGCTGCT 2690
QY 2781 GGGCTTCTCTCATCGGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2840
Db 2691 GGGCTTCTCTCATCGGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2750
QY 2841 GTCCCTTAAGCTGCCGAGAACTTCAACGAGGCTAAGTTCATCACTTCCAGATGTTGAT 2900
Db 2751 GTCCCGAAGCTGCCGAGAACTTCAATGAAGCCAAAGTTTCATCAGCTTCCAGATGCTCAT 2810
QY 2901 CTTCTTCTCATGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2960
Db 2811 CTTCTTCTCATGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2870

Search completed: November 17, 2004, 07:02:06
Job time : 339 secs

This Page Blank (uspio)

Qy	61	GCCATTACAGGAACATGCACCTACATCTGTGTTAATGAAATATTGTCAAGTATATCTGAAGGT	120
Db			
Qy	61	GCCATTACAGGAACATGCACCTACATCTGTGTTAATGAAATATTGTCAAGTATATCTGAAGGT	120
Db			
Qy	121	TATTAAATATTTCTGCAAGGATGGCTTCACGAGAAATCAATTCGTCACAGTTTCCCAT	180
Db			
Qy	121	TATTAAATATTTCTGCAAGGATGGCTTCACGAGAAATCAATTCGTCACAGTTTCCCAT	180
Db			
Qy	181	GTCAATTGTATGAATACTGACCAAGGATGTATAAATAAGCAACAAGCTGAGGACCA	240
Db			
Qy	181	GTCAATTGTATGAATACTGACCAAGGATGTATAAATAAGCAACAAGCTGAGGACCA	240
Db			
Qy	241	GTTCACCCCTTCTTGGAGCATACGATCAACCCCTGAAGGATGAAGACATTTGAGGAGAA	300
Db			
Qy	241	GTTCACCCCTTCTTGGAGCATACGATCAACCCCTGAAGGATGAAGACATTTGAGGAGAA	300
Db			
Qy	301	ATGGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCATTTACAAAGTAA	360
Db			
Qy	301	ATGGGGATTGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCATTTACAAAGTAA	360
Db			
Qy	361	GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAGGAA	420
Db			
Qy	361	GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAGGAA	420
Db			
Qy	421	CAGAGACAGGGCTGCACAATGGCTCAGCTTCACCTGCCAATCTTTATTTCTTGGATTTACA	480
Db			
Qy	421	CAGAGACAGGGCTGCACAATGGCTCAGCTTCACCTGCCAATCTTTATTTCTTGGATTTACA	480
Db			
Qy	481	CTCCTACAGTCGTACAAATGTCTCAGGATATGGTCCAAACCAAGGGCCACAGAAAGGA	540
Db			
Qy	481	CTCCTACAGTCGTACAAATGTCTCAGGATATGGTCCAAACCAAGGGCCACAGAAAGGA	540
Db			
Qy	541	GACATCATACTGGAGAGTCTCTTCCCAATACACTTTGGAGTAGCGCGCAAGGATCAGGAC	600
Db			
Qy	541	GACATCATACTGGAGAGTCTCTTCCCAATACACTTTGGAGTAGCGCGCAAGGATCAGGAC	600
Db			
Qy	601	TTAAATTCGACACGGAGGGACAAATGTATTCGGTACAAATTTTCAGAGCTTCCGATGG	660
Db			
Qy	601	TTAAATTCGACACGGAGGGACAAATGTATTCGGTACAAATTTTCAGAGCTTCCGATGG	660
Db			
Qy	661	CTCCAGCGCATGATATTTCGAAATGGAAGAGATTAAACACAGTAGTAGCTTTCTTCCGCCAAT	720
Db			
Qy	661	CTCCAGCGCATGATATTTCGAAATGGAAGAGATTAAACACAGTAGTAGCTTTCTTCCGCCAAT	720
Db			
Qy	721	ATCACCTGGGATATCCGATATTTTGACACGTTGTAACACCGTGTCCAAAGGCGCTAGAGGCA	780
Db			
Qy	721	ATCACCTGGGATATCCGATATTTTGACACGTTGTAACACCGTGTCCAAAGGCGCTAGAGGCA	780
Db			
Qy	781	ACACTCAGCTTTGTGGCCCGAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC	840
Db			
Qy	781	ACACTCAGCTTTGTGGCCCGAGAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC	840
Db			
Qy	841	TGCTCTGACCATATCCCATCCAAATAGCAGTGGTCCGGGGCAACCGGGTCAGGAATCTCC	900
Db			
Qy	841	TGCTCTGACCATATCCCATCCAAATAGCAGTGGTCCGGGGCAACCGGGTCAGGAATCTCC	900
Db			
Qy	901	ACGGCTGTGGCCCAATCTATTGGGATTTTACATTCACAGGTCAGCTATGCTCTCTCG	960
Db			
Qy	901	ACGGCTGTGGCCCAATCTATTGGGATTTTACATTCACAGGTCAGCTATGCTCTCTCG	960
Db			
Qy	961	AGCAGGCTGTACGACAAAGAAATGAGTAAAGGCTTCTCTGAGGACCAATCCCAATGAT	1020
Db			
Qy	961	AGCAGGCTGTACGACAAAGAAATGAGTAAAGGCTTCTCTGAGGACCAATCCCAATGAT	1020
Db			
Qy	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
Db			
Qy	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
Db			
Qy	1081	ACCTGTCAGCCGACGATGACTATGGCCGCCACGACATTGACAAAGTTCCGGGAGGAGGCC	1140
Db			
Qy	1081	ACCTGTCAGCCGACGATGACTATGGCCGCCACGACATTGACAAAGTTCCGGGAGGAGGCC	1140
Db			

QY	1141	GTTAAGAGGACATCTGTTATTTGACTTCAGTGAAGATGATCTCTCAGTACTACACCCAGAAG	1201
DB	1141	GTTAAGAGGACATCTGTTATTTGACTTCAGTGAAGATGATCTCTCAGTACTACACCCAGAAG	1201
QY	1201	CAGTTGAGATTTCATCGCGCAGCTCATCCAGAACTCTCGGCCCAAGGTCACTCGTGGTCTTC	1260
DB	1201	CAGTTGAGATTTCATCGCGCAGCTCATCCAGAACTCTCGGCCCAAGGTCACTCGTGGTCTTC	1260
QY	1261	TCCAATGGCCCCGACTCTGGAGCGCGCTCATCCAGGAGATGATTCCGAGAAACATCACCCGAT	1320
DB	1261	TCCAATGGCCCCGACTCTGGAGCGCGCTCATCCAGGAGATGATTCCGAGAAACATCACCCGAT	1320
QY	1321	CGGATCTGGTGGCCACGAGGGTTGGCGCAGCTCTTCGCTCATTCGCCAAGCCAGAGTAC	1380
DB	1321	CGGATCTGGTGGCCACGAGGGTTGGCGCAGCTCTTCGCTCATTCGCCAAGCCAGAGTAC	1380
QY	1381	TTCCACGTGTGGCGGCACCATCGGCTTCGCTCTCAGGGCGGGCGTATCCCAAGGTTTC	1440
DB	1381	TTCCACGTGTGGCGGCACCATCGGCTTCGCTCTCAGGGCGGGCGTATCCCAAGGTTTC	1440
QY	1441	AACAAAGTTCCTGAAGAGGTTCCACCCACAGCAGGTCTCGACAAATGGGTTTGTCCAGGAG	1500
DB	1441	AACAAAGTTCCTGAAGAGGTTCCACCCACAGCAGGTCTCGACAAATGGGTTTGTCCAGGAG	1500
QY	1501	TTCTGGGAGGAGACCTTTCAACTGCTACTTCACCGAGAAGACCCCTGACGCAGCTGGAAGAAT	1560
DB	1501	TTCTGGGAGGAGACCTTTCAACTGCTACTTCACCGAGAAGACCCCTGACGCAGCTGGAAGAAT	1560
QY	1561	TCCMAGTGCCCTCGACGAGCCGCGGCTCAAGGGAGCGGCTCCAAAGCGGGGAATCTCC	1620
DB	1561	TCCAAGTGCCCTCGACGAGCCGCGGCTCAAGGGAGCGGCTCCAAAGCGGGGAATCTCC	1620
QY	1621	AGACGGACAGCCCTAGCCACCCCTGCACCTGGGGAGGAGAAATCACACGCGTGGAGACC	1680
DB	1621	AGACGGACAGCCCTAGCCACCCCTGCACCTGGGGAGGAGAAATCACACGCGTGGAGACC	1680
QY	1681	CCCTACTGGAATTATACACACTGAGGATCTCCTACAATGTATATCGTGGCCGTTCTACTCC	1740
DB	1681	CCCTACTGGAATTATACACACTGAGGATCTCCTACAATGTATATCGTGGCCGTTCTACTCC	1740
QY	1741	ATTGCTCACGCCCTGCAGACATCCACTCTTGCAACCCGGCACCGGCATCTTTGCAAAAC	1800
DB	1741	ATTGCTCACGCCCTGCAGACATCCACTCTTGCAACCCGGCACCGGCATCTTTGCAAAAC	1800
QY	1801	GGATCTTGTGCAGATATATAAAAGTTGAGCCCTGGCAGGTCTCTCAACCATCTGCTGCAT	1860
DB	1801	GGATCTTGTGCAGATATATAAAAGTTGAGCCCTGGCAGGTCTCTCAACCATCTGCTGCAT	1860
QY	1861	CTGAAGTTTACCAACAGCATGGGTGAGCAGTTGACTTTGACGATCAAGGTACCTCAAG	1920
DB	1861	CTGAAGTTTACCAACAGCATGGGTGAGCAGTTGACTTTGACGATCAAGGTACCTCAAG	1920
QY	1921	GGGAATPACACCATTTCAACTGGCAGCTCTCCGACAGAGGATGAATCGGTGTTGTTCCAT	1980
DB	1921	GGGAATPACACCATTTCAACTGGCAGCTCTCCGACAGAGGATGAATCGGTGTTGTTCCAT	1980
QY	1981	GAGTGGGCAACTACAAACGCTTACGCTTAAGCCCAAGTGAACGATCAACATCAACGAAAAG	2040
DB	1981	GAGTGGGCAACTACAAACGCTTACGCTTAAGCCCAAGTGAACGATCAACATCAACGAAAAG	2040
QY	2041	AAATCTCTCGAGTGGCTTCTCCAAGTGGTTCTTCTTCCAACTGCAGTGCAGACTGT	2100
DB	2041	AAATCTCTCGAGTGGCTTCTCCAAGTGGTTCTTCTTCCAACTGCAGTGCAGACTGT	2100
QY	2101	GTGCGGGCACCAAGAGGGGATCATCGAGGGGGAGCCCACTGCTCTTGAATGCATG	2160
DB	2101	GTGCGGGCACCAAGAGGGGATCATCGAGGGGGAGCCCACTGCTCTTGAATGCATG	2160
QY	2161	GCAATGTCAGAGGAGATTCACTGATGAACAGATGCAAGTGCCTGTACAAAGTGCCTG	2220
DB	2161	GCAATGTCAGAGGAGATTCACTGATGAACAGATGCAAGTGCCTGTACAAAGTGCCTG	2220
QY	2221	AATGATTTCTGTCGATGAGAAACCAACGCTCTGTGATCGCCAAAGAGATTCGAGTACCTG	2280

2221	Db	GATTTCTGGTTCGAATGAAACCAACACAGTCGTGATATCCCAAGAGGATTCGAGTACCTG	2280
2281	QY	TCGTGACGAGAGCCCTTCGGGATTCGTCTGACCACTCTTCGCCGTACTCGGSCATCTCTGATC	2340
2281	Db	TCGTGACGAGAGCCCTTCGGGATTCGTCTGACCACTCTTCGCCGTACTCGGSCATCTCTGATC	2340
2341	QY	ACCTCCTTCGTGCTGGGGTCTTCATCAAGTTCAGGAACACTCCCACTCGTGAAGGCCACC	2400
2341	Db	ACCTCCTTCGTGCTGGGGTCTTCATCAAGTTCAGGAACACTCCCACTCGTGAAGGCCACC	2400
2401	QY	AACCGGAGTTGCTTACCTGCTGCTCTTCCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC	2460
2401	Db	AACCGGAGTTGCTTACCTGCTGCTCTTCCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC	2460
2461	QY	ATCTTCATCGCGAGAGCCAGGAGCTGGAACCTGTTCGGCTCGGCCAAACCGGCTTTGGGATC	2520
2461	Db	ATCTTCATCGCGAGAGCCAGGAGCTGGAACCTGTTCGGCTCGGCCAAACCGGCTTTGGGATC	2520
2521	QY	AGCTTCGTCTGTGCATCTCTCTGCATCTCTGGTGAAGACCAACCGGCTGTCTGCTGCTTCTC	2580
2521	Db	AGCTTCGTCTGTGCATCTCTCTGCATCTCTGGTGAAGACCAACCGGCTGTCTGCTGCTTCTC	2580
2581	QY	GAGGCAAGATCCCCACAGCCTCCACCGCAAGTGGTGGGCTCAACTCGAGTTCCTC	2640
2581	Db	GAGGCAAGATCCCCACAGCCTCCACCGCAAGTGGTGGGCTCAACTCGAGTTCCTC	2640
2641	QY	CTGGTCTTCTCTGCACTCTGCTGGTGAATTCGTTCACCTGCATCATCTGGCTCTACACGGG	2700
2641	Db	CTGGTCTTCTCTGCACTCTGCTGGTGAATTCGTTCACCTGCATCATCTGGCTCTACACGGG	2700
2701	QY	CTCTCCTCCAGCTACAGGAACCATGAGCTGGAGGAGAGGTTCATCTTCATCACTCGCAC	2760
2701	Db	CTCTCCTCCAGCTACAGGAACCATGAGCTGGAGGAGAGGTTCATCTTCATCACTCGCAC	2760
2761	QY	GAGGCTCGCTCATGGGCTGGGCTTCCTCATCGGCTACACCTGCCTCTCGCGGCCATC	2820
2761	Db	GAGGCTCGCTCATGGGCTGGGCTTCCTCATCGGCTACACCTGCCTCTCGCGGCCATC	2820
2821	QY	TGCTTCTTCTTCGCCCTTCAAGTCCCGTAAAGCTCCCGAGAACTTCAACGAGGCTAAGTTC	2880
2821	Db	TGCTTCTTCTTCGCCCTTCAAGTCCCGTAAAGCTCCCGAGAACTTCAACGAGGCTAAGTTC	2880
2881	QY	ATCACCTTCAGCATGTGTGATCTTCTCATTCGTCTGGAATCTTCCTTCATCCCGGCTATGTC	2940
2881	Db	ATCACCTTCAGCATGTGTGATCTTCTTCATCGTCTGGAATCTTCCTTCATCCCGGCTATGTC	2940
2941	QY	AGCACCTACGGCAAGTTTGTTCGGCGCTGGAGGTGATTGCCATCTTGGGCTCCAGCTTC	3000
2941	Db	AGCACCTACGGCAAGTTTGTTCGGCGCTGGAGGTGATTGCCATCTTGGGCTCCAGCTTC	3000
3001	QY	GGGCTGCTGGGCTGCATTACTTCAACAAGTGTATCATATCTGTTCGAAGCGTGCCTG	3060
3001	Db	GGGCTGCTGGGCTGCATTACTTCAACAAGTGTATCATATCTGTTCGAAGCGTGCCTG	3060
3061	QY	AACACCATCGAGAGTTCGGCTCAGACGGCGGCCCAACGCTTCAAGTGGGGGCCCGG	3120
3061	Db	AACACCATCGAGAGTTCGGCTCAGACGGCGGCCCAACGCTTCAAGTGGGGGCCCGG	3120
3121	QY	GCCACCTCTCGGCGCAGCGCGGCTTCGCAAGCGTTCAGACGCTTCAGACGCTGTTCGCGTCCACC	3180
3121	Db	GCCACCTCTCGGCGCAGCGCGGCTTCGCAAGCGTTCAGACGCTTCGCGTCCACC	3180
3181	QY	ATCTCTCTCGCCCGCTCTCCACTCGGGCGCGGCTCACCATGAGATGACAGCGCTGC	3240
3181	Db	ATCTCTCTCGCCCGCTCTCCACTCGGGCGCGGCTCACCATGAGATGACAGCGCTGC	3240
3241	QY	AGCACGAGAAAGTCAAGTTCGGCAGCGGCAACGCTCAACCTGTCTGCTCAGCTTCGAGGAG	3300
3241	Db	AGCACGAGAAAGTCAAGTTCGGCAGCGGCAACGCTCAACCTGTCTGCTCAGCTTCGAGGAG	3300
3301	QY	ACAGGCGGATACGGCACCTCTACGCGGACGGCCCGCAGACAGAACTCGCGGATGCGCGC	3360

[illegible]

```

RESULT 2
US-10-125-792-1
; Sequence 1, Application US/10125792
; Publication No. US20030051259A1
; GENERAL INFORMATION:
; APPLICANT: MariCal
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-007
; CURRENT APPLICATION NUMBER: US/10/125,792
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392

```

; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-792-1

Query Match 100.0%; Score 4134; DB 14; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGGTTCGTCGCTCAGTCCAGTCTCCTCCAGTGCAAAATGAGAAATGGTGGTC 60
Db |
QY 1 AATTCGGTTCGTCGCTCAGTCCAGTCTCCTCCAGTGCAAAATGAGAAATGGTGGTC 60
Db |
QY 61 GCCATTACAGGAACATGCATCATCTGTCTTAATGAATAATGTGCAAGTATCTGAAGT 120
Db |
QY 61 GCCATTACAGGAACATGCATCATCTGTCTTAATGAATAATGTGCAAGTATCTGAAGT 120
Db |
QY 121 TATTAATAATGTTTCTGCAAGATGGCTTACAGGAATCAATCTGCAAGTATCTCCATT 180
Db |
QY 121 TATTAATAATGTTTCTGCAAGATGGCTTACAGGAATCAATCTGCAAGTATCTCCATT 180
Db |
QY 181 GTCAATGTATGAATACTGACCAAGAGGATGTAACAAATGGAACAAAGCTGAGGACCAC 240
Db |
QY 181 GTCAATGTATGAATACTGACCAAGAGGATGTAACAAATGGAACAAAGCTGAGGACCAC 240
Db |
QY 241 GTTCAACCTTCTTGAGCATACGATCAACCTGTAAGAGAGATGGAAGACTTGAGAGGAA 300
Db |
QY 241 GTTCAACCTTCTTGAGCATACGATCAACCTGTAAGAGAGATGGAAGACTTGAGAGGAA 300
Db |
QY 301 ATGCGGATTCATCTCCAGAGTTCCTGTAAGAGGATCCCTCACCATTAACAAGATAA 360
Db |
QY 301 ATGCGGATTCATCTCCAGAGTTCCTGTAAGAGGATCCCTCACCATTAACAAGATAA 360
Db |
QY 361 GCAGAAATCCTCCAGGATCCTCTGTAAGAGGATCCCTCACCATTAACAAGATAA 420
Db |
QY 361 GCAGAAATCCTCCAGGATCCTCTGTAAGAGGATCCCTCACCATTAACAAGATAA 420
Db |
QY 421 CAGAGACAGGCTGCACATGCTCAGTTCAGTCCAGTCTTATTTCTGGATTTACA 480
Db |
QY 421 CAGAGACAGGCTGCACATGCTCAGTTCAGTCCAGTCTTATTTCTGGATTTACA 480
Db |
QY 481 CTCTCAGTCTGACATGCTCAGGATGATGTTCCAAACCAAGGCTCCAGGATGATGAT 540
Db |
QY 481 CTCTCAGTCTGACATGCTCAGGATGATGTTCCAAACCAAGGCTCCAGGATGATGAT 540
Db |
QY 541 GACATCATCTGGAGTCTCTCCCAATACATCTGAGTACGCTGAGTACGCTGAGTACG 600
Db |
QY 541 GACATCATCTGGAGTCTCTCTCCCAATACATCTGAGTACGCTGAGTACGCTGAGTACG 600
Db |
QY 601 TTAATAATCGAGACGGAGGCAAAATGATTCGCTGATCAATTTCTGAGGCTTCGATGG 660
Db |
QY 601 TTAATAATCGAGACGGAGGCAAAATGATTCGCTGATCAATTTCTGAGGCTTCGATGG 660
Db |
QY 661 CTCAGCGATGATATTCGCAATGAGAGATTAACAAGATGATGATCTCTGCGCCAAAT 720
Db |
QY 661 CTCAGCGATGATATTCGCAATGAGAGATTAACAAGATGATGATCTCTGCGCCAAAT 720
Db |
QY 721 ATCACTCGGATATCGCATATTTGACAGTGTAAACAGGCTGAGGCA 780
Db |
QY 721 ATCACTCGGATATCGCATATTTGACAGTGTAAACAGGCTGAGGCA 780
Db |
QY 781 ACACCTGAGTCTTGGGCCAGAAACAAATCGATCGCTGAACATGATGATGATGATGAT 840
Db |
QY 781 ACACCTGAGTCTTGGGCCAGAAACAAATCGATCGCTGAACATGATGATGATGATGAT 840
Db |
QY 841 TGCTCTGACCATATCCATCCCAATAGAGTGGTGGGGCAACCGGTCAGGAATCTCC 900
Db |

Db 841 TGCTCTGACCATATCCCATCCAAATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900
QY 901 ACGGCTGTGGCCAAATCTATTGGGATTTATTTATCATTTCCACAGGTTCAGCTATGCTCTCTCG 960
Db |
QY 901 ACGGCTGTGGCCAAATCTATTGGGATTTATTTATCATTTCCACAGGTTCAGCTATGCTCTCTCG 960
Db |
QY 961 AGCAGGCTGTCTGAGCAACAAGATGAGTCAAGGCTTCTGAGGACCATCTCCCAATGAT 1020
Db |
QY 961 AGCAGGCTGTCTGAGCAACAAGATGAGTCAAGGCTTCTGAGGACCATCTCCCAATGAT 1020
Db |
QY 1021 GAGCAACAGGCTGAGGCTGAGTATGAGGCTTCCAGTGGAACTGGGTGGGA 1080
Db |
QY 1021 GAGCAACAGGCTGAGGCTGAGTATGAGGCTTCCAGTGGAACTGGGTGGGA 1080
Db |
QY 1081 ACCCTGCGAGCGATGATATGCGCCCGCCAGGCAATGCAAGTTCGCGGAGGAGGCC 1140
Db |
QY 1081 ACCCTGCGAGCGATGATATGCGCCCGCCAGGCAATGCAAGTTCGCGGAGGAGGCC 1140
Db |
QY 1141 GTTAAGAGGACATCTCTGATTTGACTTCAGTGAGTATCTCTCAGTACTACACCCAGAAG 1200
Db |
QY 1141 GTTAAGAGGACATCTCTGATTTGACTTCAGTGAGTATCTCTCAGTACTACACCCAGAAG 1200
Db |
QY 1201 CAGTTGAGTTCATCGCGGACGTCATCCAGAACTCTCTCGGCCAAGGTTCATCGTGTCTTC 1260
Db |
QY 1201 CAGTTGAGTTCATCGCGGACGTCATCCAGAACTCTCTCGGCCAAGGTTCATCGTGTCTTC 1260
Db |
QY 1261 TCCAAATGGCCCGACCTGAGGCGCTCATCCAGGAGTATGTTGGAGAAACATCAACCGAT 1320
Db |
QY 1261 TCCAAATGGCCCGACCTGAGGCGCTCATCCAGGAGTATGTTGGAGAAACATCAACCGAT 1320
Db |
QY 1321 CGGATCTGGTTCGCGGACGAGGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Db |
QY 1321 CGGATCTGGTTCGCGGACGAGGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Db |
QY 1381 TTCAACCTGTCGCGGACCATCGGCTTCGCTCTCAGGCGGGGGGTATTCACAGGTTTC 1440
Db |
QY 1381 TTCAACCTGTCGCGGACCATCGGCTTCGCTCTCAGGCGGGGGGTATTCACAGGTTTC 1440
Db |
QY 1441 AACAGTTCCTGAGGAGGCTCCACCCAGCAGGCTCTCGACAAATGGTGTTCACAGGAG 1500
Db |
QY 1441 AACAGTTCCTGAGGAGGCTCCACCCAGCAGGCTCTCGACAAATGGTGTTCACAGGAG 1500
Db |
QY 1501 TTCTGGGAGGAGACCTTCAACTGCTACTTCCAGGAGAGACCTCTGACGAGCTGAAAGAT 1560
Db |
QY 1501 TTCTGGGAGGAGACCTTCAACTGCTACTTCCAGGAGAGACCTCTGACGAGCTGAAAGAT 1560
Db |
QY 1561 TCCAAAGTGGCTGCGAGGACCGGCTCAGGAGGACGGCTCCAGGCGGGGAACTCC 1620
Db |
QY 1561 TCCAAAGTGGCTGCGAGGACCGGCTCAGGAGGACGGCTCCAGGCGGGGAACTCC 1620
Db |
QY 1621 AGACGACAGGCTTACGCCACCTCTGACCTGGGAGGAGAACATCAACAGCTGGAGACC 1680
Db |
QY 1621 AGACGACAGGCTTACGCCACCTCTGACCTGGGAGGAGAACATCAACAGCTGGAGACC 1680
Db |
QY 1681 CCCTACCTGATATATACACCTGAGGATCTCTTCAATGATATACGTTGGCGCTCTACTCC 1740
Db |
QY 1681 CCCTACCTGATATATACACCTGAGGATCTCTTCAATGATATACGTTGGCGCTCTACTCC 1740
Db |
QY 1741 ATTCTCAGCGCTGCAAGACATCCACTTTTGCAAAACCGGCGGAGCTCTTTGCAAAAC 1800
Db |
QY 1741 ATTCTCAGCGCTGCAAGACATCCACTTTTGCAAAACCGGCGGAGCTCTTTGCAAAAC 1800
Db |
QY 1801 GGATCTTTGTCAGATATTTAAAGATTTGAGGCTTGGAGCTCTCAGGCTCTCTCAACATCTGTCAT 1860
Db |
QY 1801 GGATCTTTGTCAGATATTTAAAGATTTGAGGCTTGGAGCTCTCTCAACATCTGTCAT 1860
Db |
QY 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTGACCTTTGACGATCAAGTCAAGTCAAG 1920
Db |
QY 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTGACCTTTGACGATCAAGTCAAGTCAAG 1920
Db |
QY 1921 GGGAACTACACCATTTCAACTGGCAGCTCTCCGACAGGATGAATCGGTGTTGTTCCAT 1980
Db |
QY 1921 GGGAACTACACCATTTCAACTGGCAGCTCTCCGACAGGATGAATCGGTGTTGTTCCAT 1980
Db |

RESULT 3

US-10-125-778-1
; Sequence 1, Application US/10125778
; Publication No. US20030082574A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-005
; CURRENT APPLICATION NUMBER: US/10/125,778
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-778-1

Query Match 100.0%; Score 4134; DB 14; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AATTCGGTTCGTCGCGTTCAGTCCAGTCTCTCCAGTGCAGTAAATGAGAAATGGTGTTC	60
DB	1	AATTCGGTTCGTCGCGTTCAGTCCAGTCTCTCCAGTGCAGTAAATGAGAAATGGTGTTC	60
QY	61	GCATTACAGGAACATGCACTACATCTGTGTTAAATGAATATGTCAATATCTCAAGGT	120
DB	61	GCATTACAGGAACATGCACTACATCTGTGTTAAATGAATATGTCAATATCTCAAGGT	120
QY	121	TATTAATAATGTTCTCAGAGTGGTTCACAGGAATCAATCTGCAGTCTTCCCAT	180
DB	121	TATTAATAATGTTCTCAGAGTGGTTCACAGGAATCAATCTGCAGTCTTCCCAT	180
QY	181	GTCAATGTATGAATACTGACCAAGGGATGTAAACAAATGGAACAAAGCTGAGGACCAC	240
DB	181	GTCAATGTATGAATACTGACCAAGGGATGTAAACAAATGGAACAAAGCTGAGGACCAC	240
QY	241	GTTCCACCTTCTTGAGGATAGTCAACCTGAGGAGATGGAAGCTTCAGAGGAA	300
DB	241	GTTCCACCTTCTTGAGGATAGTCAACCTGAGGAGATGGAAGCTTCAGAGGAA	300
QY	301	ATGGGATTGATCTTCAGAGTTCGTGTAAAGCGATCCCTCACCATTACAAAGATAA	360
DB	301	ATGGGATTGATCTTCAGAGTTCGTGTAAAGCGATCCCTCACCATTACAAAGATAA	360
QY	361	GCAGAAATCTCAGGATCTCTGTAACGGGCTGGCTAGTGTGGCTTCAGGAA	420
DB	361	GCAGAAATCTCAGGATCTCTGTAACGGGCTGGCTAGTGTGGCTTCAGGAA	420
QY	421	CAGAGACAGGGCTGCACATGGCTCAGCTTCACTGCGCAATCTTATCTTGGGATTTACA	480
DB	421	CAGAGACAGGGCTGCACATGGCTCAGCTTCACTGCGCAATCTTATCTTGGGATTTACA	480
QY	481	CTCCTACAGTGTGTAATGTCTCAGGATGTGTCCAAACCAAAGGCCAGAAAGGA	540
DB	481	CTCCTACAGTGTGTAATGTCTCAGGATGTGTCCAAACCAAAGGCCAGAAAGGA	540
QY	541	GACATCATCTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600
DB	541	GACATCATCTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600

QY	601	TTAAATCGAGACCGGAGCGCAAAAATGTATTCGGTACAAATTTTCAGGCTTCCGATG	660
DB	601	TTAAATCGAGACCGGAGCGCAAAAATGTATTCGGTACAAATTTTCAGGCTTCCGATG	660
QY	661	CTCCAGGCGATGATATTCGCAATTTGAAGAGATTAAACAAGTATGACTTCTCTGCCAAT	720
DB	661	CTCCAGGCGATGATATTCGCAATTTGAAGAGATTAAACAAGTATGACTTCTCTGCCAAT	720
QY	721	ATCACCTCTGGATATGATATTTGACAGCTGTAAACCGTGTCCAAGGCGCTAGAGGCA	780
DB	721	ATCACCTCTGGATATGATATTTGACAGCTGTAAACCGTGTCCAAGGCGCTAGAGGCA	780
QY	781	ACACTCAGCTTTGTGGCCAGAAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAC	840
DB	781	ACACTCAGCTTTGTGGCCAGAAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAC	840
QY	841	TGCTCTGACCATATCCCATCCCAATAGCAGTGTGGGSCAACCGGCTCAGGAATCTCC	900
DB	841	TGCTCTGACCATATCCCATCCCAATAGCAGTGTGGGSCAACCGGCTCAGGAATCTCC	900
QY	901	ACGGCTGTGGCCAAATCTATTTGGGATTATTTTACATTTCCACAGTTCAGCTATGCTCTCG	960
DB	901	ACGGCTGTGGCCAAATCTATTTGGGATTATTTTACATTTCCACAGTTCAGCTATGCTCTCG	960
QY	961	AGCAGGCTGTCCAGACACAGAAATGATACAGGCTTCTGAGGACCATCCCAATGAT	1020
DB	961	AGCAGGCTGTCCAGACACAGAAATGATACAGGCTTCTGAGGACCATCCCAATGAT	1020
QY	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
DB	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
QY	1081	ACCTGTCAGCCGACGATGACTATGGCCGCCAGGATTTGACAAAGTTCCGGGAGGAGGC	1140
DB	1081	ACCTGTCAGCCGACGATGACTATGGCCGCCAGGATTTGACAAAGTTCCGGGAGGAGGC	1140
QY	1141	GTTAAGAGGACATCTGTTTGTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAA	1200
DB	1141	GTTAAGAGGACATCTGTTTGTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAA	1200
QY	1201	CAGTTGAGTTTCATGCGCCAGCTCATCCAGAACTCTCGGCCAAGGTCTATCGTGTCTTC	1260
DB	1201	CAGTTGAGTTTCATGCGCCAGCTCATCCAGAACTCTCGGCCAAGGTCTATCGTGTCTTC	1260
QY	1261	TCCAAATGCCCCGACCTGGAGCCGCTCATCCAGAGATAGTTCCGAGAAACATCACCGAT	1320
DB	1261	TCCAAATGCCCCGACCTGGAGCCGCTCATCCAGAGATAGTTCCGAGAAACATCACCGAT	1320
QY	1321	CGGATCTGGTGGCCAGCGAGGCTTGGGCCAGCTCTTCGCTCATTCGCAAGCAGAGTAC	1380
DB	1321	CGGATCTGGTGGCCAGCGAGGCTTGGGCCAGCTCTTCGCTCATTCGCAAGCAGAGTAC	1380
QY	1381	TTCCAGTGTGGCGGACCATCGGCTTCTCAGGGCGGGCTATCCCGAGGTTTC	1440
DB	1381	TTCCAGTGTGGCGGACCATCGGCTTCTCAGGGCGGGCTATCCCGAGGTTTC	1440
QY	1441	AACAAGTTCTGAAGAGAGTCCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG	1500
DB	1441	AACAAGTTCTGAAGAGAGTCCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG	1500
QY	1501	TTCTGGAGGAGACCTTCAACTGCTACTTCCCGAGAGACCCCTGACGAGCTGAAGAAT	1560
DB	1501	TTCTGGAGGAGACCTTCAACTGCTACTTCCCGAGAGACCCCTGACGAGCTGAAGAAT	1560
QY	1561	TCCAGGTGCTTCGACCGGAGCTCAAGGAGCGGCTCCAGGGCGGGAATCTCC	1620
DB	1561	TCCAGGTGCTTCGACCGGAGCTCAAGGAGCGGCTCCAGGGCGGGAATCTCC	1620
QY	1621	AGACGGAAGCCCTTACGCCACCCCTGCACTGGGAGAGAGAAATCAACAGCTGGAGACC	1680
DB	1621	AGACGGAAGCCCTTACGCCACCCCTGCACTGGGAGAGAGAAATCAACAGCTGGAGACC	1680
QY	1681	CCCTACCTGGATTATACACACCTGAGGATCTCTCTACAAATGATACGTGGCGCTCTACTCC	1740

Db 1681 CCTACCTGGATTATACACACCTGAGGATCTCCTCAATGTATATAGTGGCGCTTACTCC 1740
Qy 1741 ATTGCTCAGCGCCTCAAGACATCACTCTTCAAAACCGGCAAGGATCTTTGCAAAAC 1800
Db 1741 ATTGCTCAGCGCCTCAAGACATCACTCTTCAAAACCGGCAAGGATCTTTGCAAAAC 1800
Qy 1801 GGATCTTGTGAGATATTAAATAAGTTGAGGCTCGCAGGCTCTCAACATCTGTGCTGAT 1860
Db 1801 GGATCTTGTGAGATATTAAATAAGTTGAGGCTCGCAGGCTCTCAACATCTGTGCTGAT 1860
Qy 1861 CTGAAGTTTACCAACAGCATGGTGGAGGATGATTTGAGATCAAGGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATGGTGGAGGATGATTTGAGATCAAGGTGACCTCAAG 1920
Qy 1921 GGGAACTACACCATTAATCAACTGGAGCTCTCCGAGAGGATGAATCGGTGTGTTCAT 1980
Db 1921 GGGAACTACACCATTAATCAACTGGAGCTCTCCGAGAGGATGAATCGGTGTGTTCAT 1980
Qy 1981 GAGGTGGGCACTACAAAGCTTACCTTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040
Db 1981 GAGGTGGGCACTACAAAGCTTACCTTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040
Qy 2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGTTCCTTTCTCAAGTGTCTTTCTCAACTGCACTCGAGACTGT 2100
Db 2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGTTCCTTTCTCAACTGCACTCGAGACTGT 2100
Qy 2101 GTGCCGGGCAACAGGAGGATCATCGAGGGGAGCCCACTGTCTTTTGAATGCATG 2160
Db 2101 GTGCCGGGCAACAGGAGGATCATCGAGGGGAGCCCACTGTCTTTTGAATGCATG 2160
Qy 2161 GCATGTGAGAGGAGGATTCAGTGCATGAATAACGATGAAGTGCCTGACAAAGTGCCCG 2220
Db 2161 GCATGTGAGAGGAGGATTCAGTGCATGAATAACGATGAAGTGCCTGACAAAGTGCCCG 2220
Qy 2221 AATGATTTCTGTGCGAATGAGAACACACAGTGTGCATCGCCAGGAGATCGAGTACCTG 2280
Db 2221 AATGATTTCTGTGCGAATGAGAACACACAGTGTGCATCGCCAGGAGATCGAGTACCTG 2280
Qy 2281 TCGTGGAGCGGACCTTGGGATCGCTGACCATCTTGGCGGTACTGGGATCCTGATC 2340
Db 2281 TCGTGGAGCGGACCTTGGGATCGCTGACCATCTTGGCGGTACTGGGATCCTGATC 2340
Qy 2341 ACCTCTCTGCTGGGGGTCTTCAATCAAGTTTCAAGAACTCCCATCGTGAAGGCCACC 2400
Db 2341 ACCTCTCTGCTGGGGGTCTTCAATCAAGTTTCAAGAACTCCCATCGTGAAGGCCACC 2400
Qy 2401 AACCGGAGTTGCTCTACCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGTCTGCTC 2460
Db 2401 AACCGGAGTTGCTCTACCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGTCTGCTC 2460
Qy 2461 ATCTTCATCGGAGCGGACGAGCTGAGCTGCTGGCTCCGCCACCGGCTTTGGCATC 2520
Db 2461 ATCTTCATCGGAGCGGACGAGCTGAGCTGCTGGCTCCGCCACCGGCTTTGGCATC 2520
Qy 2521 AGCTTCGCTCTGCTGATCTCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Db 2521 AGCTTCGCTCTGCTGATCTCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Qy 2581 GAGGCCAAGATCCCAACAGCTTCAACCGCAAGTGGGTGGGCTCAACCTGCACTCTC 2640
Db 2581 GAGGCCAAGATCCCAACAGCTTCAACCGCAAGTGGGTGGGCTCAACCTGCACTCTC 2640
Qy 2641 CTGGTCTCTCTGATCTCTGCTGATCTGCTGATCTGCTGATCTGCTGATCTGCTGATCT 2700
Db 2641 CTGGTCTCTCTGATCTCTGCTGATCTGCTGATCTGCTGATCTGCTGATCTGCTGATCT 2700
Qy 2701 CTTCCCTCAGCTACAGGAACCATGAGCTGGAGGACGAGGTGATCTTCACTCCTGGAC 2760
Db 2701 CTTCCCTCAGCTACAGGAACCATGAGCTGGAGGACGAGGTGATCTTCACTCCTGGAC 2760
Qy 2761 GAGGCTCCTCTCACTGGCTGGCTTCTCTCATCGGCTACCTGCTCCTCGCGCCATC 2820
Db 2761 GAGGCTCCTCTCACTGGCTGGCTTCTCTCATCGGCTACCTGCTCCTCGCGCCATC 2820

Db 2761 GAGGCTCCTCTCACTGGCTGGCTTCTCTCATCGGCTACACCTGCTCCTCGCGCCATC 2820
Qy 2821 TGTCTTCTTCTCGCCTTCAAGTCCCGTAAAGTCCCGGAGAACTTCAACGAGGCTAAAGTTC 2880
Db 2821 TGTCTTCTTCTCGCCTTCAAGTCCCGTAAAGTCCCGGAGAACTTCAACGAGGCTAAAGTTC 2880
Qy 2881 ATCACTTCAAGCATGTTGATCTTCTTCACTGCTGATCTCTTCACTGCTGCTGCTGCTGCT 2940
Db 2881 ATCACTTCAAGCATGTTGATCTTCTTCACTGCTGATCTCTTCACTGCTGCTGCTGCTGCT 2940
Qy 2941 AGCACTTACGGCAAGTTTGTGCGGCTGAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Db 2941 AGCACTTACGGCAAGTTTGTGCGGCTGAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Qy 3001 GGGTGTGCTGGCTGCATTTACTTCAACAGTGTTAATCATCTGTTCAAGCGCTGCCGT 3060
Db 3001 GGGTGTGCTGGCTGCATTTACTTCAACAGTGTTAATCATCTGTTCAAGCGCTGCCGT 3060
Qy 3061 AACACCATCGAGAGGTGCGCTGCAGCAGCGGCGCCAGCCTTCAAGTGGCGGCCCG 3120
Db 3061 AACACCATCGAGAGGTGCGCTGCAGCAGCGGCGCCAGCCTTCAAGTGGCGGCCCG 3120
Qy 3121 GCCACCTTCCGGCGCAGCGCGCTGTCGAAGCGCTTCCAGCAGCTGTCGGCTCCACC 3180
Db 3121 GCCACCTTCCGGCGCAGCGCGCTGTCGAAGCGCTTCCAGCAGCTGTCGGCTCCACC 3180
Qy 3181 ATCTCTCGCGCCTGCTCCACTGCGGCGCGGCTCACCATGAGATGCAAGCTGCTC 3240
Db 3181 ATCTCTCGCGCCTGCTCCACTGCGGCGCGGCTCACCATGAGATGCAAGCTGCTC 3240
Qy 3241 AGCAGCAGAGGTTCAGTTTCCGCGCAGCGCCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Db 3241 AGCAGCAGAGGTTCAGTTTCCGCGCAGCGCCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Qy 3301 ACAGGCGGATACGCGCCTCAGCGCAAGCGCGCGGCGGCTCAGAAATCGAGCGC 3360
Db 3301 ACAGGCGGATACGCGCCTCAGCGCAAGCGCGCGGCGGCTCAGAAATCGAGCGC 3360
Qy 3361 AGCGGCGACCATCTGCGCTAGACACAGCGCGCGGCGGCTCAGAAATCGAGCGC 3420
Db 3361 AGCGGCGACCATCTGCGCTAGACACAGCGCGCGGCGGCTCAGAAATCGAGCGC 3420
Qy 3421 CAGCGCGCAACGATGCGCGATCAAGCGCGCGGCGGCGGCTCAGAAATCGAGCGC 3480
Db 3421 CAGCGCGCAACGATGCGCGATCAAGCGCGCGGCGGCGGCTCAGAAATCGAGCGC 3480
Qy 3481 GCGGCGACGAGGCGGCGGCGGCGGCGGCGGCGGCTCAGAAATCGAGCGC 3540
Db 3481 GCGGCGACGAGGCGGCGGCGGCGGCGGCGGCGGCTCAGAAATCGAGCGC 3540
Qy 3541 CCCAAGAACATCTCCACGCGCAGCGCTGCAAACTGACATCAACTCTTAAACGCTGCG 3600
Db 3541 CCCAAGAACATCTCCACGCGCAGCGCTGCAAACTGACATCAACTCTTAAACGCTGCG 3600
Qy 3601 TGCGCAACCTCTCCCTCTCCGCGACTTTCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Db 3601 TGCGCAACCTCTCCCTCTCCGCGACTTTCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Qy 3661 TCCTTTTATCCCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Db 3661 TCCTTTTATCCCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Qy 3721 ATAATGATTTGCAAAATAGGTGAGCAGAGTTCGTCAAAGTATCTGAATCTGAACT 3780
Db 3721 ATAATGATTTGCAAAATAGGTGAGCAGAGTTCGTCAAAGTATCTGAATCTGAACT 3780
Qy 3781 ATCTGAACTACTTATCTCTCGAATTTGATTAACAACATTTTGAAGTATTTTGAAGTATTTTGAAGT 3840
Db 3781 ATCTGAACTACTTATCTCTCGAATTTGATTAACAACATTTTGAAGTATTTTGAAGTATTTTGAAGT 3840
Qy 3841 TTATGTTCTAACATTTGCAAGATAATTTGTACAAATATAAGGTACCACTGAGCAGT 3900
Db 3841 TTATGTTCTAACATTTGCAAGATAATTTGTACAAATATAAGGTACCACTGAGCAGT 3900

```
QY 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATAACATTTATCAATTGAAACCTGGA 3960
Db 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATAACATTTATCAATTGAAACCTGGA 3960
QY 3961 TTGCAACAGGAATATAATGACCTGTACAAAATAATGTTGATATCTTAAAAATGCAAT 4020
Db 3961 TTGCAACAGGAATATAATGACCTGTACAAAATAATGTTGATATCTTAAAAATGCAAT 4020
QY 4021 TGTAAATCAGATGTGTAATAATGTTGTAATTAATCTCTGTACATAATTAATGCAATTTCTTGATA 4080
Db 4021 TGTAAATCAGATGTGTAATAATGTTGTAATTAATCTCTGTACATAATTAATGCAATTTCTTGATA 4080
QY 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCGACAGCAAGG 4134
Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCGACAGCAAGG 4134

RESULT 4
US-10-270-795-17
; Sequence 17, Application US/10270795
; Publication No. US20030084855A1
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT FILING DATE: US/10/270,795
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,372
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-795-17

Query Match 100.0%; Score 4134; DB 14; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGGTTGCTGCTCGGTTTCAGTCCGAGTCTCTCCAGTGCAAAATGGAATGGTGTGC 60
Db 1 AATTCGGTTGCTGCTCGGTTTCAGTCCGAGTCTCTCCAGTGCAAAATGGAATGGTGTGC 60
QY 61 GCCATTACAGGAACATGCACATACATCTGTGTTAAATGAATAATTGTCAAGTTATCTGAAGT 120
Db 61 GCCATTACAGGAACATGCACATACATCTGTGTTAAATGAATAATTGTCAAGTTATCTGAAGT 120
QY 121 TATTAAATGTTTCTCAGAGGATGGCTTACAGAAATCAATTTCTGCAGGTTTCCCAAT 180
Db 121 TATTAAATGTTTCTCAGAGGATGGCTTACAGAAATCAATTTCTGCAGGTTTCCCAAT 180
QY 181 GTCATTGTATGAATACTGACCAAGAGGATGTAAACAAAATGGAACAAAGCTGAGGACCAC 240
Db 181 GTCATTGTATGAATACTGACCAAGAGGATGTAAACAAAATGGAACAAAGCTGAGGACCAC 240
QY 241 GTTACCCCTTTCTTGAGCATACGATCAACCTGAAAGGAGATGGAAGACTTGAGAGGAA 300
Db 241 GTTACCCCTTTCTTGAGCATACGATCAACCTGAAAGGAGATGGAAGACTTGAGAGGAA 300
QY 301 ATGGGATTGATCTCCAGGATTTCTGCTGTAAGCGATCCCTCACCATTACAAAGATAA 360
Db 301 ATGGGATTGATCTCCAGGATTTCTGCTGTAAGCGATCCCTCACCATTACAAAGATAA 360
QY 361 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGTTCAGGAA 420
Db 361 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGTTCAGGAA 420
```

```
Db 361 GCAGAAATCCTCCAGGCATCCTCTGTAAACGGGCTGGCGTAGTGTGGTTCAGGAA 420
QY 421 CAGAGACAGGGCTGCACAAATGGCTCAGCTTCACTGCCAACTCTTATTTCTTGGGATTTACA 480
Db 421 CAGAGACAGGGCTGCACAAATGGCTCAGCTTCACTGCCAACTCTTATTTCTTGGGATTTACA 480
QY 481 CTCTCAGTCGTACAAATGTCTCAGGGTATGGTCCAAACCAAGAGGCCGACAGAGAAGGA 540
Db 481 CTCTCAGTCGTACAAATGTCTCAGGGTATGGTCCAAACCAAGAGGCCGACAGAGAAGGA 540
QY 541 GACATCATCTCTGGGAGGTCTCTTTCCCAATACATTTTGGAGTAGCCGCCAAGGATCAGGAC 600
Db 541 GACATCATCTCTGGGAGGTCTCTTTCCCAATACATTTTGGAGTAGCCGCCAAGGATCAGGAC 600
QY 601 TTAATAATCGAGACGGAGCGGACAAATGTATTTGGGTACAAATTTTCGAGGCTTCCGATGG 660
Db 601 TTAATAATCGAGACGGAGCGGACAAATGTATTTGGGTACAAATTTTCGAGGCTTCCGATGG 660
QY 661 CTCAGGCGGATGATATTCGCAATTTGAAGATTAACAACAGATATGACTTTTCCTGCCCAAT 720
Db 661 CTCAGGCGGATGATATTCGCAATTTGAAGATTAACAACAGATATGACTTTTCCTGCCCAAT 720
QY 721 ATCACTCTGGGATATCGCATATTTTGACAGCTGTAAACACCGTGTCCAGGCGCTAGAGGCA 780
Db 721 ATCACTCTGGGATATCGCATATTTTGACAGCTGTAAACACCGTGTCCAGGCGCTAGAGGCA 780
QY 781 ACCTCAGCTTTGTGGCCAGAAACAAATCGACTCTCTGAACCTTAGATGAGTTCTCTAAC 840
Db 781 ACCTCAGCTTTGTGGCCAGAAACAAATCGACTCTCTGAACCTTAGATGAGTTCTCTAAC 840
QY 841 TGCTCTGACCATATCCCATCCAAATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900
Db 841 TGCTCTGACCATATCCCATCCAAATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900
QY 901 ACGGCTGTGGCCAACTCTATTTGGGATTTTATCATTTCCACAGCTCAGCTATGCTCTCTCG 960
Db 901 ACGGCTGTGGCCAACTCTATTTGGGATTTTATCATTTCCACAGCTCAGCTATGCTCTCTCG 960
QY 961 AGCAGGCTGCTCAGCAACAAAGATGAGTACAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
Db 961 AGCAGGCTGCTCAGCAACAAAGATGAGTACAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
QY 1021 GAGCAACAGGCCACGGCCATGGCCGAGATCATCGACGACTTCCAGTGGAACTGGGTGGGA 1080
Db 1021 GAGCAACAGGCCACGGCCATGGCCGAGATCATCGACGACTTCCAGTGGAACTGGGTGGGA 1080
QY 1081 ACCCTGCGACGACATGACTATGGCCGCCAGGCAATGACAAAGTTCCGGGAGGAGGCC 1140
Db 1081 ACCCTGCGACGACATGACTATGGCCGCCAGGCAATGACAAAGTTCCGGGAGGAGGCC 1140
QY 1141 GTTAAGAGGACATCTGTATTGACTTTCAGTGAAGATGATCTCTCAGTACTACACCCAGAAG 1200
Db 1141 GTTAAGAGGACATCTGTATTGACTTTCAGTGAAGATGATCTCTCAGTACTACACCCAGAAG 1200
QY 1201 CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCGGCCCAAGGTCATCTGGTCTTC 1260
Db 1201 CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCGGCCCAAGGTCATCTGGTCTTC 1260
QY 1261 TCCAAATGGCCCCGACCTGGAGCGGCTCATCCAGGAGATAGTTCCGAGAAACATCAACGAT 1320
Db 1261 TCCAAATGGCCCCGACCTGGAGCGGCTCATCCAGGAGATAGTTCCGAGAAACATCAACGAT 1320
QY 1321 CGGATCTGGCTGGCCAGCGAGGCTTGGCCAGCTCTTCCGCTCATCTCCAGCCAGAGTAC 1380
Db 1321 CGGATCTGGCTGGCCAGCGAGGCTTGGCCAGCTCTTCCGCTCATCTCCAGCCAGAGTAC 1380
QY 1381 TTCCACCTGTGTGGCGGACCATCGCTTCTCAGGGCGGGGCTATCCCAAGGTTTC 1440
Db 1381 TTCCACCTGTGTGGCGGACCATCGCTTCTCAGGGCGGGGCTATCCCAAGGTTTC 1440
QY 1441 AACAGTTCTGTAAGAGGAGTCCACCCAGCAGGTCCTCGGACAAATGGGTTTGTCAAGGAG 1500
Db 1441 AACAGTTCTGTAAGAGGAGTCCACCCAGCAGGTCCTCGGACAAATGGGTTTGTCAAGGAG 1500
```



```
Db 3661 TCCTTTTATCCCTGATTTCTGATCTGGATATTTACTAGTGTGCGATGGAATATCACAC 3720
Qy 3721 ATAATGAGTTGCAATTAAGGTGAGCAGAGTTGTGTCAAAAGTATCTGAAGT 3780
Db 3721 ATAATGAGTTGCAATTAAGGTGAGCAGAGTTGTGTCAAAAGTATCTGAAGT 3780
Qy 3781 ATCTGAACACTTATCTCTCGAATTTGATTTACAAACATTTGAAGTATTTTACTGACA 3840
Db 3781 ATCTGAACACTTATCTCTCGAATTTGATTTACAAACATTTGAAGTATTTTACTGACA 3840
Qy 3841 TTATGTTCTAAACATTTCTCAAGTAAATTTGTTTACACATATAAGTACCACCTGAAGCAGT 3900
Db 3841 TTATGTTCTAAACATTTCTCAAGTAAATTTGTTTACACATATAAGTACCACCTGAAGCAGT 3900
Qy 3901 GACTGAGATGGCACTGTGATGACAGAACTGTTTATAACATTTATCAATTTGAACCTGGA 3960
Db 3901 GACTGAGATGGCACTGTGATGACAGAACTGTTTATAACATTTATCAATTTGAACCTGGA 3960
Qy 3961 TTGCAACAGGAATATTAATGACTGTAAACAAAAAATTTGTTGATTTCTTAAAAATGCAAT 4020
Db 3961 TTGCAACAGGAATATTAATGACTGTAAACAAAAAATTTGTTGATTTCTTAAAAATGCAAT 4020
Qy 4021 TGTAATCAGATGTGTAATTTGTAATTTGTAATTTCTCTGATACATTAATTTCTTGATA 4080
Db 4021 TGTAATCAGATGTGTAATTTGTAATTTGTAATTTCTCTGATACATTAATTTCTTGATA 4080
Qy 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCGACGCAACGG 4134
Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCGACGCAACGG 4134
```

RESULT 5

```
US-10-270-876-17
; Sequence 17, Application US/10270876
; Publication No.: US20030116096A1
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/10/270,876
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,477
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-876-17
```

```
Query Match 100.0%; Score 4134; DB 15; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 AATTCGGTTGCTGCTCGGTTTCAGTCCAGTCTCTCCAGTGCAAAATGAGAAATGGTGTC 60
Db 1 AATTCGGTTGCTGCTCGGTTTCAGTCCAGTCTCTCCAGTGCAAAATGAGAAATGGTGTC 60
Qy 61 GCATTTACAGGAACATGCACACTACTCTGTGTTAAATGAATATTTGCAATTTCTGAAGT 120
Db 61 GCATTTACAGGAACATGCACACTACTCTGTGTTAAATGAATATTTGCAATTTCTGAAGT 120
Qy 121 TATTAATGTTTCTGCAAGGATGGCTTCCACAGAAATCAATTTCTGACGTTTCCCAT 180
Db 121 TATTAATGTTTCTGCAAGGATGGCTTCCACAGAAATCAATTTCTGACGTTTCCCAT 180
```

```
Qy 181 GTCAATCTATGAATACTGACCAAGGATGTAAACAAATGGAACCAAGCTGAGGACCAC 240
Db 181 GTCAATCTATGAATACTGACCAAGGATGTAAACAAATGGAACCAAGCTGAGGACCAC 240
Qy 241 GTTCACCCCTTTCTTGGAGCATACGATCAACCCCTGAAGAGATGGAAGACTTGGAGGAA 300
Db 241 GTTCACCCCTTTCTTGGAGCATACGATCAACCCCTGAAGAGATGGAAGACTTGGAGGAA 300
Qy 301 ATGGGATTCATCTTCAGAGTTCTGCTGTAAGGATCCCTCACCATTACAAAGATAA 360
Db 301 ATGGGATTCATCTTCAGAGTTCTGCTGTAAGGATCCCTCACCATTACAAAGATAA 360
Qy 361 GCAGAAATCTCCAGGATCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
Db 361 GCAGAAATCTCCAGGATCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
Qy 421 CAGAGACAGGGCTGCACAAATGGCTCAGCTTCACCTGCCAATCTTATTTCTGGGATTTACA 480
Db 421 CAGAGACAGGGCTGCACAAATGGCTCAGCTTCACCTGCCAATCTTATTTCTGGGATTTACA 480
Qy 481 CTCCTACAGTCGTACAAATGTCTCAGGGTATGTTCCAAACCAAGGGCCCAAGAAAGGA 540
Db 481 CTCCTACAGTCGTACAAATGTCTCAGGGTATGTTCCAAACCAAGGGCCCAAGAAAGGA 540
Qy 541 GACATCATCTGGAGGTCTCTTCCCAATACATTTGGAGTAGCCGCCAAGGATCAGGAC 600
Db 541 GACATCATCTGGAGGTCTCTTCCCAATACATTTGGAGTAGCCGCCAAGGATCAGGAC 600
Qy 601 TTAATAATCGAGCCGGAGCGGACAAATGTATTCGGTACAAATTTTCGAGGCTTCCCATG 660
Db 601 TTAATAATCGAGCCGGAGCGGACAAATGTATTCGGTACAAATTTTCGAGGCTTCCCATG 660
Qy 661 CTCAGGCGATGATTTGCAATTTGAAGAGATTAAACACAGTATGATTTCTCTGCCCAAT 720
Db 661 CTCAGGCGATGATTTGCAATTTGAAGAGATTAAACACAGTATGATTTCTCTGCCCAAT 720
Qy 721 ATCACTCTGGGATATCGCATATTTGACAGCTGTAAACACCGTGTCCAGGCGCTAGAGCA 780
Db 721 ATCACTCTGGGATATCGCATATTTGACAGCTGTAAACACCGTGTCCAGGCGCTAGAGCA 780
Qy 781 ACCTCAGCTTTGTGGCCCAAGAAACAAATCGACTCGCTGAACTTAGATGATGTTCTGTAAC 840
Db 781 ACCTCAGCTTTGTGGCCCAAGAAACAAATCGACTCGCTGAACTTAGATGATGTTCTGTAAC 840
Qy 841 TGCTCTGACCATATCCCATCCAATAGCAGTGGTGGGGCAACCGGGTCAGAAATCTCC 900
Db 841 TGCTCTGACCATATCCCATCCAATAGCAGTGGTGGGGCAACCGGGTCAGAAATCTCC 900
Qy 901 ACGGCTGTGGCCAAATCTATTGGGATTTATTACATTTCCACAGTTCAGTATGCTCTCG 960
Db 901 ACGGCTGTGGCCAAATCTATTGGGATTTATTACATTTCCACAGTTCAGTATGCTCTCG 960
Qy 961 AGCAGGCTGTCTCAGCAACAGAAATGATCAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
Db 961 AGCAGGCTGTCTCAGCAACAGAAATGATCAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
Qy 1021 GAGCAACAGCCACGCGCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Db 1021 GAGCAACAGCCACGCGCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Qy 1081 ACCCTGCGAGCCACGATGACTATGGCCGCCAGGCAATGACAAGTTCCGGGAGGAGGCC 1140
Db 1081 ACCCTGCGAGCCACGATGACTATGGCCGCCAGGCAATGACAAGTTCCGGGAGGAGGCC 1140
Qy 1141 GTTAAGAGGACATCTGTATTGATTTAGTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Db 1141 GTTAAGAGGACATCTGTATTGATTTAGTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Qy 1201 CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCTGGCCCAAGGTCATCTGTGTTCTTC 1260
Db 1201 CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCTGGCCCAAGGTCATCTGTGTTCTTC 1260
Qy 1261 TCCAATGGCCCCGACCTGGAGCGGCTCATCCAGGAGATAGTTCGGAGAAACATCCCGAT 1320
```

Db 1261 TCCAAATGGCCCGACCTGAGCGCTCATCAGAGAGATAGTTCGAGAGAAACATCACCGAT 1320
Qy 1321 CGGATCTGGCTGGCCAGGAGGCTTGGCCAGCTCTTGGCTCATTTGCCCAAGCCAGAGTAC 1380
Db 1321 CGGATCTGGCTGGCCAGGAGGCTTGGCCAGCTCTTGGCTCATTTGCCCAAGCCAGAGTAC 1380
Qy 1381 TTCCACGCTGGTGGGGGACCACTCGGCTTCGCTCTCAGGGGGGGCGGTATCCCAAGGGTTC 1440
Db 1381 TTCCACGCTGGTGGGGGACCACTCGGCTTCGCTCTCAGGGGGGGCGGTATCCCAAGGGTTC 1440
Qy 1441 AACAAATCTCTGAAGAGGTGCACCCGACAGGTCTCTGGCAATATGGGTTTGTCAAGGAG 1500
Db 1441 AACAAATCTCTGAAGAGGTGCACCCGACAGGTCTCTGGCAATATGGGTTTGTCAAGGAG 1500
Qy 1501 TTCTGGGAGGAGCTTCAACTGCTTACTTCCGAGAGAGACCTCAGCAGCTGAAGAAT 1560
Db 1501 TTCTGGGAGGAGCTTCAACTGCTTACTTCCGAGAGAGACCTCAGCAGCTGAAGAAT 1560
Qy 1561 TCCAAAGGTGCCCTCGCACGGACCGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCC 1620
Db 1561 TCCAAAGGTGCCCTCGCACGGACCGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCC 1620
Qy 1621 AGACGGACAGCCCTACGCCACCCCTGCACCTGGGAGGAGACATCACAGAGTGGAGACC 1680
Db 1621 AGACGGACAGCCCTACGCCACCCCTGCACCTGGGAGGAGACATCACAGAGTGGAGACC 1680
Qy 1681 CCTACCTGGATATACACACCTGAGGATCTCTACAATGTATACGTGGCGCTTACTCC 1740
Db 1681 CCTACCTGGATATACACACCTGAGGATCTCTACAATGTATACGTGGCGCTTACTCC 1740
Qy 1741 ATTGCTCAGCCCTCGAAGACATCGACTCTTCCAAACCGGACCGGGCATCTTTGCAAAAC 1800
Db 1741 ATTGCTCAGCCCTCGAAGACATCGACTCTTCCAAACCGGACCGGGCATCTTTGCAAAAC 1800
Qy 1801 GGATCTTGTGAGATATTAATAAGTTGAGGCTTGGAGCTCCTCAACCATCTGCTGCAT 1860
Db 1801 GGATCTTGTGAGATATTAATAAGTTGAGGCTTGGAGCTCCTCAACCATCTGCTGCAT 1860
Qy 1861 CTGAAGTTTACCAACAGCATGGTGAGCAGGTGATCTTTGACGATCAAGGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATGGTGAGCAGGTGATCTTTGACGATCAAGGTGACCTCAAG 1920
Qy 1921 GGGAACTACACATTATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCAT 1980
Db 1921 GGGAACTACACATTATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCAT 1980
Qy 1981 GAGGTGGGCAACTACAAACGCTTACGTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040
Db 1981 GAGGTGGGCAACTACAAACGCTTACGTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040
Qy 2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCGAGTCACTGT 2100
Db 2041 AAAATCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCGAGTCACTGT 2100
Qy 2101 GTCCGGGACACAGGAGGGATCATCGAGGGGGACCCACCTGCTGTCTTGAATGCAATG 2160
Db 2101 GTCCGGGACACAGGAGGGATCATCGAGGGGGACCCACCTGCTGTCTTGAATGCAATG 2160
Qy 2161 GCATGTGCAGAGGAGATTCAAGTATGAAACGATGCAAGTGCCTGTATCAAAAGTGCCCG 2220
Db 2161 GCATGTGCAGAGGAGATTCAAGTATGAAACGATGCAAGTGCCTGTATCAAAAGTGCCCG 2220
Qy 2221 AATGATTTCTGTCGATGAGAACACAGTGTGATCGCAGGAGATCGAGTACCTG 2280
Db 2221 AATGATTTCTGTCGATGAGAACACAGTGTGATCGCAGGAGATCGAGTACCTG 2280
Qy 2281 TCGTGACAGAGCCCTTCGGGATCGCTCTGACCATCTTCGCGGTACTGGGCATCTGTATC 2340
Db 2281 TCGTGACAGAGCCCTTCGGGATCGCTCTGACCATCTTCGCGGTACTGGGCATCTGTATC 2340
Qy 2341 ACCTCCTTCTGGGTCTTTCATCAAGTTTCAGGAACATCTCCATCTGTGAAGGCCACC 2400

Db 2341 ACCTCCTTCTGGGTCTTTCATCAAGTTTCAGGAACATCTCCATCTGTAAGGCCACC 2400
Qy 2401 AACCGGAGTTGCTTACCTGCTGCTTCTTCCCTCATCTGCTGCTTCTCCAGCTGCTC 2460
Db 2401 AACCGGAGTTGCTTACCTGCTGCTTCTTCCCTCATCTGCTGCTTCTCCAGCTGCTC 2460
Qy 2461 ATCTTCATCGCGAGGCCAGGAGCTGGAACCTGTGCGGTGCGCAACCGGCTTTTGGCATC 2520
Db 2461 ATCTTCATCGCGAGGCCAGGAGCTGGAACCTGTGCGGTGCGCAACCGGCTTTTGGCATC 2520
Qy 2521 AGCTTCGCTGCTGCTATCTCTGATCTCTGATGCAACCAACCGGCTGCTGCTGCTTTC 2580
Db 2521 AGCTTCGCTGCTGCTATCTCTGATCTCTGATGCAACCAACCGGCTGCTGCTGCTTTC 2580
Qy 2581 GAGGCCAAGATCCCAACAGCTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCCCTC 2640
Db 2581 GAGGCCAAGATCCCAACAGCTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCCCTC 2640
Qy 2641 CTGGTCTTCTGCTGCTATCTCTGATCTCTGATGCAACCTGCACTGCTCTACACGGCG 2700
Db 2641 CTGGTCTTCTGCTGCTATCTCTGATCTCTGATGCAACCTGCACTGCTCTACACGGCG 2700
Qy 2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGGAGACGAGTCTATCTTCATCACTCGAC 2760
Db 2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGGAGACGAGTCTATCTTCATCACTCGAC 2760
Qy 2761 GAGGGTCTGCTCATGCGGCTGGGCTTCTCATCGGCTACACCTGCTCTTCCGCGCATC 2820
Db 2761 GAGGGTCTGCTCATGCGGCTGGGCTTCTCATCGGCTACACCTGCTCTTCCGCGCATC 2820
Qy 2821 TGCTTCTTCTCGCTTCAAGTCCCGTAAGCTCCGAGAACTTCAACGAGGCTAAAGTTC 2880
Db 2821 TGCTTCTTCTCGCTTCAAGTCCCGTAAGCTCCGAGAACTTCAACGAGGCTAAAGTTC 2880
Qy 2881 ATCACTTTCAGCATGTTGATCTTTCATCGTCTGATCTCTTCATCTCCCGCTATGTC 2940
Db 2881 ATCACTTTCAGCATGTTGATCTTTCATCGTCTGATCTCTTCATCTCCCGCTATGTC 2940
Qy 2941 AGCACTTACGGCAAGTTTGTGCGCGTGAGGTGATTTGGCATCTCGGCTCCAGGCTTC 3000
Db 2941 AGCACTTACGGCAAGTTTGTGCGCGTGAGGTGATTTGGCATCTCGGCTCCAGGCTTC 3000
Qy 3001 GGGTCTGCTGGCTGCTATTTACTTCAACAAGTTTACATCATCTGTTTCAAGCCGTCCGT 3060
Db 3001 GGGTCTGCTGGCTGCTATTTACTTCAACAAGTTTACATCATCTGTTTCAAGCCGTCCGT 3060
Qy 3061 AACACCATCAGAGAGTGGCTGAGCACGGGGCCACCGCTTCAAGGTGGGCGCCGG 3120
Db 3061 AACACCATCAGAGAGTGGCTGAGCACGGGGCCACCGCTTCAAGGTGGGCGCCGG 3120
Qy 3121 GCCACCTCCGGCGCAGCGCGCTCTCGCAAGCGTCCAGAGCTTCCGGCTCCACC 3180
Db 3121 GCCACCTCCGGCGCAGCGCGCTCTCGCAAGCGTCCAGAGCTTCCGGCTCCACC 3180
Qy 3181 ATCTCCTCGCCGCTCTGCTCCACCTGCGGCGCGGCTCACCATGGAGATGCAAGCGTGC 3240
Db 3181 ATCTCCTCGCCGCTCTGCTCCACCTGCGGCGCGGCTCACCATGGAGATGCAAGCGTGC 3240
Qy 3241 AGCAGCAGAAAGTCACTTGGCAGCGGCACCGTCAACCTGCTGCTCAGCTTCGAGGAG 3300
Db 3241 AGCAGCAGAAAGTCACTTGGCAGCGGCACCGTCAACCTGCTGCTCAGCTTCGAGGAG 3300
Qy 3301 ACAGGCGATACAGCAACCTCAGCGGCACCGCGCCGAGCAGGAACCTCGGCGATGGCCGC 3360
Db 3301 ACAGGCGATACAGCAACCTCAGCGGCACCGCGCCGAGCAGGAACCTCGGCGATGGCCGC 3360
Qy 3361 AGCGGCGAGCTTGCATCTAGACACACGACCGGGCCGCTCAGAAATGCGAGCCC 3420
Db 3361 AGCGGCGAGCTTGCATCTAGACACACGACCGGGCCGCTCAGAAATGCGAGCCC 3420
Qy 3421 CAGCCCGCAACGATGCCCGATCAAGCGCGCGGACCAAGGCGACCTTAGAGTCCCG 3480
Db 3421 CAGCCCGCAACGATGCCCGATCAAGCGCGCGGACCAAGGCGACCTTAGAGTCCCG 3480

QY 3481 GGCGGAGCAAGAGGCGGCCCACTATGAGGAAACCTAATCCAACTCTCTCCATCAAC 3540
 Db 3481 GGCGGAGCAAGAGGCGGCCCACTATGAGGAAACCTAATCCAACTCTCTCCATCAAC 3540
 QY 3541 CCCAAGAACATCTCCACGCGCAGCAGCGTCGACCACTGACATCAACTCTCTAACCGGTGCG 3600
 Db 3541 CCCAAGAACATCTCCACGCGCAGCAGCGTCGACCACTGACATCAACTCTCTAACCGGTGCG 3600
 QY 3601 TGCCCAACCTCTCCCTCTCCGCGCACTTTGCGTTTGTGAAAGTATGAGCATCTGCAAT 3660
 Db 3601 TGCCCAACCTCTCCCTCTCCGCGCACTTTGCGTTTGTGAAAGTATGAGCATCTGCAAT 3660
 QY 3661 TCCCTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCACAA 3720
 Db 3661 TCCCTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGTGCGATGGAATATCACAA 3720
 QY 3721 ATAAATGAGTTGCAAAATAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT 3780
 Db 3721 ATAAATGAGTTGCAAAATAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT 3780
 QY 3781 ATCTGAACCTATTTATCTCTCGAATTTCTTACAAACATTTTGAAGTATTTTGTGACA 3840
 Db 3781 ATCTGAACCTATTTATCTCTCGAATTTCTTACAAACATTTTGAAGTATTTTGTGACA 3840
 QY 3841 TTATGTTCTAAACATTTCTGCAAGATAATTTGTTTAAACATATAAGGTACCCTGAAAGCAGT 3900
 Db 3841 TTATGTTCTAAACATTTCTGCAAGATAATTTGTTTAAACATATAAGGTACCCTGAAAGCAGT 3900
 QY 3901 GACTGAGATTGCCATGTGATGACAGAACTGTTTATTAACATTTATCAATGAAACCTGGA 3960
 Db 3901 GACTGAGATTGCCATGTGATGACAGAACTGTTTATTAACATTTATCAATGAAACCTGGA 3960
 QY 3961 TTCCCAACAGAAATATAATGACTGTACAAACAAATTTGTTATCTTAAATGCAAAAT 4020
 Db 3961 TTCCCAACAGAAATATAATGACTGTACAAACAAATTTGTTATCTTAAATGCAAAAT 4020
 QY 4021 TGTAATCAGATGTGTAATTTGTTATTTACTTCTGTACATTAATGCAATTTCTTGATA 4080
 Db 4021 TGTAATCAGATGTGTAATTTGTTATTTACTTCTGTACATTAATGCAATTTCTTGATA 4080
 QY 4081 AAAGCGCGCAGCAACGG 4134
 Db 4081 AAAGCGCGCAGCAACGG 4134

RESULT 6
 ; Sequence 7, Application US/10268051
 ; Publication No. US20030124090A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harris, H. William
 ; APPLICANT: Jury, Steven
 ; APPLICANT: Russell, David R.
 ; APPLICANT: Nearing, Jacqueline A
 ; APPLICANT: Betka, Marlies
 ; APPLICANT: Linley, Timothy
 ; APPLICANT: Brown, Edward M
 ; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
 ; FILE REFERENCE: 2213.2004-001
 ; CURRENT APPLICATION NUMBER: US/10/268,051
 ; PRIOR FILING DATE: 2003-01-24
 ; PRIOR APPLICATION NUMBER: 60/328,464
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 4134
 ; TYPE: DNA
 ; ORGANISM: Squalus acanthias
 ; us-10-268-051-7

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AATTCCTGCTGTCGGTTCAGTCCAACTCTCTCCAGTCCAAATAGAGAAATGGTGGTC 60
 Db 1 AATTCCTGCTGTCGGTTCAGTCCAACTCTCTCCAGTCCAAATAGAGAAATGGTGGTC 60
 QY 61 GCCATTACAGGAATGCTACATCTGCTTAAATGAAATATTGCTAGTATCTGAGGT 120
 Db 61 GCCATTACAGGAATGCTACATCTGCTTAAATGAAATATTGCTAGTATCTGAGGT 120
 QY 121 TATTAAATATGTTCTGCAAGGATGGCTTCACGAGAAATCAATTCGACGTTTCCCAT 180
 Db 121 TATTAAATATGTTCTGCAAGGATGGCTTCACGAGAAATCAATTCGACGTTTCCCAT 180
 QY 181 GTCAATGTAATTAATGACCAAGGATGTAACAAATGGAACAAAGCTGAGGACCA 240
 Db 181 GTCAATGTAATTAATGACCAAGGATGTAACAAATGGAACAAAGCTGAGGACCA 240
 QY 241 GTTCACCTTTCTTGGAGCATACGATCAACCTGAAGGATGGAAGATCTGAGGAGGA 300
 Db 241 GTTCACCTTTCTTGGAGCATACGATCAACCTGAAGGATGGAAGATCTGAGGAGGA 300
 QY 301 ATGGGATGATCTTCAGGATTTCTGCTTAAAGGATCCCTCACCATTACAAAGATA 360
 Db 301 ATGGGATGATCTTCAGGATTTCTGCTTAAAGGATCCCTCACCATTACAAAGATA 360
 QY 361 GCAGAAATCTCCAGGATCTCTGTAACGGCTGCGTAGTGGTTCAGAGGA 420
 Db 361 GCAGAAATCTCCAGGATCTCTGTAACGGCTGCGTAGTGGTTCAGAGGA 420
 QY 421 CAGAGACAGGGCTGCACAAATGCTCAGCTTCACTGCCAACTCTTATTTGGGATTACA 480
 Db 421 CAGAGACAGGGCTGCACAAATGCTCAGCTTCACTGCCAACTCTTATTTGGGATTACA 480
 QY 481 CTCTCAGTCTGATACATGCTCAGGATATGTTCCAAACCAAGGCGCCAGAGGAAGA 540
 Db 481 CTCTCAGTCTGATACATGCTCAGGATATGTTCCAAACCAAGGCGCCAGAGGAAGA 540
 QY 541 GACATCATCTGGAGGTCTCTTCCCAATACATTTGGAGTAGCCGCAAGGATCAGGAC 600
 Db 541 GACATCATCTGGAGGTCTCTTCCCAATACATTTGGAGTAGCCGCAAGGATCAGGAC 600
 QY 601 TTAATTCGAGACCGGAGGCGCAAAATGATTTGCGTACAAATTTTCAGGCTTCCATG 660
 Db 601 TTAATTCGAGACCGGAGGCGCAAAATGATTTGCGTACAAATTTTCAGGCTTCCATG 660
 QY 661 CTCAGGCGATGATATTTGCAATTTGAAGATTAACAAAGTATGACTTCTCTGCCCAAT 720
 Db 661 CTCAGGCGATGATATTTGCAATTTGAAGATTAACAAAGTATGACTTCTCTGCCCAAT 720
 QY 721 ATCACTCTGGATATGCAATTTGACAGGTGTAACACCGGTGTCAGGCGCTAGAGGCA 780
 Db 721 ATCACTCTGGATATGCAATTTGACAGGTGTAACACCGGTGTCAGGCGCTAGAGGCA 780
 QY 781 ACCTCAGCTTTGTCGCGCAACAAATCGACTCTGTAACCTGATGATGATGTTCTGTAAC 840
 Db 781 ACCTCAGCTTTGTCGCGCAACAAATCGACTCTGTAACCTGATGATGATGTTCTGTAAC 840
 QY 841 TGCTCTGACCATATCCATCCCAATAGCAGTGTGCGGCAACCGGGTCAGGAATCTCC 900
 Db 841 TGCTCTGACCATATCCATCCCAATAGCAGTGTGCGGCAACCGGGTCAGGAATCTCC 900
 QY 901 AGCGTGTGCGCAATCTATTTGGGATTTTACATTTCCACAGTTCAGCTATGCTCTCG 960
 Db 901 AGCGTGTGCGCAATCTATTTGGGATTTTACATTTCCACAGTTCAGCTATGCTCTCG 960
 QY 961 AGCAGGCTGTCTGAGCAACAAAGATGATGATGATGATGATGATGATGATGATGAT 1020
 Db 961 AGCAGGCTGTCTGAGCAACAAAGATGATGATGATGATGATGATGATGATGATGAT 1020
 QY 1021 GAGCAACAGGCGCGCGCATGCGCGAGATCATCGAGACTTCCAGTGGAACTCGGTGGGA 1080

Db 1021 GAGCAACAGCGCCACGCGCATGCCCGAGATCATCGAGCATCTCCAGTGGAACTGGGTGGGA 1080
Qy 1081 ACCCTGGACCGCAGCATGACTATAGCCGCCCGCAGGCAATTGACAACTTCGGGAGAGGCC 1140
Db 1081 ACCCTGGACCGCAGCATGACTATAGCCGCCCGCAGGCAATTGACAACTTCGGGAGAGGCC 1140
Qy 1141 GTTAAGAGGGAATCTGTATTGACTTCACTTCACTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Db 1141 GTTAAGAGGGAATCTGTATTGACTTCACTTCACTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Qy 1201 CAGTTGGAGTTTATCGCCAGCGTATCCAGAACTCTCGGCCAAGGTATCTGTGTCTTC 1260
Db 1201 CAGTTGGAGTTTATCGCCAGCGTATCCAGAACTCTCGGCCAAGGTATCTGTGTCTTC 1260
Qy 1261 TCCAAATGGCCCCGACCTCGAGCCGCTCATCCAGGAGATAGTTTCGAGAAAATCAACGAT 1320
Db 1261 TCCAAATGGCCCCGACCTCGAGCCGCTCATCCAGGAGATAGTTTCGAGAAAATCAACGAT 1320
Qy 1321 CGGATCTGGCTGGCCAGCAGAGCTTGGGCCAGCTTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Db 1321 CGGATCTGGCTGGCCAGCAGAGCTTGGGCCAGCTTTCGCTCATTTGCCAAGCCAGAGTAC 1380
Qy 1381 TTCCAGCTGGTGGCGGCCACCATCGGCTTCGCTCTCAGGCGGGGGGTATCCACGGTTC 1440
Db 1381 TTCCAGCTGGTGGCGGCCACCATCGGCTTCGCTCTCAGGCGGGGGGTATCCACGGTTC 1440
Qy 1441 AACAGTTCTGAAGAGTCCACCCAGCAGGTCTCGGACAAATGGGTTTGTCAAGAG 1500
Db 1441 AACAGTTCTGAAGAGTCCACCCAGCAGGTCTCGGACAAATGGGTTTGTCAAGAG 1500
Qy 1501 TTCTGGAGGAGACCTTCAACTGCTACTTTCACCGAAGACCTGACGAGCTGAAGAT 1560
Db 1501 TTCTGGAGGAGACCTTCAACTGCTACTTTCACCGAAGACCTGACGAGCTGAAGAT 1560
Qy 1561 TCCAAAGTCCCTCGCACCGACCGCGCTCAAGGGACGGTCCAAAGCGGGGAACCTCC 1620
Db 1561 TCCAAAGTCCCTCGCACCGACCGCGCTCAAGGGACGGTCCAAAGCGGGGAACCTCC 1620
Qy 1621 AGACGACAGCCCTACGCCACCCCTGCACTGGGGAGGAGAAATCACAGCGTGGAGACC 1680
Db 1621 AGACGACAGCCCTACGCCACCCCTGCACTGGGGAGGAGAAATCACAGCGTGGAGACC 1680
Qy 1681 CCTACTGGATATACACACTGAGGATCTCTCAATGTATAGTGGCGCTTACTCC 1740
Db 1681 CCTACTGGATATACACACTGAGGATCTCTCAATGTATAGTGGCGCTTACTCC 1740
Qy 1741 ATTGCTCAGCCCTGGAAGATCCTCTCTGGAACCCCGCAGCGGATCTTGGAAAC 1800
Db 1741 ATTGCTCAGCCCTGGAAGATCCTCTCTGGAACCCCGCAGCGGATCTTGGAAAC 1800
Qy 1801 GGATCTGTGCATATTAATAAAGTTGAGGCTGGCAGGTCTCAACCATCTGTGCAT 1860
Db 1801 GGATCTGTGCATATTAATAAAGTTGAGGCTGGCAGGTCTCAACCATCTGTGCAT 1860
Qy 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTGACTTTGAGCATCAAGGTGACCTCAAG 1920
Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTGACTTTGAGCATCAAGGTGACCTCAAG 1920
Qy 1921 GGGAACTTACCACTATCACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTTTCAT 1980
Db 1921 GGGAACTTACCACTATCACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTTTCAT 1980
Qy 1981 GAGGTGGCAACTACCAACGCTACCGTAAAGCCAGTGAACGATCAACATCAACGAAAG 2040
Db 1981 GAGGTGGCAACTACCAACGCTACCGTAAAGCCAGTGAACGATCAACATCAACGAAAG 2040
Qy 2041 AAAATCTCTGAGTGGCTTCTCAAGTGGTTCCTTCTCNACTCGAGTGGAGCTGT 2100
Db 2041 AAAATCTCTGAGTGGCTTCTCAAGTGGTTCCTTCTCNACTCGAGTGGAGCTGT 2100
Qy 2101 GTCCCGGGACCAAGGAGGATCATCGAGGGGAGCCACCTGCTTGAATGCATG 2160
Db 2101 GTCCCGGGACCAAGGAGGATCATCGAGGGGAGCCACCTGCTTGAATGCATG 2160

Qy 2161 GCATGTCCAGAGGAGAGTTTCAGTGTGATAAAAAAGATGCAAGTGGTGTGTA AAAAGTGGCCG 2220
Db 2161 GCATGTCCAGAGGAGAGTTTCAGTGTGATAAAAAAGATGCAAGTGGTGTGTA AAAAGTGGCCG 2220
Qy 2221 AATGATTTCTGGTTCGATGAGAACCAACAGCTCGTGTGATCGCCAAAGAGATCGAGTACTG 2280
Db 2221 AATGATTTCTGGTTCGATGAGAACCAACAGCTCGTGTGATCGCCAAAGAGATCGAGTACTG 2280
Qy 2281 TCGTGGACGAGCCCTTCGGGATCGCTTCACCATCTTCGCCCTACTTGGGCATCTGATC 2340
Db 2281 TCGTGGACGAGCCCTTCGGGATCGCTTCACCATCTTCGCCCTACTTGGGCATCTGATC 2340
Qy 2341 ACCTCCTTCGTGTGGGGTCTTCATCAAGTTGAGGAACACTCCCATCTGTAAGGCCACC 2400
Db 2341 ACCTCCTTCGTGTGGGGTCTTCATCAAGTTGAGGAACACTCCCATCTGTAAGGCCACC 2400
Qy 2401 AACCGGAGTTGTCTTCACTGCTCTTCTTCTCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
Db 2401 AACCGGAGTTGTCTTCACTGCTCTTCTTCTCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
Qy 2461 ATCTTCATCGCGAGCCAGGACTGGAACCTGTGCGCTCGGCCAACCGGCTTTGGCATC 2520
Db 2461 ATCTTCATCGCGAGCCAGGACTGGAACCTGTGCGCTCGGCCAACCGGCTTTGGCATC 2520
Qy 2521 AGCTTCGCTCTGTCATCTCTGTCATCTCTGTAAGAACCAACCGGCTGCTGCTGCTTC 2580
Db 2521 AGCTTCGCTCTGTCATCTCTGTCATCTCTGTAAGAACCAACCGGCTGCTGCTGCTTC 2580
Qy 2581 GAGCCCAAGATCCCAACCGCTCCACCGAAGTGGGTGGGCTCAACCTGCAAGTTCCTC 2640
Db 2581 GAGCCCAAGATCCCAACCGCTCCACCGAAGTGGGTGGGCTCAACCTGCAAGTTCCTC 2640
Qy 2641 CTGCTCTCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTGCTCTACACCGC 2700
Db 2641 CTGCTCTCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTGCTCTACACCGC 2700
Qy 2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGAGAGACGAGGTCACTTCATCACCTGGAC 2760
Db 2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGAGAGACGAGGTCACTTCATCACCTGGAC 2760
Qy 2761 GAGGGCTCGCTCATGGCGCTGGGCTTCTCATCGGCTACACCTGCTCTCGCGGCCATC 2820
Db 2761 GAGGGCTCGCTCATGGCGCTGGGCTTCTCATCGGCTACACCTGCTCTCGCGGCCATC 2820
Qy 2821 TGCTTCTTCTTTCGCTTCAAGTCCCGTAAGCTGCCGAGAACTTCAACGAGGCTAAGTTC 2880
Db 2821 TGCTTCTTCTTTCGCTTCAAGTCCCGTAAGCTGCCGAGAACTTCAACGAGGCTAAGTTC 2880
Qy 2881 ATCACTTCAGCATGTTGATCTTCTTCTCATCGTGTGATCTCTTTCATCCCGCTATGTC 2940
Db 2881 ATCACTTCAGCATGTTGATCTTCTTCTCATCGTGTGATCTCTTTCATCCCGCTATGTC 2940
Qy 2941 AGCACCTACGCAAGTTTGTGCGCGCTGGAGTATTCGCATCTCGGCTCCAGCTTC 3000
Db 2941 AGCACCTACGCAAGTTTGTGCGCGCTGGAGTATTCGCATCTCGGCTCCAGCTTC 3000
Qy 3001 GGGTGTCTGGCTGCATTTACTTCAACAAGTGTTCATCATCTCTGTTCAAGCCGTGCGGT 3060
Db 3001 GGGTGTCTGGCTGCATTTACTTCAACAAGTGTTCATCATCTCTGTTCAAGCCGTGCGGT 3060
Qy 3061 AACACCATCGAGAGTGGCTGAGCAGCGGCCCCACCGCTTCAGAGTGGCGGCCGG 3120
Db 3061 AACACCATCGAGAGTGGCTGAGCAGCGGCCCCACCGCTTCAGAGTGGCGGCCGG 3120
Qy 3121 GCCACCTTCGGCGCAGCGCGCTCTCGCAAGGCTCCAGACGCTGTGGGCTCCACC 3180
Db 3121 GCCACCTTCGGCGCAGCGCGCTCTCGCAAGGCTCCAGACGCTGTGGGCTCCACC 3180
Qy 3181 ATCTCTCGCCGCTGTCTCACTGCGGCGCGGCTTCAACATGAGATGCAAGGCTGC 3240
Db 3181 ATCTCTCGCCGCTGTCTCACTGCGGCGCGGCTTCAACATGAGATGCAAGGCTGC 3240

3241 AGCAGCAGAGGTCAGCTTCGCGCAGCGGACCGTCAACCTGTGCTCAGCTTCAGGAG 3300
 Db AGCAGCAGAGGTCAGCTTCGCGCAGCGGACCGTCAACCTGTGCTCAGCTTCAGGAG 3300
 Qy ACAGCGCGATACCGCCCTCAGCGCAGCGGCGCGCAGCAGGAACTCGCGGATGCGCG 3360
 Db ACAGCGCGATACCGCCCTCAGCGCAGCGGCGCGCAGCAGGAACTCGCGGATGCGCG 3360
 Qy AGCGCGCAGACCTGCGCATCTAGACACCGACCGCGCGCGCTCAGAAATGCGAGGCC 3420
 Db AGCGCGCAGACCTGCGCATCTAGACACCGACCGCGCGCGCTCAGAAATGCGAGGCC 3420
 Qy CAGCGCGCAGACCTGCGCATCTAGACACCGACCGCGCGCGCTCAGAAATGCGAGGCC 3480
 Db CAGCGCGCAGACCTGCGCATCTAGACACCGACCGCGCGCGCTCAGAAATGCGAGGCC 3480
 Qy GCGCGCAGCAGAGGCG 3540
 Db GCGCGCAGCAGAGGCG 3540
 Qy CCAAGAACTCTCTCAGCGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3600
 Db CCAAGAACTCTCTCAGCGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3600
 Qy TGCCCAACT 3660
 Db TGCCCAACT 3660
 Qy TCTTTTATCT 3720
 Db TCTTTTATCT 3720
 Qy ATATGAGTGTGCAATAGGTGAGCAGAGTGTGTGCAAGTATCTGAACTATCTGAAGT 3780
 Db ATATGAGTGTGCAATAGGTGAGCAGAGTGTGTGCAAGTATCTGAACTATCTGAAGT 3780
 Qy ATCTGAACACTTATCT 3840
 Db ATCTGAACACTTATCT 3840
 Qy TTAGTGTCTAAGTGTGCAATAGGTGAGCAGAGTGTGTGCAAGTATCTGAACTATCTGAAGT 3900
 Db TTAGTGTCTAAGTGTGCAATAGGTGAGCAGAGTGTGTGCAAGTATCTGAACTATCTGAAGT 3900
 Qy GACTGAGATGCGCAGTGTGCAAGTGTGTGCAAGTATCTGAACTATCTGAAGT 3960
 Db GACTGAGATGCGCAGTGTGCAAGTGTGTGCAAGTATCTGAACTATCTGAAGT 3960
 Qy TTGCAACAGGATATATGCTGTGCAAGTGTGTGCAAGTATCTGAACTATCTGAAGT 4020
 Db TTGCAACAGGATATATGCTGTGCAAGTGTGTGCAAGTATCTGAACTATCTGAAGT 4020
 Qy TGTAAATCAGATGTGAAATGTGAAATGTGAAATGTGAAATGTGAAATGTGAAATGTGAA 4080
 Db TGTAAATCAGATGTGAAATGTGAAATGTGAAATGTGAAATGTGAAATGTGAAATGTGAA 4080
 Qy AAAGCGCGCGCGCG 4134
 Db AAAGCGCGCGCGCG 4134

RESULT 7
 US-10-125-772-1
 ; Sequence 1, Application US/10125772
 ; Publication No. US20030124657A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MariCal
 ; APPLICANT: Harris, H. William
 ; APPLICANT: Nearing, Jacqueline A.
 ; APPLICANT: Betka, Marlies
 ; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
 ; FILE REFERENCE: 2213.1006-006
 ; CURRENT APPLICATION NUMBER: US/10/125,772

; CURRENT FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: 10/121,441
 ; PRIOR FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: PCT/US01/31704
 ; PRIOR FILING DATE: 2001-10-11
 ; PRIOR APPLICATION NUMBER: 60/240,392
 ; PRIOR FILING DATE: 2000-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,003
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 4134
 ; TYPE: DNA
 ; ORGANISM: Squalus acanthias
 US-10-125-772-1
 Query Match 100.0%; Score 4134; DB 15; Length 4134;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATTCCTGCTGTCGCTTTCAGTCCAAAGTCTCTCCAGTCCAAATGAGAAATGTTGGTTC 60
 Db 1 AATTCCTGCTGTCGCTTTCAGTCCAAAGTCTCTCCAGTCCAAATGAGAAATGTTGGTTC 60
 Qy 61 GCCATTACAGAACATGCTACATCTGTTTAAATGAAATATTGTCAGTTATCTGAAGT 120
 Db 61 GCCATTACAGAACATGCTACATCTGTTTAAATGAAATATTGTCAGTTATCTGAAGT 120
 Qy 121 TATTAAATATGTTTTCGAGGATGGCTTACGAGAAATCAATTCCTGACGTTTCCCAT 180
 Db 121 TATTAAATATGTTTTCGAGGATGGCTTACGAGAAATCAATTCCTGACGTTTCCCAT 180
 Qy 181 GTCTTCTATGAAATGCTACCAAGGATGTAACAAATGGAACAAAGCTGAGGAGCCAC 240
 Db 181 GTCTTCTATGAAATGCTACCAAGGATGTAACAAATGGAACAAAGCTGAGGAGCCAC 240
 Qy 241 GTTCACCTTTTTCGAGGATGATGATCAACCTTGAAGGATGGAAGATGGAAGGAA 300
 Db 241 GTTCACCTTTTTCGAGGATGATGATCAACCTTGAAGGATGGAAGATGGAAGGAA 300
 Qy 301 ATGGGATGATCTTTCAGGATGCTGCTTAAAGGATCCCTCAGCATTAACAAGATAA 360
 Db 301 ATGGGATGATCTTTCAGGATGCTGCTTAAAGGATCCCTCAGCATTAACAAGATAA 360
 Qy 361 GCAGAAATCTTCAGGATGCTGCTTAAAGGATGCTGCTTAAAGGATGCTGCTTAAAGGAA 420
 Db 361 GCAGAAATCTTCAGGATGCTGCTTAAAGGATGCTGCTTAAAGGATGCTGCTTAAAGGAA 420
 Qy 421 CAGAGACGGGCTGCAATGCTGCTTAAAGGATGCTGCTTAAAGGATGCTGCTTAAAGGAT 480
 Db 421 CAGAGACGGGCTGCAATGCTGCTTAAAGGATGCTGCTTAAAGGATGCTGCTTAAAGGAT 480
 Qy 481 CTCCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db 481 CTCCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Qy 541 GACATCATCTGCGAGGCTCTCTTCCCAATACACTTTGGAGTAGCCCGCAAGGATCAGGAC 600
 Db 541 GACATCATCTGCGAGGCTCTCTTCCCAATACACTTTGGAGTAGCCCGCAAGGATCAGGAC 600
 Qy 601 TTAATTCGAGACCGGAGGCGCAAAATGATTTCGGTACAAATTTTCGAGGCTTCCGATG 660
 Db 601 TTAATTCGAGACCGGAGGCGCAAAATGATTTCGGTACAAATTTTCGAGGCTTCCGATG 660
 Qy 661 CTCAGGCGGATGATATTGCAATTTGAAGATTAACAACAGATATGACTTTCTGCGCCCAAT 720
 Db 661 CTCAGGCGGATGATATTGCAATTTGAAGATTAACAACAGATATGACTTTCTGCGCCCAAT 720
 Qy 721 ATCACCCTGGGATATGCTATATTGACAGTGTAAACCGTGTCCAGGCGCTAGAGGCA 780
 Db 721 ATCACCCTGGGATATGCTATATTGACAGTGTAAACCGTGTCCAGGCGCTAGAGGCA 780

QY 781 ACACTCAGCTTTGTGGCCAGAACAAATCGACTCGCTGAACCTTAGATGAGTTCTGTAAAC 840
Db |||||
QY 781 ACACTCAGCTTTGTGGCCAGAACAAATCGACTCGCTGAACCTTAGATGAGTTCTGTAAAC 840
Db |||||
QY 841 TCGCTGACCATATCCCATCCCAATAGCAGTGGTGGGGGCAACCGGGTCAAGGAATCTCC 900
Db |||||
QY 841 TCGCTGACCATATCCCATCCCAATAGCAGTGGTGGGGGCAACCGGGTCAAGGAATCTCC 900
Db |||||
QY 901 ACGGCTGTGGCCAACTATTGGGATATTATTTACATTCACAGGTTCAGTATGCTCTCTCG 960
Db |||||
QY 901 ACGGCTGTGGCCAACTATTGGGATATTATTTACATTCACAGGTTCAGTATGCTCTCTCG 960
Db |||||
QY 961 AGCAGCTGCTCAGCAACAAGAAATGAGTACAAGGCTCTTCTGAGGACCATCCCCAATGAT 1020
Db |||||
QY 961 AGCAGCTGCTCAGCAACAAGAAATGAGTACAAGGCTCTTCTGAGGACCATCCCCAATGAT 1020
Db |||||
QY 1021 GAGCAACAGGCCACGCGCATGCGGAGATCATCGAGCACTTCGAGCACTTCGAGTGAATGGGTGGGA 1080
Db |||||
QY 1021 GAGCAACAGGCCACGCGCATGCGGAGATCATCGAGCACTTCGAGCACTTCGAGTGAATGGGTGGGA 1080
Db |||||
QY 1081 ACCCTGGCAGCGACGATGACTATGGCCGCCAGGCATTGACAACTTCGGGAGAGAGGCC 1140
Db |||||
QY 1081 ACCCTGGCAGCGACGATGACTATGGCCGCCAGGCATTGACAACTTCGGGAGAGAGGCC 1140
Db |||||
QY 1141 GTTAAGAGGGA CATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Db |||||
QY 1141 GTTAAGAGGGA CATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Db |||||
QY 1201 CAGTTGGAGTTCACTCGCCAGCTCATCCAGAACTCTCGGCCAAGTTCATCGTGTCTTC 1260
Db |||||
QY 1201 CAGTTGGAGTTCACTCGCCAGCTCATCCAGAACTCTCGGCCAAGTTCATCGTGTCTTC 1260
Db |||||
QY 1261 TCCAAATGGCCCGACCTGAGCGCTCATCCAGGAGATAGTTTCGAGAAACATACCGAT 1320
Db |||||
QY 1261 TCCAAATGGCCCGACCTGAGCGCTCATCCAGGAGATAGTTTCGAGAAACATACCGAT 1320
Db |||||
QY 1321 CGGATCTGCTGGCCAGCAGAGCTTGGCCAGCTCTCGCTCATTCGCAAGCAGAGTAC 1380
Db |||||
QY 1321 CGGATCTGCTGGCCAGCAGAGCTTGGCCAGCTCTCGCTCATTCGCAAGCAGAGTAC 1380
Db |||||
QY 1381 TTCCAGTGGTGGCGGACCACTCGGCTTCGCTCTCAGGGCGGGGCTATCCAGGGTTC 1440
Db |||||
QY 1381 TTCCAGTGGTGGCGGACCACTCGGCTTCGCTCTCAGGGCGGGGCTATCCAGGGTTC 1440
Db |||||
QY 1441 AACAAATTCCTGAAGAGGTCCACCCAGCAGGTCTCGGACAAATGGGTTTCTCAAGGAG 1500
Db |||||
QY 1441 AACAAATTCCTGAAGAGGTCCACCCAGCAGGTCTCGGACAAATGGGTTTCTCAAGGAG 1500
Db |||||
QY 1501 TTCTGGGAGAGACCTTCACTGCTACTTCCAGAGAGACCTTCAGCAGCTGAAGAT 1560
Db |||||
QY 1501 TTCTGGGAGAGACCTTCACTGCTACTTCCAGAGAGACCTTCAGCAGCTGAAGAT 1560
Db |||||
QY 1561 TCCAAAGGTGCTTCGACGAGCCGGGCTCAAGGGACGGCTCCAAAGCGGGGAATCC 1620
Db |||||
QY 1561 TCCAAAGGTGCTTCGACGAGCCGGGCTCAAGGGACGGCTCCAAAGCGGGGAATCC 1620
Db |||||
QY 1621 AGACGAGACCTTACGCAACCCCTGCTCACTGGGAGGAGAAATCACACGCTGAGAGC 1680
Db |||||
QY 1621 AGACGAGACCTTACGCAACCCCTGCTCACTGGGAGGAGAAATCACACGCTGAGAGC 1680
Db |||||
QY 1681 CCTACTGGAATATACACCTGAGGATCTCCTACAATGTATAGTGGCCGCTTACTCC 1740
Db |||||
QY 1681 CCTACTGGAATATACACCTGAGGATCTCCTACAATGTATAGTGGCCGCTTACTCC 1740
Db |||||
QY 1741 ATTGCTCAGCCCTGCAAGACATCCACTCTTTGCAAAACCCGGGACGGGATCTTTGCAAAAC 1800
Db |||||
QY 1741 ATTGCTCAGCCCTGCAAGACATCCACTCTTTGCAAAACCCGGGACGGGATCTTTGCAAAAC 1800
Db |||||
QY 1801 GGAATCTTGCAATATTAAGGTTGAGGCTGCGAGTCTCTCAACCATCTGCTGAT 1860
Db |||||
QY 1801 GGAATCTTGCAATATTAAGGTTGAGGCTGCGAGTCTCTCAACCATCTGCTGAT 1860
Db |||||
QY 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
Db |||||

Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
QY |||||
QY 1921 GGGAACTACACCATTAACCTGCGAGCTCTCCGAGAGATGAATCGGTGTTGTTCCAT 1980
Db |||||
QY 1921 GGGAACTACACCATTAACCTGCGAGCTCTCCGAGAGATGAATCGGTGTTGTTCCAT 1980
Db |||||
QY 1981 GAGTGGGCAACTACAACGCTTACGCTAAGCCAGTGAACGACTCAACATCAACGAAAAG 2040
Db |||||
QY 1981 GAGTGGGCAACTACAACGCTTACGCTAAGCCAGTGAACGACTCAACATCAACGAAAAG 2040
Db |||||
QY 2041 AATATCTCTGGAGTGGCTTCTCAAGTGGTTCCTTCTCAACCTGCGAGTCCGAGTGT 2100
Db |||||
QY 2041 AATATCTCTGGAGTGGCTTCTCAAGTGGTTCCTTCTCAACCTGCGAGTCCGAGTGT 2100
Db |||||
QY 2101 GTGCGGGCACACAGGAAGGGAATCATCGAGGGGAGCCACCTGCTGCTTTGTAATGATG 2160
Db |||||
QY 2101 GTGCGGGCACACAGGAAGGGAATCATCGAGGGGAGCCACCTGCTGCTTTGTAATGATG 2160
Db |||||
QY 2161 GCATGTGAGAGGAGGATTCAGTGATGAAAAAGATGAAAGTGGTGTACAAAAGTGGCCG 2220
Db |||||
QY 2161 GCATGTGAGAGGAGGATTCAGTGATGAAAAAGATGAAAGTGGTGTACAAAAGTGGCCG 2220
Db |||||
QY 2221 AATGATTTCTGGTGAATGAGAACCAACGCTGCTGATCGCCAAGGAGATCGAGTACCTG 2280
Db |||||
QY 2221 AATGATTTCTGGTGAATGAGAACCAACGCTGCTGATCGCCAAGGAGATCGAGTACCTG 2280
Db |||||
QY 2281 TCGTGGACGAGGCCCTTCGGGATCGCTTCACCATCTTCGCCGTACTGGGCACTCTGATC 2340
Db |||||
QY 2281 TCGTGGACGAGGCCCTTCGGGATCGCTTCACCATCTTCGCCGTACTGGGCACTCTGATC 2340
Db |||||
QY 2341 ACCTCTCTGCTGCTGGGGTCTTCATCAAGTTGAGGAACACTCCCATCTGTAAGGCCACC 2400
Db |||||
QY 2341 ACCTCTCTGCTGCTGGGGTCTTCATCAAGTTGAGGAACACTCCCATCTGTAAGGCCACC 2400
Db |||||
QY 2401 AACCGGAGTTGCTCTACCTGCTGCTCTTCTCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
Db |||||
QY 2401 AACCGGAGTTGCTCTACCTGCTGCTCTTCTCCTCATCTGCTGCTTCTCAGCTCGCTC 2460
Db |||||
QY 2461 ATCTTCAATCGGCGAGGCCAGGAGCTGACCTGCGGCTCGGCCAACCGGCTTTGGGATC 2520
Db |||||
QY 2461 ATCTTCAATCGGCGAGGCCAGGAGCTGACCTGCGGCTCGGCCAACCGGCTTTGGGATC 2520
Db |||||
QY 2521 AGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Db |||||
QY 2521 AGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Db |||||
QY 2581 GAGGCCAAGATCCCAACAGCCTCCACCGCAAGTGGGTGGGCTCAACCTGCGAGTTCCTC 2640
Db |||||
QY 2581 GAGGCCAAGATCCCAACAGCCTCCACCGCAAGTGGGTGGGCTCAACCTGCGAGTTCCTC 2640
Db |||||
QY 2641 CTGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Db |||||
QY 2641 CTGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Db |||||
QY 2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGAGGAGCAGAGTTCATCTTTCATCACCTGGAC 2760
Db |||||
QY 2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGAGGAGCAGAGTTCATCTTTCATCACCTGGAC 2760
Db |||||
QY 2761 GAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
Db |||||
QY 2761 GAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
Db |||||
QY 2821 TGCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
Db |||||
QY 2821 TGCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
Db |||||
QY 2881 ATCACTTCAAGCTGTTGATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Db |||||
QY 2881 ATCACTTCAAGCTGTTGATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Db |||||
QY 2941 AGCACCTACGGAAGTTGCTGCGCGGTGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Db |||||

Db 2941 AGCACCTACGGCAAGTTTGTTCGGCGGTGGAGGTGATTGCCATCTCGCCTCCAGCTTC 3000
Qy 3001 GGCTCTGCTGGCTGCAATTTACTTTCAACAAGTGTATCATCATCTGTTCAAGCGCTGCCGT 3060
Db 3001 GGCTCTGCTGGCTGCAATTTACTTTCAACAAGTGTATCATCATCTGTTCAAGCGCTGCCGT 3060
Qy 3061 AACACCATCGAGGAGTGGCTCGACACGCGCGCCACGCTTCAAGTGGCGCCGG 3120
Db 3061 AACACCATCGAGGAGTGGCTCGACACGCGCGCCACGCTTCAAGTGGCGCCGG 3120
Qy 3121 GCCACCTCGCGCGACGCGCGCTCTCGCAAGCGCTCCAGCAGCGCTGCGCGCTCCACC 3180
Db 3121 GCCACCTCGCGCGACGCGCGCTCTCGCAAGCGCTCCAGCAGCGCTGCGCGCTCCACC 3180
Qy 3181 ATCTCTCGCGCGCTCTCGCAAGCGCTCCAGCAGCGCTGCGCGCTCCACC 3240
Db 3181 ATCTCTCGCGCGCTCTCGCAAGCGCTCCAGCAGCGCTGCGCGCTCCACC 3240
Qy 3241 AGCAGCAGAGGTTCAGCTTCGCGAGCGGCGCTGCTCAGCTTCAGGAG 3300
Db 3241 AGCAGCAGAGGTTCAGCTTCGCGAGCGGCGCTGCTCAGCTTCAGGAG 3300
Qy 3301 ACAGCGCGATACCGCAACCTTCAGCGGCGCGCGCTGCTCAGGAGTGGCGG 3360
Db 3301 ACAGCGCGATACCGCAACCTTCAGCGGCGCGCGCTGCTCAGGAGTGGCGG 3360
Qy 3361 AGCGGCGAGCTGCGCATCTAGACACCGCGCGCGCTGCTCAGGAGTGGCGG 3420
Db 3361 AGCGGCGAGCTGCGCATCTAGACACCGCGCGCGCTGCTCAGGAGTGGCGG 3420
Qy 3421 CAGCCCGCCAAAGATCCCGGATACAGGCGCGCGCGCTGCTCAGGAGTGGCGG 3480
Db 3421 CAGCCCGCCAAAGATCCCGGATACAGGCGCGCGCGCTGCTCAGGAGTGGCGG 3480
Qy 3481 GCGGCGAGCAGGAGCGCGCGCTGCTCAGGAGTGGCGGCTGCTCAGGAGTGGCGG 3540
Db 3481 GCGGCGAGCAGGAGCGCGCGCTGCTCAGGAGTGGCGGCTGCTCAGGAGTGGCGG 3540
Qy 3541 CCCAAGAACTCTCCAGCGCAGCGCTGCTCAGGAGTGGCGGCTGCTCAGGAGTGGCGG 3600
Db 3541 CCCAAGAACTCTCCAGCGCAGCGCTGCTCAGGAGTGGCGGCTGCTCAGGAGTGGCGG 3600
Qy 3601 TGCCCAACCTCTCCCGCACTTTGCGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3660
Db 3601 TGCCCAACCTCTCCCGCACTTTGCGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3660
Qy 3661 TCCTTTTATCCCTGATTTTCTGACTTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3720
Db 3661 TCCTTTTATCCCTGATTTTCTGACTTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3720
Qy 3721 ATATGAGTTGCAATATGAGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3780
Db 3721 ATATGAGTTGCAATATGAGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3780
Qy 3781 ATCTGAACTACTTTATCTCTGAAATTTATACAAACATTTGAAATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3840
Db 3781 ATCTGAACTACTTTATCTCTGAAATTTATACAAACATTTGAAATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3840
Qy 3841 TTATGTTTCAACATTTGAAATTTATACAAACATTTGAAATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3900
Db 3841 TTATGTTTCAACATTTGAAATTTATACAAACATTTGAAATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3900
Qy 3901 GACTGAGTGGCACTGATGAGCAGACTGTTTATACAAACATTTGAAATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3960
Db 3901 GACTGAGTGGCACTGATGAGCAGACTGTTTATACAAACATTTGAAATTTAGTGGATATTTAGTGGATATTTAGTGGAT 3960
Qy 3961 TTGCAACAGGAAATATTAATGACTGTAAACAAACATTTGAAATTTAGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 4020
Db 3961 TTGCAACAGGAAATATTAATGACTGTAAACAAACATTTGAAATTTAGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 4020
Qy 4021 TGTAATCAGATGTGTAATTTGTAATTTACTTCTGTACATTAATTAATTTAGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 4080
Db 4021 TGTAATCAGATGTGTAATTTGTAATTTACTTCTGTACATTAATTAATTTAGTGGATATTTAGTGGATATTTAGTGGATATTTAGTGGAT 4080

Qy 4081 AAGCGCCGCAAGCAACGG 4134
Db 4081 AAGCGCCGCAAGCAACGG 4134

RESULT 8

US-10-016-496-1
; Sequence 1, Application US/10016496
; Publication No. US20030166908A1
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; FILE OF INVENTION: Species and Methods of Use Thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/10/016,496
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US/09/162,021B
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: squalus acanthias
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (439)...(3522)
US-10-016-496-1

Query Match 100.0%; Score 4134; DB 15; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTCCGTTGCTGTCGGTTTCAGTCCCAAGTCTCTCCAGTGCACAAATGAGAAATGGTGGTC 60
Db 1 AATTCCGTTGCTGTCGGTTTCAGTCCCAAGTCTCTCCAGTGCACAAATGAGAAATGGTGGTC 60
Qy 61 GCCATTACAGAAATGACATGATCTGTTTAAATGAAATATTTGTCAGTTATCTGAAGGT 120
Db 61 GCCATTACAGAAATGACATGATCTGTTTAAATGAAATATTTGTCAGTTATCTGAAGGT 120
Qy 121 TATTAAATCTTCTGCAAGGATGGCTTCACGAGAAATCAATTCGACGTTTTCCTCAT 180
Db 121 TATTAAATCTTCTGCAAGGATGGCTTCACGAGAAATCAATTCGACGTTTTCCTCAT 180
Qy 181 GTCAATTGATGAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGACCAC 240
Db 181 GTCAATTGATGAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGACCAC 240
Qy 241 GTTCACCTTTCTTGAGCATGATCAACCTTGAGGAGATGGAAGCTTGAGGAGGAA 300
Db 241 GTTCACCTTTCTTGAGCATGATCAACCTTGAGGAGATGGAAGCTTGAGGAGGAA 300
Qy 301 ATGGGATTCATCTTCCAGGATCTGCTGTAAGGATCCCTCACCATTACAAAGATAA 360
Db 301 ATGGGATTCATCTTCCAGGATCTGCTGTAAGGATCCCTCACCATTACAAAGATAA 360
Qy 361 GCAGAAATCTCCAGGATCTCTGTAAGCGGCTGCGGTAGTGGCTTGGTCAAGGAA 420
Db 361 GCAGAAATCTCCAGGATCTCTGTAAGCGGCTGCGGTAGTGGCTTGGTCAAGGAA 420
Qy 421 CAGAGCAGGCTGCAATGCTGCTGTAAGCGGCTGCGGTAGTGGCTTGGTCAAGGAA 480
Db 421 CAGAGCAGGCTGCAATGCTGCTGTAAGCGGCTGCGGTAGTGGCTTGGTCAAGGAA 480
Qy 481 CTCCTACAGTCGTACAAATGCTCAGGATGCTCAGGATGCTGCTGTAAGCGGCTGCGGTAGTGGCTTGGTCAAGGAA 540


```
QY 2701 CTTCCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTGATCTTTCATCACTCCGAC 2760
DB 2701 CTTCCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTGATCTTTCATCACTCCGAC 2760
QY 2761 GAGGGCTCGCTCATGGCGCTGGGCTTCTCATCGGCTACACCTGCGCTCCCTCCGCGCATC 2820
DB 2761 GAGGGCTCGCTCATGGCGCTGGGCTTCTCATCGGCTACACCTGCGCTCCCTCCGCGCATC 2820
QY 2821 TGTCTTCTTTCGCTTCAAGTCCCGTAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC 2880
DB 2821 TGTCTTCTTTCGCTTCAAGTCCCGTAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC 2880
QY 2881 ATCACCTTCAGCATGTTGATCTTTCATCGCTGCGATCTCTTCAATCCCGCTATGTC 2940
DB 2881 ATCACCTTCAGCATGTTGATCTTTCATCGCTGCGATCTCTTCAATCCCGCTATGTC 2940
QY 2941 AGCACCTACGGCAAGTTTGTGTCGGCGTGGAGGTGATTCATCCCTCCGCTCCAGCTTC 3000
DB 2941 AGCACCTACGGCAAGTTTGTGTCGGCGTGGAGGTGATTCATCCCTCCGCTCCAGCTTC 3000
QY 3001 GGGCTGTGGCTGCATTTACTTTCACAGGTGTTACATCATCTGTTCAAGCGGTGCGGT 3060
DB 3001 GGGCTGTGGCTGCATTTACTTTCACAGGTGTTACATCATCTGTTCAAGCGGTGCGGT 3060
QY 3061 AACACCATCGAGGAGTGGCTGCAGCAGCGGCGCCAGCCCTTCAAGTGGCGCCCGG 3120
DB 3061 AACACCATCGAGGAGTGGCTGCAGCAGCGGCGCCAGCCCTTCAAGTGGCGCCCGG 3120
QY 3121 GCCACCTTCGGCGAGCGCGGTCTCGAAGCGCTCCAGAGCTGTCGCGCTCCACC 3180
DB 3121 GCCACCTTCGGCGAGCGCGGTCTCGAAGCGCTCCAGAGCTGTCGCGCTCCACC 3180
QY 3181 ATCTCTCGCCCTGCTCCACTTGGCGCGGCTCCACATGAGATGAGCGGTGC 3240
DB 3181 ATCTCTCGCCCTGCTCCACTTGGCGCGGCTCCACATGAGATGAGCGGTGC 3240
QY 3241 AGCAGCAGAGTTCAGCTTCGCGAGCGGACCGTCACTCGCTGCTGCTGCTGAGAG 3300
DB 3241 AGCAGCAGAGTTCAGCTTCGCGAGCGGACCGTCACTCGCTGCTGCTGCTGAGAG 3300
QY 3301 ACAGGCGGATACCCACCTTCAGCGCGCGCGCGAGGAACTCGCGGATGCGCG 3360
DB 3301 ACAGGCGGATACCCACCTTCAGCGCGCGCGCGAGGAACTCGCGGATGCGCG 3360
QY 3361 AGCGGCGAGCACTGCGCATCTAGACACCAACGAGGCGCGCTCAGAAATGCGAGGCC 3420
DB 3361 AGCGGCGAGCACTGCGCATCTAGACACCAACGAGGCGCGCTCAGAAATGCGAGGCC 3420
QY 3421 CAGCGCGCAACCATGCGGATACAGGCGCGCGCGACCAAGGCACTAGAGTCGCG 3480
DB 3421 CAGCGCGCAACCATGCGGATACAGGCGCGCGCGACCAAGGCACTAGAGTCGCG 3480
QY 3481 GCGGCGAGCAAGGAGCGCGCCCAACTATGAGGAGAACTTAATCCAACTCTCCATCAAC 3540
DB 3481 GCGGCGAGCAAGGAGCGCGCCCAACTATGAGGAGAACTTAATCCAACTCTCCATCAAC 3540
QY 3541 CCCAAGAAATCTCCAGCGGAGCAGCGTGCAGCACTGACATCACTCTAACCCTGCG 3600
DB 3541 CCCAAGAAATCTCCAGCGGAGCAGCGTGCAGCACTGACATCACTCTAACCCTGCG 3600
QY 3601 TGCCCAACTCTCCCTCTCCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
DB 3601 TGCCCAACTCTCCCTCTCCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
QY 3661 TCCCTTTATCCCTGATTTTCTGATTTGATATTTACTAGTGGGATGGAATATCAAC 3720
DB 3661 TCCCTTTATCCCTGATTTTCTGATTTGATATTTACTAGTGGGATGGAATATCAAC 3720
QY 3721 ATAACTGAGTTCACAAATTAGGTGAGCAGAGTGTGTCAGAGTATCTGAACTATCTGAAGT 3780
DB 3721 ATAACTGAGTTCACAAATTAGGTGAGCAGAGTGTGTCAGAGTATCTGAACTATCTGAAGT 3780
```

```
QY 3781 ATCTGAACCTACTTTATTCTCTCGAATTTGATTTACAAACATTTTGAAGTATTTTAGTGACA 3840
DB 3781 ATCTGAACCTACTTTATTCTCTCGAATTTGATTTACAAACATTTTGAAGTATTTTAGTGACA 3840
QY 3841 TTATGTTCTAACATTTGTCAAGATAAATTTGTTTCAACATATAAGGTACCACTGAAGCAGT 3900
DB 3841 TTATGTTCTAACATTTGTCAAGATAAATTTGTTTCAACATATAAGGTACCACTGAAGCAGT 3900
QY 3901 GACTGAGATTCGCCACTGTGATGACAGAACTGTTTATAACATTTATCAATTTGAAACCTGGA 3960
DB 3901 GACTGAGATTCGCCACTGTGATGACAGAACTGTTTATAACATTTATCAATTTGAAACCTGGA 3960
QY 3961 TTGCAACAGGAATAATAATGACTGTAAACAAAAAATTTGTTGATTATCTTAAAAATGCAAAAT 4020
DB 3961 TTGCAACAGGAATAATAATGACTGTAAACAAAAAATTTGTTGATTATCTTAAAAATGCAAAAT 4020
QY 4021 TGTAAATCAGATGTGTAATAATTTGTTAAATTTCTGTACATTAATGCAATTTCTTGATA 4080
DB 4021 TGTAAATCAGATGTGTAATAATTTGTTAAATTTCTGTGTACATTAATGCAATTTCTTGATA 4080
QY 4081 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 4134
DB 4081 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 4134
```

RESULT 9
US-10-411-076-23
; Sequence 23, Application US/10411076
; Publication No. US2003026516A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Growing Marine Fish in Freshwater
; FILE REFERENCE: 2213.1003007
; CURRENT APPLICATION NUMBER: US/10/411,076
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US01/31625
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/687,373
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Mustelus canis
US-10-411-076-23

Query Match 100.0%; Score 4134; DB 15; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AATTCCTGCTGTCGGTTCCAGTCCAGTCTCTCCAGTCAAAATGAGAAATGGTGGTC 60
DB 1 AATTCCTGCTGTCGGTTCCAGTCCAGTCTCTCCAGTCAAAATGAGAAATGGTGGTC 60
QY 61 GCCATTCAGAACATGCACTACATCTGTTTAAATGAAATATTGTGATTTATCTGAAGGT 120
DB 61 GCCATTCAGAACATGCACTACATCTGTTTAAATGAAATATTGTGATTTATCTGAAGGT 120
QY 121 TATTAATGTTTTCGACGAGTGGTTCACGAGAAATCAATTCGACGTTTCCCAT 180
DB 121 TATTAATGTTTTCGACGAGTGGTTCACGAGAAATCAATTCGACGTTTCCCAT 180
QY 181 GTCAATTCATGAATACTGACCAAGGATGTTAAACAAATGGAACAAAGCTGAGGACCAC 240
DB 181 GTCAATTCATGAATACTGACCAAGGATGTTAAACAAATGGAACAAAGCTGAGGACCAC 240
QY 241 GTTCACCTTTCTTGGAGCATACATCAACCTGAGGAGATGGAAGCTTTGAGGAGAA 300
DB 241 GTTCACCTTTCTTGGAGCATACATCAACCTGAGGAGATGGAAGCTTTGAGGAGAA 300
```

301 ATGGGGATTGATCTTCCAGGAGTTCTGTGTAAAGGATCCCTCACCAATTACAAAGATAA 360
301 ATGGGGATTGATCTTCCAGGAGTTCTGTGTAAAGGATCCCTCACCAATTACAAAGATAA 360
361 GAGAAATCCTCAGGATCCTCTGTAAACGGCTGGGTAGTGGTCTGTCAAGGAA 420
361 GAGAAATCCTCAGGATCCTCTGTAAACGGCTGGGTAGTGGTCTGTCAAGGAA 420
421 CAGAGACAGGGTGCACAATAGCTCAGCTTCACTGCAACTCTTATTTCTGGGATTTACA 480
421 CAGAGACAGGGTGCACAATAGCTCAGCTTCACTGCAACTCTTATTTCTGGGATTTACA 480
481 CTCCTACAGTCTACAAATGCTCAGGATGCTCCAAACCAAGGGCCAGAAAGGA 540
481 CTCCTACAGTCTACAAATGCTCAGGATGCTCCAAACCAAGGGCCAGAAAGGA 540
541 GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCGCCCAAGGATCAGGAC 600
541 GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCGCCCAAGGATCAGGAC 600
601 TTAATAATCAGACCGGAGCGGACAAATGATTTGGTACAAATTTTCGAGGCTTCCGATGG 660
601 TTAATAATCAGACCGGAGCGGACAAATGATTTGGTACAAATTTTCGAGGCTTCCGATGG 660
661 CTCAGGCGATGATATTCCCAATTTGAAGAGATTAAACAAGTATGACTTTCCTGCCCAAT 720
661 CTCAGGCGATGATATTCCCAATTTGAAGAGATTAAACAAGTATGACTTTCCTGCCCAAT 720
721 ATCACCTGGGATATCGCATATTTGACAGGTGTAACACCGTGTCCAAAGCGGTAGAGGCA 780
721 ATCACCTGGGATATCGCATATTTGACAGGTGTAACACCGTGTCCAAAGCGGTAGAGGCA 780
781 ACACCTCAGCTTTGGCCCGAGACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
781 ACACCTCAGCTTTGGCCCGAGACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840
841 TGTCTTGACCATATCCCATCCCAATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900
841 TGTCTTGACCATATCCCATCCCAATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900
901 AGGCTGTGGCCAACTATTTGGATTATTTTACATTCACAGGTGAGCTATGCTTCCCTCG 960
901 AGGCTGTGGCCAACTATTTGGATTATTTTACATTCACAGGTGAGCTATGCTTCCCTCG 960
961 AGCAGGCTGCTCAGCAACAAGATGATGTAAGGGCTTCTCAGGACCAATCCCAATGAT 1020
961 AGCAGGCTGCTCAGCAACAAGATGATGTAAGGGCTTCTCAGGACCAATCCCAATGAT 1020
1021 GAGCAACAGGCCACCGCCATGGCCGAGATCATCGAGCATTCAGTGGAACTGGGTGGGA 1080
1021 GAGCAACAGGCCACCGCCATGGCCGAGATCATCGAGCATTCAGTGGAACTGGGTGGGA 1080
1081 ACCCTGGCAGCCGACGATGACTATGGCCCGCCAGGCAATGACAAGTTCCGGAGAGGCC 1140
1081 ACCCTGGCAGCCGACGATGACTATGGCCCGCCAGGCAATGACAAGTTCCGGAGAGGCC 1140
1141 GTTAAGAGGACATCTGTATTGACTTCACTTCACTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
1141 GTTAAGAGGACATCTGTATTGACTTCACTTCACTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
1201 CAGTTGGAGTTATCGCCGAGTCACTCAGAACTCTCGGCCCAAGTCACTGTGTCTTC 1260
1201 CAGTTGGAGTTATCGCCGAGTCACTCAGAACTCTCGGCCCAAGTCACTGTGTCTTC 1260
1261 TCCAAATGGCCCCGACCTGGAGCGCTCATCCAGGAGATAGTTCCGAGAAACATCACCGAT 1320
1261 TCCAAATGGCCCCGACCTGGAGCGCTCATCCAGGAGATAGTTCCGAGAAACATCACCGAT 1320
1321 CGGATCTGGCTGCCAGCGAGGCTTGGGCCAGCTCTTTCGCTCATTTGCCAAGCCAGAGTAC 1380
1321 CGGATCTGGCTGCCAGCGAGGCTTGGGCCAGCTCTTTCGCTCATTTGCCAAGCCAGAGTAC 1380

1381 TTCCACGTGTCGGCGCACCATCGGCTTCGCTCTCAGGGCGGGCGGTATCCAGGGTTC 1440
1381 TTCCACGTGTCGGCGCACCATCGGCTTCGCTCTCAGGGCGGGCGGTATCCAGGGTTC 1440
1441 AACAAAGTTCCTGAGGAGGTCCACCCAGCAGGTCTCTCGACAATGGTTTGTCAAGGAG 1500
1441 AACAAAGTTCCTGAGGAGGTCCACCCAGCAGGTCTCTCGACAATGGTTTGTCAAGGAG 1500
1501 TTCTGGGAGAGACCTTTCACTGCTACTTCAACGAGAGACCTCTGACGAGCTGAGAAT 1560
1501 TTCTGGGAGAGACCTTTCACTGCTACTTCAACGAGAGACCTCTGACGAGCTGAGAAT 1560
1561 TCCAAAGTTCGCTCGACGAGACCGGCGCTCAAGGGGACGGCTCCAAAGGCGGGAACTCC 1620
1561 TCCAAAGTTCGCTCGACGAGACCGGCGCTCAAGGGGACGGCTCCAAAGGCGGGAACTCC 1620
1621 AGACGAGACGCGCTTACGCCACCCCTGCACTGGGGAGAGAAACATCACACGCTGGAGAC 1680
1621 AGACGAGACGCGCTTACGCCACCCCTGCACTGGGGAGAGAAACATCACACGCTGGAGAC 1680
1681 CCTTACCTGGATTATACACACCTGAGGATCTCTTACAATGTATACGTGGCGCTTACTCC 1740
1681 CCTTACCTGGATTATACACACCTGAGGATCTCTTACAATGTATACGTGGCGCTTACTCC 1740
1741 ATTGCTCACGCGCTTGAAGACATCCACTCTTTGCAAAACCCGGCAGCGGCACTTTTGAAC 1800
1741 ATTGCTCACGCGCTTGAAGACATCCACTCTTTGCAAAACCCGGCAGCGGCACTTTTGAAC 1800
1801 GGATCTTGTGAGATATTAAGAGTTGAGCGCTGGCAGGTCTCTCAACCATCTCTGCTCAT 1860
1801 GGATCTTGTGAGATATTAAGAGTTGAGCGCTGGCAGGTCTCTCAACCATCTCTGCTCAT 1860
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
1921 GGGAACTTACCAATTTCACTGSCAGCTCTCCGACAGGATGATCGGTGTTGTTCCAT 1980
1921 GGGAACTTACCAATTTCACTGSCAGCTCTCCGACAGGATGATCGGTGTTGTTCCAT 1980
1981 GAGTGGGCACTACAACGCTTACGCTAAGCCAGTACCGACTCAACATCAACGAAAG 2040
1981 GAGTGGGCACTACAACGCTTACGCTAAGCCAGTACCGACTCAACATCAACGAAAG 2040
2041 AAAATCTCTGGAGTGGCTTCTCAAAGTGGTCTCTTCTCAAACCTGAGTCAAGTGT 2100
2041 AAAATCTCTGGAGTGGCTTCTCAAAGTGGTCTCTTCTCAAACCTGAGTCAAGTGT 2100
2101 GTGCGGGCACCAAGAGGGATCATCGAGGGGAGCCACCTGCTCTTTGAATGCATG 2160
2101 GTGCGGGCACCAAGAGGGATCATCGAGGGGAGCCACCTGCTCTTTGAATGCATG 2160
2161 GCATGTGCAGAGGAGAGTTCAAGTGAATAAAGATGCAAGTGGCTGTACAAAGTGCCCG 2220
2161 GCATGTGCAGAGGAGAGTTCAAGTGAATAAAGATGCAAGTGGCTGTACAAAGTGCCCG 2220
2221 AATGATTTCTGGTGCATGAGAACCAACGTCGTGATCGCAAGGAGATCGAGTACTG 2280
2221 AATGATTTCTGGTGCATGAGAACCAACGTCGTGATCGCAAGGAGATCGAGTACTG 2280
2281 TCCTGGACGAGCCCTTCGGGATCGCTGACCATCTTCGCCGTACTGGGCACTCTGATC 2340
2281 TCCTGGACGAGCCCTTCGGGATCGCTGACCATCTTCGCCGTACTGGGCACTCTGATC 2340
2341 ACCTCTTCTGCTGGGGTCTTCAAGTTTGAAGAACTCCCATCTGTAAGGCGCAC 2400
2341 ACCTCTTCTGCTGGGGTCTTCAAGTTTGAAGAACTCCCATCTGTAAGGCGCAC 2400
2401 AACCGGAGTTGCTCTACCTGCTCTTCTCCCTCATCTGCTCTCTTCTCAGGCTCGCTC 2460
2401 AACCGGAGTTGCTCTACCTGCTCTTCTCCCTCATCTGCTCTCTTCTCAGGCTCGCTC 2460
2461 ATCTTATCGGCGAGCCCGAGGACTGGAACCTGTGCGGTTCGCCAACCGGCGCTTTTGGCATC 2520

QY 1 AATCCGTTGTCGGTTCAGTCCAAAGTCTCCTCCAGTGCAGAAATGAGAAATGGTGGTC 60
Db |||||
1 AATCCGTTGTCGGTTCAGTCCAAAGTCTCCTCCAGTGCAGAAATGAGAAATGGTGGTC 60
QY |||||
61 GCATTACAGGAACATGACATACATCTGTGTTAATGAATATGTCAGTTATCTGAAGGT 120
Db |||||
61 GCATTACAGGAACATGACATACATCTGTGTTAATGAATATGTCAGTTATCTGAAGGT 120
QY |||||
121 TATTAATAATGTTCTGCAAGGATGCTTCACAGAGAAATCAATTCGACGTTTTCCCAAT 180
Db |||||
121 TATTAATAATGTTCTGCAAGGATGCTTCACAGAGAAATCAATTCGACGTTTTCCCAAT 180
QY |||||
181 GTCATTGATGAATAACTGACCAAGAGGATGTAAACAAATGGAACAAAGCTGAGGACAC 240
Db |||||
181 GTCATTGATGAATAACTGACCAAGAGGATGTAAACAAATGGAACAAAGCTGAGGACAC 240
QY |||||
241 GTTCAACCTTCTTGGAGCATACGATCAACCTGGAAGGATGGAAGACTTGGAGAGGAA 300
Db |||||
301 ATGGGGATTGATCTTCCAGGATCTGCTGTAAAGCGATCCCTCACCAATTAACAAGATAA 360
Db |||||
301 ATGGGGATTGATCTTCCAGGATCTGCTGTAAAGCGATCCCTCACCAATTAACAAGATAA 360
QY |||||
361 GCAGAAATCCTCCAGGATCTCTGTAAAGCGGCTGGGCTAGTGGCTTGGTCAAGGAA 420
Db |||||
361 GCAGAAATCCTCCAGGATCTCTGTAAAGCGGCTGGGCTAGTGGCTTGGTCAAGGAA 420
QY |||||
421 CAGACACAGGCTGCACAAATGCTCAGCTTCACTGCCAACTTATTCTTGGGATTTACA 480
Db |||||
421 CAGACACAGGCTGCACAAATGCTCAGCTTCACTGCCAACTTATTCTTGGGATTTACA 480
QY |||||
481 CTCCTACAGTCGTAATGCTCAGGGTATGTTCCCAATACACTTTGGAGTAGCGCCAGGAC 540
Db |||||
481 CTCCTACAGTCGTAATGCTCAGGGTATGTTCCCAATACACTTTGGAGTAGCGCCAGGAC 540
QY |||||
541 GACATCACTGGGAGGCTCTTCCCAATACACTTTGGAGTAGCGCCAGGAC 600
Db |||||
541 GACATCACTGGGAGGCTCTTCCCAATACACTTTGGAGTAGCGCCAGGAC 600
QY |||||
601 TTAAATTCAGACCGGAGCGCAAAATGATATTCGGTACATTTTCGAGGCTTCGGATGG 660
Db |||||
601 TTAAATTCAGACCGGAGCGCAAAATGATATTCGGTACATTTTCGAGGCTTCGGATGG 660
QY |||||
661 CTCACAGGCGATGATATTCGCAATTCGAGATTAACAACAGTATGACTTCTCGCCCAAT 720
Db |||||
661 CTCACAGGCGATGATATTCGCAATTCGAGATTAACAACAGTATGACTTCTCGCCCAAT 720
QY |||||
721 ATCACCTGGGATATCGCATATTTGACAGTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780
Db |||||
721 ATCACCTGGGATATCGCATATTTGACAGTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780
QY |||||
781 ACACCTCAGCTTTGTGGCCAGAACAAATCGACTCGCTGAACCTTAGATGAGTTCTGTAAAC 840
Db |||||
781 ACACCTCAGCTTTGTGGCCAGAACAAATCGACTCGCTGAACCTTAGATGAGTTCTGTAAAC 840
QY |||||
841 TGCTCTGACCATATCCCATCCCAATAGCAGTGGTGGGGCAACCGGGTCAGGAAATCTCC 900
Db |||||
841 TGCTCTGACCATATCCCATCCCAATAGCAGTGGTGGGGCAACCGGGTCAGGAAATCTCC 900
QY |||||
901 AGCGTGTGGCAATCTATTGGATTAATTTACATTCACAGGTGAGCTATGCTTCCTCG 960
Db |||||
901 AGCGTGTGGCAATCTATTGGATTAATTTACATTCACAGGTGAGCTATGCTTCCTCG 960
QY |||||
961 AGCAGGCTCTCAGCAACAAAGATGAGTACAAAGGCTTCTCAGGACCATCCCAATGAT 1020
Db |||||
961 AGCAGGCTCTCAGCAACAAAGATGAGTACAAAGGCTTCTCAGGACCATCCCAATGAT 1020
QY |||||
1021 GAGCAACAGGCCACCGCCATGCGCGAGATCATCGAGCATCTCCAGTGGAACCTGGGTGGGA 1080
Db |||||
1021 GAGCAACAGGCCACCGCCATGCGCGAGATCATCGAGCATCTCCAGTGGAACCTGGGTGGGA 1080
QY |||||
1081 ACCCTGGACCGACGATGACTATGGCCGCCAGGCAATTTGACAAAGTTCGGGAGGAGGCC 1140

Db |||||
1081 ACCCTGGACCGACGATGACTATGGCCGCCAGGCAATTTGACAAAGTTCGGGAGGAGGCC 1140
QY |||||
1141 GTTAAGAGGACATCTGTATTGATTTAGTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
Db |||||
1141 GTTAAGAGGACATCTGTATTGATTTAGTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200
QY |||||
1201 CAGTTGAGGATTCATCGCCGACGTCATCCAGAACTCTCCGCCAAGGTCATCGTGGTCTTC 1260
Db |||||
1201 CAGTTGAGGATTCATCGCCGACGTCATCCAGAACTCTCCGCCAAGGTCATCGTGGTCTTC 1260
QY |||||
1261 TCCAAATGGCCCGACCTGGAGCGGCTCATCCAGAGATAGTTCCGAGAAACATCACCGAT 1320
Db |||||
1261 TCCAAATGGCCCGACCTGGAGCGGCTCATCCAGAGATAGTTCCGAGAAACATCACCGAT 1320
QY |||||
1321 CGGATCTGGCTGGCCAGCGAGGCTTGGGCCAGCTCTTCGGCTATTCGCCAAGCCAGAGTAC 1380
Db |||||
1321 CGGATCTGGCTGGCCAGCGAGGCTTGGGCCAGCTCTTCGGCTATTCGCCAAGCCAGAGTAC 1380
QY |||||
1381 TTCCAGTGGTTCGGCGCACCATCGGCTTCGCTCAGGGCGGGGCTATCCAGGGTTC 1440
Db |||||
1381 TTCCAGTGGTTCGGCGCACCATCGGCTTCGCTCAGGGCGGGGCTATCCAGGGTTC 1440
QY |||||
1441 AACAAAGTTCCTGAAGGAGGTCACCCAGCAGGTCTCTCGGACAAATGGTGTCAAGGAG 1500
Db |||||
1441 AACAAAGTTCCTGAAGGAGGTCACCCAGCAGGTCTCTCGGACAAATGGTGTCAAGGAG 1500
QY |||||
1501 TTCTGGAGGAGACCTTCAATCTGCTACTTACCGAGAGACCTCTGACGAGCTGAGAAAT 1560
Db |||||
1501 TTCTGGAGGAGACCTTCAATCTGCTACTTACCGAGAGACCTCTGACGAGCTGAGAAAT 1560
QY |||||
1561 TCCAAAGTGGCTTCGACGAGCGGGGCTCAAGGGGACCGGCTCCAAAGCGGGGAACTCC 1620
Db |||||
1561 TCCAAAGTGGCTTCGACGAGCGGGGCTCAAGGGGACCGGCTCCAAAGCGGGGAACTCC 1620
QY |||||
1621 AGACGACAGCCCTAGCCACCCCTGCACTGCGGGAGGAGAACATCACAGCGTGGAGACC 1680
Db |||||
1621 AGACGACAGCCCTAGCCACCCCTGCACTGCGGGAGGAGAACATCACAGCGTGGAGACC 1680
QY |||||
1681 CCTTACCTGATTTATACACACTGAGATCTCTCAATGTATACGTGGCCGCTACTCTCC 1740
Db |||||
1681 CCTTACCTGATTTATACACACTGAGATCTCTCAATGTATACGTGGCCGCTACTCTCC 1740
QY |||||
1741 ATTGCTCACCCCTGCAAGACATCCACTCTTTGCAAAACCCCGGACCGGCACTTTTGAAC 1800
Db |||||
1741 ATTGCTCACCCCTGCAAGACATCCACTCTTTGCAAAACCCCGGACCGGCACTTTTGAAC 1800
QY |||||
1801 GGATCTTGTGACATATTAATAAAGTTGAGCCCTGCGAGGCTCTCAACCATCTGCTGCAT 1860
Db |||||
1801 GGATCTTGTGACATATTAATAAAGTTGAGCCCTGCGAGGCTCTCAACCATCTGCTGCAT 1860
QY |||||
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTTGACGATCAAGGTGACCTCAAG 1920
Db |||||
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTTGACGATCAAGGTGACCTCAAG 1920
QY |||||
1921 GGGAACTACACCATTAATCAACTGGCAGCTCTCGCGAGAGATGAATCGGTGTTGTTCCAT 1980
Db |||||
1921 GGGAACTACACCATTAATCAACTGGCAGCTCTCGCGAGAGATGAATCGGTGTTGTTCCAT 1980
QY |||||
1981 GAGTGGGCAACTACACGCTAGCTAAGCCCAAGTACCGACTCAACATCAACGAAAG 2040
Db |||||
1981 GAGTGGGCAACTACACGCTAGCTAAGCCCAAGTACCGACTCAACATCAACGAAAG 2040
QY |||||
2041 AAAATCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCCAACTGCGAGTGGAGTGT 2100
Db |||||
2041 AAAATCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCCAACTGCGAGTGGAGTGT 2100
QY |||||
2101 GTCCCGGACACAGGAGGGATCATCGAGGGGAGCCACCTGCTGCTTTGATGATG 2160
Db |||||
2101 GTCCCGGACACAGGAGGGATCATCGAGGGGAGCCACCTGCTGCTTTGATGATG 2160
QY |||||
2161 GCATGTGCAGAGGAGAGTTTCAGTGTGATGAAAGATGCAAGTGGCTGTACAAAGTGGCCG 2220

Db 2161 GCATGTGACAGGAGAGTTCAGTGTGATGAAACGATGCAAGTGCCTGTATCAAAAGTGCCTG 2220
QY 2221 AATGATTTCTGTGTCGAATCAGAACACACAGTGTGTCATGCCAACAGAGATCAGTACCTG 2280
Db 2221 AATGATTTCTGTGTCGAATCAGAACACACAGTGTGTCATGCCAACAGAGATCAGTACCTG 2280
QY 2281 TCGTGACGAGCCCTTCGGGATCGCTCTGACATCTTCGCCGTACTCGGCTACTCTGATC 2340
Db 2281 TCGTGACGAGCCCTTCGGGATCGCTCTGACATCTTCGCCGTACTCGGCTACTCTGATC 2340
QY 2341 ACCTCCTCTGCTGCGGGTCTTCATCAAGTTTCAGGAACACCTCCATCGTGAAGGCCACC 2400
Db 2341 ACCTCCTCTGCTGCGGGTCTTCATCAAGTTTCAGGAACACCTCCATCGTGAAGGCCACC 2400
QY 2401 AACCGGAGTTGTCCTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460
Db 2401 AACCGGAGTTGTCCTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460
QY 2461 ATCTTCATCGGAGCCGAGGACTGGACCTGTGCGCTCCGCAACCGGCTTTGGCATC 2520
Db 2461 ATCTTCATCGGAGCCGAGGACTGGACCTGTGCGCTCCGCAACCGGCTTTGGCATC 2520
QY 2521 AGCTTCGCTCTGTCATCTCTGTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 2580
Db 2521 AGCTTCGCTCTGTCATCTCTGTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 2580
QY 2581 GAGGCCAAGATCCCAACAGCTTCAACGCAAGTGGTGGGCTCAACCTGAGTTCCTC 2640
Db 2581 GAGGCCAAGATCCCAACAGCTTCAACGCAAGTGGTGGGCTCAACCTGAGTTCCTC 2640
QY 2641 CTGGTCTCTGTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2700
Db 2641 CTGGTCTCTGTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2700
QY 2701 CTTCTCTCAGCTACAGGAACATGAGCTGGAGGACGAGGTCACTTCATCACTTCGAC 2760
Db 2701 CTTCTCTCAGCTACAGGAACATGAGCTGGAGGACGAGGTCACTTCATCACTTCGAC 2760
QY 2761 GAGGCTCTGCTCATGCGCTGGGCTCTTCATCGCTACACCTGCTCTCTGCGGCCATC 2820
Db 2761 GAGGCTCTGCTCATGCGCTGGGCTCTTCATCGCTACACCTGCTCTCTGCGGCCATC 2820
QY 2821 TGTCTCTCTGCGCTTCAAGTCCCGTAAAGTCCCGGAGAACTTCAAGAGGCTAAGTTC 2880
Db 2821 TGTCTCTCTGCGCTTCAAGTCCCGTAAAGTCCCGGAGAACTTCAAGAGGCTAAGTTC 2880
QY 2881 ATCACTTCAGCATGTGATCTCTTCATCGTCTGATCTCTTCATCGCTCTGCTCTGCT 2940
Db 2881 ATCACTTCAGCATGTGATCTCTTCATCGTCTGATCTCTTCATCGCTCTGCTCTGCT 2940
QY 2941 AGCACCTACGGCAAGTTTGTGTCGCGCGTGGAGGTGATTCGCTCTGCGCTTCCAGCTTC 3000
Db 2941 AGCACCTACGGCAAGTTTGTGTCGCGCGTGGAGGTGATTCGCTCTGCGCTTCCAGCTTC 3000
QY 3001 GGGCTCTGGGCTGATTTACTTCAACAGTGTATCATCTCTGTTCAAGCCGTGCGCT 3060
Db 3001 GGGCTCTGGGCTGATTTACTTCAACAGTGTATCATCTCTGTTCAAGCCGTGCGCT 3060
QY 3061 AACACCATCGAGAGTGTGCTGACAGCGCGGCCCGCTTCAAGTGTGCGGCCCGG 3120
Db 3061 AACACCATCGAGAGTGTGCTGACAGCGCGGCCCGCTTCAAGTGTGCGGCCCGG 3120
QY 3121 GGCACCTCCGGCGAGCCCGCTCTCGAAGCGCTCCAGAGCTCTGCGGCTTCCACC 3180
Db 3121 GGCACCTCCGGCGAGCCCGCTCTCGAAGCGCTCCAGAGCTCTGCGGCTTCCACC 3180
QY 3181 ATCTCTCTCGCCGCTCTGCTACCTCTGCGGCGCGGCTTCAACATGAGATGAGCGCTC 3240
Db 3181 ATCTCTCTCGCCGCTCTGCTACCTCTGCGGCGCGGCTTCAACATGAGATGAGCGCTC 3240
QY 3241 AGCAGCAGAGGTCTGAGTCTCGGCGAGCGGCTTCAACCTCTGCTCTGCTCTGAGGAG 3300
Db 3241 AGCAGCAGAGGTCTGAGTCTCGGCGAGCGGCTTCAACCTCTGCTCTGCTCTGAGGAG 3300

QY 3301 ACAGCCGATACGCCACCTCTCAGCCGACGCGCCGACGAGGAACCTCGCGGATGCGCGC 3360
Db 3301 ACAGCCGATACGCCACCTCTCAGCCGACGCGCCGACGAGGAACCTCGCGGATGCGCGC 3360
QY 3361 AGCGGCGACACCTGCTCTAGACACACGACGAGCGCGCCGCTCAGAAATGCGAGCCC 3420
Db 3361 AGCGGCGACACCTGCTCTAGACACACGACGAGCGCGCCGCTCAGAAATGCGAGCCC 3420
QY 3421 CAGCCGCCCAACGATGCGCGATCAAGGCGCGCCGACCAAGGCGCCCTTAGAGTGCCTG 3480
Db 3421 CAGCCGCCCAACGATGCGCGATCAAGGCGCGCCGACCAAGGCGCCCTTAGAGTGCCTG 3480
QY 3481 GCGGCGAGGAGGCGCGCCCAACATATGAGAGGAACCTTAATCCAACTCTCTCAAC 3540
Db 3481 GCGGCGAGGAGGCGCGCCCAACATATGAGAGGAACCTTAATCCAACTCTCTCAAC 3540
QY 3541 CCCAAGAACATCTCTCAGCGGACGCGCTCGCAACATCACTCAACTCTCTAAACCGGTGC 3600
Db 3541 CCCAAGAACATCTCTCAGCGGACGCGCTCGCAACATCACTCAACTCTCTAAACCGGTGC 3600
QY 3601 TGCCCAACCTCTCCCTCTCCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Db 3601 TGCCCAACCTCTCCCTCTCCGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
QY 3661 TCCCTTTATCCCTGATTTCTGACTTGGATTTACTAGTGTGCGATGGAATATCAAC 3720
Db 3661 TCCCTTTATCCCTGATTTCTGACTTGGATTTACTAGTGTGCGATGGAATATCAAC 3720
QY 3721 ATAATGAGTTGCAAAATAGGTGAGCAGAGTGTGTCAAAAGTATCTGAACTATCTGAAGT 3780
Db 3721 ATAATGAGTTGCAAAATAGGTGAGCAGAGTGTGTCAAAAGTATCTGAACTATCTGAAGT 3780
QY 3781 ATCTGAACTACTTTATCTCTCGAATTTATTAACAACATTTGAAGTATTTTAGTGACA 3840
Db 3781 ATCTGAACTACTTTATCTCTCGAATTTATTAACAACATTTGAAGTATTTTAGTGACA 3840
QY 3841 TTATGTTTCAACATTTGCAAGATAATTTGTTCAACATATAAGGTACCTGAAGCAGT 3900
Db 3841 TTATGTTTCAACATTTGCAAGATAATTTGTTCAACATATAAGGTACCTGAAGCAGT 3900
QY 3901 GACTGAGTTGCACTGTGATGACAGAACTGTTTTATACATTTATCATTTGAACCTGGA 3960
Db 3901 GACTGAGTTGCACTGTGATGACAGAACTGTTTTATACATTTATCATTTGAACCTGGA 3960
QY 3961 TTGCAACAGGAATATATGACTGTAAACAAAATTTGTTGATTTCTTAAATGCAAAAT 4020
Db 3961 TTGCAACAGGAATATATGACTGTAAACAAAATTTGTTGATTTCTTAAATGCAAAAT 4020
QY 4021 TGTAAATCAGATGTGAAAATTTGTTGATTTCTTACATTTAAATGCAATTTCTTGATA 4080
Db 4021 TGTAAATCAGATGTGAAAATTTGTTGATTTCTTACATTTAAATGCAATTTCTTGATA 4080
QY 4081 AAGCGG 4134
Db 4081 AAGCGG 4134

RESULT 11

US-10-410-885-1
; Sequence 1, Application US/10410885
; Publication No. US20030232366A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-008
; CURRENT APPLICATION NUMBER: US/10/410,885
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 10/125,778
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/125,772

<p> ; PRIOR FILING DATE: 2002-04-18 ; PRIOR APPLICATION NUMBER: 10/125,792 ; PRIOR FILING DATE: 2002-04-18 ; PRIOR APPLICATION NUMBER: 10/121,441 ; PRIOR FILING DATE: 2002-04-11 ; PRIOR APPLICATION NUMBER: PCT/US01/31704 ; PRIOR FILING DATE: 2001-10-11 ; PRIOR APPLICATION NUMBER: 60/240,392 ; PRIOR FILING DATE: 2000-10-12 ; PRIOR APPLICATION NUMBER: 60/240,003 ; PRIOR FILING DATE: 2000-10-12 ; NUMBER OF SEQ ID NOS: 40 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 1 ; LENGTH: 4134 ; TYPE: DNA ; ORGANISM: Squalus acanthias ; US-10-410-885-1 </p>		<p> Query Match 100.0%; Score 4134; DB 15; Length 4134; Best Local Similarity 100.0%; Pred. No. 0; Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0; </p>	
QY	1	AATTCGGTGTCTGCGGTTCAGTCCAGTCTCTCAGTGCAGAAATGAGAAATGGTGGTC	60
DB	1	AATTCGGTGTCTGCGGTTCAGTCCAGTCTCTCAGTGCAGAAATGAGAAATGGTGGTC	60
QY	61	GCATTACAGGAACATGACTACATCTGTGTTAAATGAAATATGTCAGTATCTGAAGGT	120
DB	61	GCATTACAGGAACATGACTACATCTGTGTTAAATGAAATATGTCAGTATCTGAAGGT	120
QY	121	TATTAATATGTTTCTGCAAGGATGCTTCAAGAGATGCTTCAAGAGATCAATCTTGGACGTTTCCCAAT	180
DB	121	TATTAATATGTTTCTGCAAGGATGCTTCAAGAGATGCTTCAAGAGATCAATCTTGGACGTTTCCCAAT	180
QY	181	GTCATTGATGAATAACTGACCAAGGATGTAACAAATGAAATGAAATGAGAGCCAC	240
DB	181	GTCATTGATGAATAACTGACCAAGGATGTAACAAATGAAATGAGAGCCAC	240
QY	241	GTTCCACCTTCTTGGAGCATACGATCAACCTGGAAGGATGGAAGACTTGGAGGAA	300
DB	241	GTTCCACCTTCTTGGAGCATACGATCAACCTGGAAGGATGGAAGACTTGGAGGAA	300
QY	301	ATGGGGATGATCTTCCAGGATCTGCTGTAAGCGATCCCTCAACCATTAACAAGATAA	360
DB	301	ATGGGGATGATCTTCCAGGATCTGCTGTAAGCGATCCCTCAACCATTAACAAGATAA	360
QY	361	CGAGAAATCCTCCAGGATCTCTGTAAACGGCTGGCGTAGTGTGGCTTGGTCAAGGAA	420
DB	361	CGAGAAATCCTCCAGGATCTCTGTAAACGGCTGGCGTAGTGTGGCTTGGTCAAGGAA	420
QY	421	CAGACAGGGGTGCACAAATGCTCAGCTTCACTGCGCAACTCTTATCTTGGGATTTACA	480
DB	421	CAGACAGGGGTGCACAAATGCTCAGCTTCACTGCGCAACTCTTATCTTGGGATTTACA	480
QY	481	CTCCCTACGCTGACAAATGCTCAGGATGATGTCACAAACCAAGGGCCAGAAAGGA	540
DB	481	CTCCCTACGCTGACAAATGCTCAGGATGATGTCACAAACCAAGGGCCAGAAAGGA	540
QY	541	GACATCATACTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600
DB	541	GACATCATACTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600
QY	601	TTAAATTCAGACCGGAGCGGCAAAATGATTCGGTACAAATTTTCGAGGCTTCGGATGG	660
DB	601	TTAAATTCAGACCGGAGCGGCAAAATGATTCGGTACAAATTTTCGAGGCTTCGGATGG	660
QY	661	CTCCAGGCGATGATATTCGCAATGGAAGATTAACAACAGATGATGACTTTCTGCGCCCAAT	720
DB	661	CTCCAGGCGATGATATTCGCAATGGAAGATTAACAACAGATGATGACTTTCTGCGCCCAAT	720
QY	721	ATCACCTCGGATATCGCATATTTGACAGTGTAAACACCGTGTCCAGGCGCTAGAGCA	780
DB	721	ATCACCTCGGATATCGCATATTTGACAGTGTAAACACCGTGTCCAGGCGCTAGAGCA	780
QY	781	ACACTCAGCTTGTGGCCAGAAACAAATTCGCTCGCTGAACCTTAGATGAGTTCTGTAAC	840
DB	781	ACACTCAGCTTGTGGCCAGAAACAAATTCGCTCGCTGAACCTTAGATGAGTTCTGTAAC	840
QY	841	TGCTCTGACCATATCCCATCCACATAGCAGTGTGCGGGCAACCGGCTCAGGAATCTCC	900
DB	841	TGCTCTGACCATATCCCATCCACATAGCAGTGTGCGGGCAACCGGCTCAGGAATCTCC	900
QY	901	ACGGCTGTGGCAATCTATTTGGGATTTATTTTACATTCACAGTCAAGTATGCTCTCTCG	960
DB	901	ACGGCTGTGGCAATCTATTTGGGATTTATTTTACATTCACAGTCAAGTATGCTCTCTCG	960
QY	961	AGCAGGCTGTCTCAGCAACAGAAATGAGTACAAAGGCTTCTCTGAGGACCATCCCAATGAT	1020
DB	961	AGCAGGCTGTCTCAGCAACAGAAATGAGTACAAAGGCTTCTCTGAGGACCATCCCAATGAT	1020
QY	1021	GAGCAACAGCCACGGCCATGCGCGAGATCATCGAGCACTTCCAGTGGAACTGGTGGGA	1080
DB	1021	GAGCAACAGCCACGGCCATGCGCGAGATCATCGAGCACTTCCAGTGGAACTGGTGGGA	1080
QY	1081	ACCTGSCACGCGACGATGACTATGCGCGCCAGGCAATTGACAAAGTTCCGGGAGGAGGCC	1140
DB	1081	ACCTGSCACGCGACGATGACTATGCGCGCCAGGCAATTGACAAAGTTCCGGGAGGAGGCC	1140
QY	1141	GTTAAGAGGACATCTGTATTGACTTCACTGAGATGATCTCTCAGTACTACACCCAGAG	1200
DB	1141	GTTAAGAGGACATCTGTATTGACTTCACTGAGATGATCTCTCAGTACTACACCCAGAG	1200
QY	1201	CAGTTGGAGTTCACTCGCGACGTCATCCAGAACTCTCGSCCAAGGTCACTCGTGTCTTC	1260
DB	1201	CAGTTGGAGTTCACTCGCGACGTCATCCAGAACTCTCGSCCAAGGTCACTCGTGTCTTC	1260
QY	1261	TCCAATGGCCCGACCTGGAGCGCTCATCCAGGAGATAGTTCGGAGAAACATCACCGAT	1320
DB	1261	TCCAATGGCCCGACCTGGAGCGCTCATCCAGGAGATAGTTCGGAGAAACATCACCGAT	1320
QY	1321	CGATCTGGCTGGCCAGCGAGGCTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380
DB	1321	CGATCTGGCTGGCCAGCGAGGCTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380
QY	1381	TTCCACGCTGTGGCGCACCATTCGGCTTCTCAGGGCGGGCGGTATCCAGGGGTTTC	1440
DB	1381	TTCCACGCTGTGGCGCACCATTCGGCTTCTCAGGGCGGGCGGTATCCAGGGGTTTC	1440
QY	1441	AACAAGTCTCTGAGGAGGTCCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG	1500
DB	1441	AACAAGTCTCTGAGGAGGTCCACCCAGCAGGTCTCTCGGACAAATGGGTTTGTCAAGGAG	1500
QY	1501	TTCTGGAGGAGACCTTCAACTGCTTCACTTCCAGGAGACCCCTGACGAGCTGAAGAAT	1560
DB	1501	TTCTGGAGGAGACCTTCAACTGCTTCACTTCCAGGAGACCCCTGACGAGCTGAAGAAT	1560
QY	1561	TCCAAGTGTGCTCGCACCGACCGGGCTCAAGGGGACGGCTCCAGGCGGGGAACTCC	1620
DB	1561	TCCAAGTGTGCTCGCACCGACCGGGCTCAAGGGGACGGCTCCAGGCGGGGAACTCC	1620
QY	1621	AGACGACAGCCCTTACGCCACCCCTGCACTGGGAGGAGAAACATCACCAGCTGGAGAC	1680
DB	1621	AGACGACAGCCCTTACGCCACCCCTGCACTGGGAGGAGAAACATCACCAGCTGGAGAC	1680
QY	1681	CCCTACCTGGATTATACACACCTGAGGATCTCTACAAATGATATATCGTGGCGCTACTCC	1740
DB	1681	CCCTACCTGGATTATACACACCTGAGGATCTCTACAAATGATATATCGTGGCGCTACTCC	1740
QY	1741	ATTGCTCAGCCCTTGCAAGACATCCACTTTTGCAAAACCCCGGACGGGCACTTTTGCNAAC	1800
DB	1741	ATTGCTCAGCCCTTGCAAGACATCCACTTTTGCAAAACCCCGGACGGGCACTTTTGCNAAC	1800
QY	1801	GGATCTTGTGAGATATTTAAAGTTGAGGCGCTTGGCAGGCTCTCTCAACCATCTGCTGCAT	1860
DB	1801	GGATCTTGTGAGATATTTAAAGTTGAGGCGCTTGGCAGGCTCTCTCAACCATCTGCTGCAT	1860

1861 CTGAAGTTTACCAACGATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
1861 CTGAAGTTTACCAACGATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920
1921 GGGAACTTACACCATTTCAACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTGTTCCAT 1980
1921 GGGAACTTACACCATTTCAACTGGCAGCTCTCGCAGAGGATGAATCGGTGTTGTTCCAT 1980
1981 GAGGTGGGCAACTACAAAGCTTACGTAAGCCAGTGAACGACTCAACATCAACGAAAG 2040
1981 GAGGTGGGCAACTACAAAGCTTACGTAAGCCAGTGAACGACTCAACATCAACGAAAG 2040
2041 AATACTCTGGAAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAAGTGCAGACTGT 2100
2041 AATACTCTGGAAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAAGTGCAGACTGT 2100
2101 GTCCGGGCAACGAGGAGGATCATCGAGGGGAGCCACCTGCTGCTTTGAAATGCAATG 2160
2101 GTCCGGGCAACGAGGAGGATCATCGAGGGGAGCCACCTGCTGCTTTGAAATGCAATG 2160
2161 GCATGTGCAGAGGAGGATTCAGTGTGAACGATGAAGTGAAGTGCATGAAGTGCAGG 2220
2161 GCATGTGCAGAGGAGGATTCAGTGTGAACGATGAAGTGCATGAAGTGCAGG 2220
2221 AATGATTTCTGTGCGAATGAGAACCAACAGTGTGTCATCGCCAAAGGAGATCGAGTACCTG 2280
2221 AATGATTTCTGTGCGAATGAGAACCAACAGTGTGTCATCGCCAAAGGAGATCGAGTACCTG 2280
2281 TCGTGAAGGAGCCCTTGGGATTCGTGACCAATCTTCCGCTACTGCGGATTCCTGATC 2340
2281 TCGTGAAGGAGCCCTTGGGATTCGTGACCAATCTTCCGCTACTGCGGATTCCTGATC 2340
2341 ACCTCTTCTGTGCTGGGCTTCTTCACTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 2400
2341 ACCTCTTCTGTGCTGGGCTTCTTCACTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 2400
2401 AACCGGAGTTGTCCTACCTGCTGCTTCTTCTCCCTCATCTGCTGCTTCTTCCAGTTCGCTC 2460
2401 AACCGGAGTTGTCCTACCTGCTGCTTCTTCTCCCTCATCTGCTGCTTCTTCCAGTTCGCTC 2460
2461 ATCTTCTATCGGAGCCCGAGGACTGAGCTGTCGCTCCGCTCCGCTCCGCTCCGCTCCGCTC 2520
2461 ATCTTCTATCGGAGCCCGAGGACTGAGCTGTCGCTCCGCTCCGCTCCGCTCCGCTCCGCTC 2520
2521 AGCTTCTGCTGTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 2580
2521 AGCTTCTGCTGTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 2580
2581 GAGGCCAAGTCCCAACGATCTCCAGCAGAGTGGTGGGCTCAACCTGAGTTCCTC 2640
2581 GAGGCCAAGTCCCAACGATCTCCAGCAGAGTGGTGGGCTCAACCTGAGTTCCTC 2640
2641 CTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 2700
2641 CTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 2700
2701 CTTCCCTCCAGCTACAGGAACATGAGCTGGAGGAGGATCATCTTCACTGCTGCTGCTGCTGCT 2760
2701 CTTCCCTCCAGCTACAGGAACATGAGCTGGAGGAGGATCATCTTCACTGCTGCTGCTGCTGCT 2760
2761 GAGGGCTCGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 2820
2761 GAGGGCTCGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 2820
2821 TGCTTCTTCTGCTTCAAGTCCCGTAAAGCTGCGGAGAACTTCAAGAGGCTAAAGTTC 2880
2821 TGCTTCTTCTGCTTCAAGTCCCGTAAAGCTGCGGAGAACTTCAAGAGGCTAAAGTTC 2880
2881 ATCACCTTCAGCATGTGTGATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2881 ATCACCTTCAGCATGTGTGATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940

2941 AGCACCTACCGCAAGTTTGTGTCGGCGTGAGGTGATTGCCATCTGGCTCCAGCTTC 3000
2941 AGCACCTACCGCAAGTTTGTGTCGGCGTGAGGTGATTGCCATCTGGCTCCAGCTTC 3000
3001 GGGTGTGCTGGCTGCAATTTACTTTCAACAAGTGTGTATCATCTCTGTTCAAGCGTGCCTG 3060
3001 GGGTGTGCTGGCTGCAATTTACTTTCAACAAGTGTGTATCATCTCTGTTCAAGCGTGCCTG 3060
3061 AACACATCGAGAGGTGCTGCTGAGCAGCGCGCCACGCTTCAAGTGGGGCGCCG 3120
3061 AACACATCGAGAGGTGCTGCTGAGCAGCGCGCCACGCTTCAAGTGGGGCGCCG 3120
3121 GCCACCTCTCGGGCAGCGCGGCTCTCGCAAGCGTCCAGCAGCCTGTCGCGCTCCACC 3180
3121 GCCACCTCTCGGGCAGCGCGGCTCTCGCAAGCGTCCAGCAGCCTGTCGCGCTCCACC 3180
3181 ATCTCTCTCGCGCTGCTGCTGCTGCGCGCGGCTTCAACATGAGATGAGCGCTGC 3240
3181 ATCTCTCTCGCGCTGCTGCTGCTGCGCGCGGCTTCAACATGAGATGAGCGCTGC 3240
3241 AGCACGAGAGGTGCTGCTGCGCAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
3241 AGCACGAGAGGTGCTGCTGCGCAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
3301 ACAGGCGATACGCCACCTCTCAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
3301 ACAGGCGATACGCCACCTCTCAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
3361 AGCGGCAAGCT 3420
3361 AGCGGCAAGCT 3420
3421 CAGCGCGCACTGCT 3480
3421 CAGCGCGCACTGCT 3480
3481 GCGGCAAGCT 3540
3481 GCGGCAAGCT 3540
3541 CCCAAGCACTGCT 3600
3541 CCCAAGCACTGCT 3600
3601 TGCCCAACCTGCT 3660
3601 TGCCCAACCTGCT 3660
3661 TCTTTTATCCCTGATTTCTGCT 3720
3661 TCTTTTATCCCTGATTTCTGCT 3720
3721 ATAATGAGTTGCAAAATAGGTGAGCAGTGTGTCGCAAGTGTGTCGAACTTCTGAACTTCTGAACT 3780
3721 ATAATGAGTTGCAAAATAGGTGAGCAGTGTGTCGCAAGTGTGTCGAACTTCTGAACTTCTGAACT 3780
3781 ATCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACT 3840
3781 ATCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACTTCTGAACT 3840
3841 TTAATGTTCTAACAATGTCGAAAGTAAATTTGTTTACAACATATAAGGTACCCTGAAGCAGT 3900
3841 TTAATGTTCTAACAATGTCGAAAGTAAATTTGTTTACAACATATAAGGTACCCTGAAGCAGT 3900
3901 GACTGAGATGCGCACTGCTGATGACAGACTGTTTTTATACATTTATCATTTGAACTGGA 3960
3901 GACTGAGATGCGCACTGCTGATGACAGACTGTTTTTATACATTTATCATTTGAACTGGA 3960
3961 TTGCAACAGGAATATATGACTGTAAACAAAATTTGTTGATTATCTTAAAAATGCAAAAT 4020
3961 TTGCAACAGGAATATATGACTGTAAACAAAATTTGTTGATTATCTTAAAAATGCAAAAT 4020
4021 TGTAAATCAGATGTGTAATAATTTGTTGTTTCTGTTACATTAATGATATTTCTTGATA 4080

963	GGCAGACATCATCGAGTATTTCGCTGGAATCGGCTGGCCACAAATTCAGCTGATGACGA	1022
1101	CTATGGCCGCCCAGGCAATTGACAAGTTCGCGGAGGAGCGCGTTAAGAGGGACATCTGTAT	1160
1023	CTATGGCGCGCGGGATTGAGAAATTCGAGAGGAAGCTGAGGAAAGGGATATCTGCAT	1082
1161	TGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAGCAGTTGAGTTTCATCGCGCA	1220
1083	CGAATTTCAGTGAATCATCTCCAGTACTCTGATGAGGAAGAGATCCAGCATGTGGTAGA	1142
1221	CGTCATCCAGAACTCCTCGGCCAAGTCATCGTGGTCTTCTCCAATGGCCCCGACCTGGA	1280
1143	GGTGATTCAAAATTCACGGGCCAAAGTCATCGTGGTGTTCCTCAGTGGCCAGATCTTGA	1202
1281	GCCGCTCATCCAGGAGATAGTTCCGGAAGAACATCACCGATCGGATCTGGCTGGCCAGCGA	1340
1203	GCCCTTCATCAAGGAGATTTCGGGCGCAATATCACGGGCAAGATCTGGCTGGCCAGCGA	1262
1341	GGCTTGGGCAGGCTCTTCGCTCATTTGCCAAGCCAGAGTACTTCCACGTGGTCGCGGCAC	1400
1263	GGCTGGGCCAGGCTCCTCCCTGATCGCGCATGCCTCAGTACTTCCACGTGGTTGGCGGCAC	1322
1401	CATCGGCTTCGCTCATCGCGGGGGCGTATCCAGGGTTCACAAGTTTCCTGAAGGAGGT	1460
1323	CATTGGATTTCGCTCTGAAGGCTGGCGAGATCCAGGCTTCGGGAAATTCCTTGAAGAAGT	1382
1461	CCACCCAGCAGGTCCTCCGACAATGGGTTTGTCAAGGAGTTCCTGGAGGAGACCTTCAA	1520
1383	CCATCCGAGGAAGTCTCTCCAAATGGTTTTCGCAAGGAGTTTGGGAAGAAACATTAA	1442
		1500

Db	1443	CTGCCACTCCAAGA-----AGGTGC AAAAGGACCTTTACCTGTGGACACCTTTCTG	1494
Qy	1581	ACGGCGGCTCAAGGGGACGGCTCCAAAGGCGGGGAACTCCAGACGGACAGCCCTACGGCA	1640
Db	1495	AGGG----TCACGAAGAAATGGCGACAGCTTTAGCAACAGCTCGACAGCCTTCGGACC	1550
Qy	1641	CCCTCGCACTGGGAGGAGAGAACATCACACGGCTGGAGACCCCTACCTGGATTATACACA	1700
Db	1551	CCTCTGTACAGGGAGTACGAAACATCAGACGTGTGAGACCCCTACATAGATTACACGA	1610
Qy	1701	CCTGAGGATCTCCTACAATGTATACGTGGGGCTTACTTCCATTGCTACGGCCTGCAAGA	1760
Db	1611	TTTACGGATATCCTTACAATGTGTACTTAGCAGTCTACTTCCATTGCCACGGCTTGCAAGA	1670
Qy	1761	CATCCACTCTTGCAAAACCCGSCAGGCACTCTTTGCAAAACGGATCTTGTGCAGATATTAA	1820
Db	1671	TATATATACCTGTTACTCTGGGAGAGGCTCTTCACCAATGGCTCTGTGCAGACATCAA	1730
Qy	1821	AAAAGTTGAGGCTGGCAGTCTCTCAACCAATCTGCTGCATCTGAAGTTTACCAACAGAT	1880
Db	1731	GAAAGTTGAGGCTGGCAGGTCCTGGAAGCACCTACGGCATCTAAACTTTTACAAAACATAT	1790
Qy	1981	GGGTGACAGGTTGACTTTTCAGCATCAAGTGAACCTCAAGGGGAACATACACCTATTCAA	1940
Db	1791	GGGGAGCAGGTGACCTTTTGATGAGTGTGTGACCTGTTGGGGAACTATTTCATCATCA	1850
Qy	1941	CTGGCAGCTCTCCGACAGGATGAATCGGTGTTGTTCCATGAGTGGGCAACTACACGC	2000
Db	1851	CTGGCACTCTCCGACAGGATGGCTCCATCGTGTTTAAGGAAGTCGGGTATTACAAGT	1910
Qy	2001	CTACGCTTAAGCCAGTCACGACTCAACATCAAGCAAGAAAGAAATCCTCTGGATGGCTT	2060
Db	1911	CTATGSCAAGAAGGAGAAAGACTCTTCATCAACGAGGAGAAATCCTCTGTGAGTGGGTT	1970
Qy	2061	CTCCAAAGTGGTTCTCTTCTCCAACTGCAGTCGAGACTGTGTGCGGGCAACGAGAAAGG	2120
Db	1971	CTCCAGGAGGTGCCCTTCTCCAACTGCAGCCGAGACTGCTCGCAGGACGAGGAAAGG	2030
Qy	2121	GATCATGAGGGGAGCCCACTGCTGCTTTGAATGCATGCCATGTCAGAGGGAGATT	2180
Db	2031	GATCAITGAGGGGAGCCCACTGCTGCTTTGAGTGTGTGAGTGTCTCTGATGGGAGTA	2090

QY	3201	CACCTGCGGGCGGCGCTCACCATGGAGATGCGGCTGCGAGCAGCGAGAAGTCAAGCTT	3260
Db	2739	CATCAGCAGCAAGAGCAACA-----GCGAAGACCCATTCCCAACAGCCCGAGAGGCAGAAG	2793
QY	3261	CGGCAAGCGCACCGTCAACCTGTGCTCAGCTTCGAGGAGACAGGCCGATAGCCACCCT	3320
Db	2794	CAGCAGCAGCGCTGGCCCTAACCCCAACAAAGAGCAGCAGCCCTGACCCCTCCCA	2853
QY	3321	CAGCGGCACGCGCCCGCAGCAGGAATCGGCGGATGGCGGCGAG	3362
Db	2854	CAGCAGCAACAATCGCAGCAGCGCCAGATCGCAGCAGAAG	2895

Search completed: November 17, 2004, 11:44:47
Job time : 2335 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 21:14:43 ; Search time 11876 Seconds
(without alignments)
12684.561 Million cell updates/sec

Title: US-10-016-496-1
Perfect score: 4134
Sequence: 1 aattccgtgtctgtcgttc.....aagcggccgacagcaacgg 4134

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171.4	28.3	3115	3 AK029770	Mus muscu
2	548	13.3	745	9 CE057024	tigr-g8s-
3	535.4	13.0	746	9 CE057025	tigr-g8s-
4	495.4	12.0	637	9 CE303215	tigr-g8s-
5	452.2	10.9	581	6 CD608331	56076771J
6	440.2	10.6	579	6 CD608332	56076771J
7	431.6	10.4	670	9 CE504040	tigr-g8s-
8	415.6	10.1	600	6 CD608327	56021515H
9	415.2	10.0	654	6 CD608330	56048444J
10	403	9.7	622	6 CD608328	56048444H
11	393.2	9.5	602	6 CD608328	56021515J
12	369	8.9	813	7 CK805060	AGENCOURT
13	336.4	8.1	567	5 BP766221	BP766221
14	329.8	8.0	776	7 CK483822	AGENCOURT
15	313.8	7.6	653	2 BS615658	BS615658
16	312.4	7.6	498	2 AW051287	AW051287
17	293.4	7.1	464	1 AA937218	AA937218
18	283.4	6.9	2262	3 AK029734	Mus muscu
19	280.8	6.8	675	9 AG297995	Mus muscu
20	246.2	6.0	923	4 BJ730259	BJ730259
21	234.6	5.7	1037	9 CL093343	ISBI-2362
22	233.6	5.7	525	9 CC546019	CH240_428
23	231.8	5.6	374	8 BH303533	CH230-167
24	229.4	5.5	939	9 CL091501	ISBI-2012

C	25	221.4	5.4	659	1	AI766210	wh6804.X
	26	220	5.3	1033	9	CL033878	CH216-37C
	27	218.4	5.3	2239	3	AK030224	Mus muscu
C	28	217.8	5.3	1038	9	CNS0508R	Tetradon
	29	217	5.2	973	9	CL057415	CH216-85G
	30	214.4	5.2	1026	9	CL113420	ISBI-5813
	31	212.2	5.1	3849	3	AK084934	Mus muscu
	32	210.8	5.1	1018	9	CL091265	ISBI-20C1
C	33	210.2	5.1	888	9	CNS03200	AL225177 Tetradon
	34	209.6	5.1	1026	8	CC214498	CH261-116
C	35	208.6	5.0	974	8	BZ117727	CH230-460
	36	208.4	5.0	1033	9	CL036219	CH216-22W
C	37	208	5.0	602	1	AI434785	CH216-22W
	38	208	5.0	1013	9	CL112721	ISBI-5711
C	39	204.8	5.0	1048	9	CL039415	CH216-47N
	40	199.6	4.8	861	9	CL028116	CH216-27B
C	41	195.8	4.7	2071	3	AK017298	Mus muscu
	42	195.4	4.7	643	5	EX866121	EX866121
	43	190.8	4.6	971	9	CL091702	ISBI-2003
	44	189.6	4.6	833	9	CR254908	Reverse s
	45	189.6	4.6	928	9	CR233802	Forward s

ALIGNMENTS

RESULT 1
LOCUS AK029770 3115 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493054218 product:calcium-sensing receptor, full insert sequence.
ACCESSION AK029770
VERSION AK029770.1 GI:26325707
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
93273253
REFERENCE 2
10349636
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
REFERENCE 3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
REFERENCE 4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 688-690 (2001)
REFERENCE 5
The FANTOM Consortium and the RIKEN Genome Exploration Research


```
Db 1069 CTCTGCTCTTCTCACTCTCTGCTGCTTCTCCAGCTCCCTGTTCTTCAATGGGAGCC 1128
Qy 2479 AGGACTGGACCTTCTGGCTCCGCCAACCGGCTTTGGCATCAGCTTCGCTGTGCATC 2538
Db 1129 CAGGACTGGACCTTCCGCTCGCAGACCGGCTTGGCATCAGCTTCGCTGTGCATC 1188
Qy 2539 TCCTGCACTCTGCTGGAAGCAACCGGCTGCTGCTGCTTTCAGGCGCAAGATCCCAACC 2598
Db 1189 TCGTGCACTCTGCTGGAAGCAACCGGCTGCTGCTGCTTTCAGGCGCAAGATCCCAACC 1248
Qy 2599 AGCTTCCACCGCAAGTGGTGGGCTCAACCTGCACTGCTTCTCTGCTTCTCTGCTGATC 2658
Db 1249 AGCTTCCACCGCAAGTGGTGGGCTCAACCTGCACTGCTTCTCTGCTTCTCTGCTGATC 1308
Qy 2659 CTGCTGCAATCTGCTCACTGCACTGCTGCTTACACCGGCTTCTCTGCTTCTCTGCTGATC 2718
Db 1309 TCGTGCACTCTGCTGGAAGCAACCGGCTGCTGCTGCTTTCAGGCGCAAGATCCCAACC 1368
Qy 2719 AACCATGAGCTGAGGAGGAGGCTCACTTTCATCACTTCCGACGAGGCTCGCTCAAGGCG 2778
Db 1369 AACCATGAGCTGAGGAGGAGGCTCACTTTCATCACTTCCGACGAGGCTCGCTCAAGGCG 1428
Qy 2779 CTGGGCTTCTCATGCGCTTACCTGCTTCTCGCGCATCTGCTTCTTCTGCTGCTTCT 2838
Db 1429 CTGGGCTTCTCATGCGCTTACCTGCTTCTCGCGCATCTGCTTCTTCTGCTGCTTCT 1488
Qy 2839 AAGTCCGTAAGCTGCGGAGAACTTCAACGAGGCTAAGTTTCATCACTTCACTGATG 2898
Db 1489 AAGTCTCGGAGCTGCGGAGAACTTCAACGAGGCTAAGTTTCATCACTTCACTGATG 1548
Qy 2899 ATCTTCTTCACTGCTGATCTCTTCACTTCCGCTTATGTCAGCACTTACGCAAGTTT 2958
Db 1549 ATCTTCTTCACTGCTGATCTCTTCACTTCCGCTTATGTCAGCACTTACGCAAGTTT 1608
Qy 2959 GTGTCGCGGAGGAGGATGATGCTTCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 3018
Db 1609 GTCTCTGCGGAGGAGGATGATGCTTCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 1668
Qy 3019 TACTTCAACAAAGTTTACATCATCTGTTTAAAGCGCTGCGCTTAAACATGAGGAGG 3078
Db 1669 TTCTTCAACAAAGTTTACATCATCTGTTTAAAGCGCTGCGCTTAAACATGAGGAGG 1728
Qy 3079 CGCTGACGAGCGGCGGCGGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3138
Db 1729 CGCTGACGAGCGGCGGCGGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1788
Qy 3139 GCGGCGCTTCCGAGCGCTTCCAGAGCGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCG 3198
Db 1789 AACATCTCCGAGAGCGGCTCCAGAGCGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCG 1848
Qy 3199 TCCACCTGCGGCGGCGGCTTCCAGATGGA 3227
Db 1849 TCCATCAGCAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG
```

```
RESULT 2
CE057024 745 bp DNA linear GSS 24-SEP-2003
LOCUS tigr-gss-dog-17000322442683 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE057024
VERSION CE057024.1 GI:35104959
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 745)
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
The dog genome: survey sequencing and comparative analysis
TITLE
```

```
JOURNAL Science 301 (5641), 1899-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TiGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
source Location/Qualifiers
1..745
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
ORIGIN
Query Match 13.3%; Score 548; DB 9; Length 745;
Best Local Similarity 84.8%; Pred. No. 1.3e-111;
Matches 614; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 2181 CAGTGATGAAAAAGATGCAAGTGGTGATGACAAAGTGGCGGATGATTTCTGTCGATCA 2240
Db 22 CTGGAATATTACAGATGCAAGTGGCTGTGACAAGTGGCGGATGATTTCTGTCGATCA 81
Qy 2241 GAACACACAGTCTGTGATCGCAAGGAGATCAGATACCTGTGTGACGAGCGCTTCGG 2300
Db 82 AACCACACATTTGTGATTTGCCAAGAGATTCAGTTTCTGTCTGACAGAGCGCTTTGG 141
Qy 2301 GATCGCTCTGACCATTTCCCGCTACTGGGATCTGTGATCACTCTCTTCTGCTGGGGT 2360
Db 142 GATTGCACTCACCTCTTTGCTGTGTGGGCTTTTCTCTGACAGCTTTCTGCTGGGGT 201
Qy 2361 CTTTCATCAAGTTTCAGAACACTCCCATCTGTAAGGCCACCAACCGGAGTGTGCTACCT 2420
Db 202 CTTTCATCAAGTTTCAGAACACTCCCATCTGTAAGGCCACCAACCGGAGCTTCTGATCT 261
Qy 2421 GCTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2480
Db 262 CTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 321
Qy 2481 GATCTGGAAGTGTGGCTCCGCAACCGGCTTTGGCATCAGTTCTGCTGTGATCTC 2540
Db 322 GGAATGAGCTTGGCGCTTGGCGGCTTGGCATCAGTTCTGCTGTGATCTC 381
Qy 2541 CTGCATCTCTGTAAGCAACCAACCGGCTGTGTGCTTTCGAGGCCAAGATCCCAACAG 2600
Db 382 ATGCATCTCTGTAAGCAACCAACCGGCTGTGTGCTTTCGAGGCCAAGATCCCAACAG 441
Qy 2601 CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTTTCTCTCTCTCTCTCTCTCTCTCTCT 2660
Db 442 CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 501
Qy 2661 GGTGCAATCTCTCACTGATCATCTGCTCTTACACCGGCTTCTCTCTCTCTCTCTCTCT 2720
Db 502 CATGCAAGTTGTCATCTGTGATCTGCTCTTACACGGGCTTCTCTCTCTCTCTCTCTCT 561
Qy 2721 CCATGAGCTGGAGGAGGATCATCTTATCATCTGCAAGGCTCTCTCTCTCTCTCTCTCT 2780
Db 562 CCATGAGCTGGAGGAGGATCATCTTATCATCTGCAAGGCTCTCTCTCTCTCTCTCTCTCT 621
Qy 2781 GGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2840
Db 622 GGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 681
Qy 2841 GTCCCGTAAGCTCCGAGAACTTCAACGAGGCTTAAGTTTCATCACCTTCTGATTTGAT 2900
Db 682 GTCCCGTAAGCTCCGAGAACTTCAACGAGGCTTAAGTTTCATCACCTTCTGATTTGAT 741
```

JOURNAL Science 301 (5641), 1899-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TiGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source Location/Qualifiers
1..745
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 13.3%; Score 548; DB 9; Length 745;
Best Local Similarity 84.8%; Pred. No. 1.3e-111;
Matches 614; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 2181 CAGTGATGAAAAAGATGCAAGTGGTGATGACAAAGTGGCGGATGATTTCTGTCGATCA 2240
Db 22 CTGGAATATTACAGATGCAAGTGGCTGTGACAAGTGGCGGATGATTTCTGTCGATCA 81
Qy 2241 GAACACACAGTCTGTGATCGCAAGGAGATCAGATACCTGTGTGACGAGCGCTTCGG 2300
Db 82 AACCACACATTTGTGATTTGCCAAGAGATTCAGTTTCTGTCTGACAGAGCGCTTTGG 141
Qy 2301 GATCGCTCTGACCATTTCCCGCTACTGGGATCTGTGATCACTCTCTTCTGCTGGGGT 2360
Db 142 GATTGCACTCACCTCTTTGCTGTGTGGGCTTTTCTCTGACAGCTTTCTGCTGGGGT 201
Qy 2361 CTTTCATCAAGTTTCAGAACACTCCCATCTGTAAGGCCACCAACCGGAGTGTGCTACCT 2420
Db 202 CTTTCATCAAGTTTCAGAACACTCCCATCTGTAAGGCCACCAACCGGAGCTTCTGATCT 261
Qy 2421 GCTGCTCTTCT 2480
Db 262 CTTCT 321
Qy 2481 GATCTGGAAGTGTGGCTCCGCAACCGGCTTTGGCATCAGTTCTGCTGTGATCTC 2540
Db 322 GGAATGAGCTTGGCGCTTGGCGGCTTGGCATCAGTTCTGCTGTGATCTC 381
Qy 2541 CTGCATCTCTGTAAGCAACCAACCGGCTGTGTGCTTTCGAGGCCAAGATCCCAACAG 2600
Db 382 ATGCATCTCTGTAAGCAACCAACCGGCTGTGTGCTTTCGAGGCCAAGATCCCAACAG 441
Qy 2601 CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTTTCTCTCTCTCTCTCTCTCTCTCTCT 2660
Db 442 CTTCCACCGCAAGTGGTGGGCTCAACCTGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 501
Qy 2661 GGTGCAATCTCTCACTGATCATCTGCTCTTACACCGGCTTCTCTCTCTCTCTCTCTCT 2720
Db 502 CATGCAAGTTGTCATCTGTGATCTGCTCTTACACGGGCTTCTCTCTCTCTCTCTCTCT 561
Qy 2721 CCATGAGCTGGAGGAGGATCATCTTATCATCTGCAAGGCTCTCTCTCTCTCTCTCTCT 2780
Db 562 CCATGAGCTGGAGGAGGATCATCTTATCATCTGCAAGGCTCTCTCTCTCTCTCTCTCTCT 621
Qy 2781 GGGCTTCT 2840
Db 622 GGGCTTCT 681
Qy 2841 GTCCCGTAAGCTCCGAGAACTTCAACGAGGCTTAAGTTTCATCACCTTCTGATTTGAT 2900
Db 682 GTCCCGTAAGCTCCGAGAACTTCAACGAGGCTTAAGTTTCATCACCTTCTGATTTGAT 741

```

Qy      2901 CTTTC 2904
Db      742 CTTTC 745

RESULT 3
LOCUS   CE057025          746 bp   DNA      linear   GSS 24-SEP-2003
DEFINITION tigr-gss-dog-1700032242684 Dog Library Canis familiaris genomic,
ACCESSION CE057025
VERSION   CE057025.1 GI:35104961
KEYWORDS  GSS.
SOURCE    Canis familiaris (dog)
ORGANISM  Canis familiaris
REFERENCE 1 (bases 1 to 746)
AUTHORS   Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae; Canis.
          Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
          Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
          Venter,J.C.
          The dog genome: survey sequencing and comparative analysis
          Science 301 (5641), 1898-1903 (2003)
JOURNAL   MEDLINE
PUBMED    14512627
COMMENT   Contact: Kirkness EF
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0200
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.

FEATURES             Location/Qualifiers
     source           1..746
     organism="Canis familiaris"
     mol_type="genomic DNA"
     strain="Standard Poodle"
     db_xref="taxon:9615"
     clone_lib="Dog Library"
     note="Site 1: BstXI; Libraries were prepared from
           peripheral blood"

ORIGIN
Query Match      13.0%; Score 535.4; DB 9; Length 746;
Best Local Similarity 84.6%; Pred. No. 8.5e-109;
Matches 613; Conservative 0; Mismatches 111; Indels 1; Gaps 1;

Qy      2181 CAGTCATGAACGATGCGTGTACAAAGTGGCCGGAATTTCTGTCGATGA 2240
Db      22 CTGGAATATTACAGATGAAGTGCCTGTGACAAAGTGCCTGATGACTTCTGGTCCAAATGA 81

Qy      2241 GAACACACAGCTCGTCATCGCCAGAGATCGAGTACCTGTCGTGGACGAGCCCTTCGG 2300
Db      82 AAACACACTTCGTGCAATGCCAAGAGATTGAGTTCTGCTCTGGACAGAGCCCTTTGG 141

Qy      2301 GATCCTCTGACCATCTTCGGCGTACTGGGGATCCTGATACCTCTTCGTGCTGGGGGT 2360
Db      142 GATTCACATCACTTCCTTTGCTGTGCTGGGATTTCTCTGACAGCTTCGTGCTGGGGGT 201

Qy      2361 CTTTATCAAGTTACAGAACTCCCATCGTGAAGCCACCAACCGGAGTTGCTCTACCT 2420
Db      202 CTTTATCAAGTTCCGTACACAGCCCATCGTCAAGCCACCAACCGAGAGCTTCGTACCT 261

Qy      2421 GCTGCTCTTCCTTCATCTGCTGCTTCCTCAGCTCGCTCATCTTCATCGCGGAGCCCAAG 2480
Db      262 CCTCCTCTCTCTCTGCTGCTGCTCTCTCCAGCTCCCTGCTCTTCATTCATTCGCGAGCCCA 321

Qy      2481 GGACTGGACCTGTGGCTCCGCCAACCGGCTTTGGGATCAGCTTCGCTGTCATCTC 2540
Db      322 GGACTGGACCTGCCGCTTGGCCAGCCGCGCTTTGGGATCAGCTTCGCTGTCATCTC 381

```

```

Qy      2541 CTGCATCTCTGTTGAAGACCAACCGGGTGTGCTGTTCTTCGAGGCCAAGATCCCCACCAG 2600
Db      382 ATGCATCTCTGTTGAAGACCAACCGGTGTGCTCTCTGTTGTTGAGGCCAAGATCCCCACAAG 441

Qy      2601 CTTCCACCGCAAGTGGGTGGGCTCAACCTGCAGTTCTTCCTCTGCTGCTCTCTGCTGCT 2660
Db      442 CTTCCACCGCAAGTGGTGGGGCTCAACCTGCAGTTCTTCCTCTGCTGCTCTCTCTGCTGCT 501

Qy      2661 GGTGCAAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2720
Db      502 CATGCGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561

Qy      2721 CCATGAGCTGGAGGACGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2780
Db      562 CCATGAGCTGGAGGACGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621

Qy      2781 GGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2840
Db      622 GGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681

Qy      2841 GT-CCGTAAGTCCGAGAGACTTCAACGAGGCTAAAGTTTCATCAGCTTCAGCATGTTGA 2899
Db      682 GTCCCCGAGAGTCCGAGAGACTTCAACGAGGCTAAAGTTTCATCAGCTTCAGCATGTTGA 741

Qy      2900 TCTTC 2904
Db      742 TCTTC 746

RESULT 4
LOCUS   CE303215          637 bp   DNA      linear   GSS 26-SEP-2003
DEFINITION tigr-gss-dog-17000360222011 Dog Library Canis familiaris genomic,
ACCESSION CE303215
VERSION   CE303215.1 GI:36094287
KEYWORDS  GSS.
SOURCE    Canis familiaris (dog)
ORGANISM  Canis familiaris
REFERENCE 1 (bases 1 to 637)
AUTHORS   Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae; Canis.
          Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
          Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
          Venter,J.C.
          The dog genome: survey sequencing and comparative analysis
          Science 301 (5641), 1898-1903 (2003)
JOURNAL   MEDLINE
PUBMED    14512627
COMMENT   Contact: Kirkness EF
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0200
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.

FEATURES             Location/Qualifiers
     source           1..637
     organism="Canis familiaris"
     mol_type="genomic DNA"
     strain="Standard Poodle"
     db_xref="taxon:9615"
     clone_lib="Dog Library"
     note="Site 1: BstXI; Libraries were prepared from
           peripheral blood"

ORIGIN
Query Match      12.0%; Score 495.4; DB 9; Length 637;
Best Local Similarity 87.1%; Pred. No. 7.6e-100;
Matches 555; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

Qy      2408 AGTTGCTTACTGCTGCTCTCTCTCCCTCATGCTGCTTCCAGCTCGCTCATCTTCA 2467

```


JOURNAL
COMMENT

extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3150 Porter Dr., Palo Alto, CA 94303
Tel: 6508454102
Email: gfu@incyte.com.

ORIGIN

[illegible]


```

RESULT 12
CK805060
LOCUS
DEFINITION
AGENCOURT 19147865 NICHX XGC Te2 Xenopus laevis cDNA clone
IMAGE:7211077 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 813)
NIH-MGC http://mgc.mci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Igor B. Dawid
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLaM15101 row: c column: 11
High quality sequence start: 9
High quality sequence stop: 695.
Location/Qualifiers
1..813
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:7211077"
/tissue_type="Pooled samples from 6 adult Xenopus testis"
/lab_host="DH10B TonA"
/clone_lib="NICHX XGC Te2"
/Note="Organ: testis; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from 6 adult male testis. cDNA
was primed using oligo-dT primer:
5'-pGACTAGTCTAGATCGGAGCGCGGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1kb
resulted in an average insert size of 1.25 kb. This is a
primary library (normalized primary library is
NICHX XGC Te2N) and was constructed by Express Genomics
(Fredrick, MD). Note: this is a NIH_MGC library"

ORIGIN
Query Match 8.9%; Score 369; DB 7; Length 813;
Best Local Similarity 73.0%; Pred. No. 1.8e-71;
Matches 474; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 1733 TCTACTCCATTGCTCAGCCCTGCAAGACATCCACTCTTTGCAAAACCCGGCAGGCGCATCT 1792
DB 13 TCTCCGGATGCGTTATGCTCTGCAGATATATATCTCTGACCCCTGGGAAGGGCTGT 72
QY 1793 TTGCAACCGGATCTTGTGAGATATTAAAAAAGTTGAGCCCTGGCAGGTCCTCAACCATC 1852
DB 73 TTGCCAACAAATTCCTGTGCCGACATAAAGAAAGTGAAGCCTGGCAGTTGCTGAAACACT 132
QY 1853 TGCTGATCTGAGTTTACACAGCATGGTGACGAGTTTACATTTGACGATCAGGTG 1912
DB 133 TGCGGCATCTCAATTTCAACAATATATGGGGAGCAGGTGACTCAATGACTCAGGGG 192
QY 1913 ACTCAAGGGGAACACTACACATTATCAACTGGCAGCTCTCCGAGAGGATGAATCGGTGT 1972
DB 193 ACTTGTTGGGAACACTACTCCATCATCACTGCGACCTGTCACAGGAGGACACTCCATTG 252

```

```

QY 1973 TGTTCATGAGGTGGGCAACTCAACGCCCTACGCTAAGCCAGTACCAGCTCAACATCA 2032
DB 253 TGTTCAGGAGGTGGGGTACTCAACGCTCTATGCCAAGGTGGCGGAGCGGCTTTTCATCA 312
QY 2033 ACCAAAGAAAATCCCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTCTCCAACTGCAGTC 2092
DB 313 ACGAAGCAAAATCCCTGTGGAGAGGCTTCTCCGAGTGGTCCCAATTTCCAACCTGCAGTC 372
QY 2093 GAGACTGTGTGCGGGGACCCAGGAAGGGATCATCGAGGGGGAGCCACCTGCTGCTTTG 2152
DB 373 AAATCTGCCAGGAAGGCACCCGGAAAGGCATCATTTGAAGGGAACCCACCTGCTGCTTTG 432
QY 2153 AATGCATGGCATGTGCAGAGGGAGAGTTCAAGTGCATGATGAAACGATCAAGTGCCTGTACAA 2212
DB 433 AATGTGTTGACTGCCCGACGGGATACAGTGTATGACAGATGCGCAGTGCCTGTGAGA 492
QY 2213 AGTGCCCGAATGATTTCTGTGCGAATGAGAACACACACGCTGTGCATCGCAAGGAGATCG 2272
DB 493 AATGTGCCAAGGATTAAGTGTGCTCAATGAAACACACACTTCTGCAITTCGCAAGCAGATCG 552
QY 2333 TCCTGATCACCTCTCTGCTCGGGGTCTTCATCAAGTTTCAGGAACAC 2381
DB 613 TAATGCTCATTTCAATTTGTTCTCGGTGTTTCATCAAAATTCGCAACAC 661

RESULT 13
BP766221
LOCUS
DEFINITION
BP766221 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mid09082 5',
mRNA sequence.
ACCESSION
VERSION BP766221.1 GI:50224919
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 567)
Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioka, H.,
Takeda, J., Ohara, O. and Seino, S.
TITLE
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL
Unpublished (2004)
COMMENT
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..567
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="mid09082"
/sex="male"
/tissue_type="pancreatic islet"
/dev_stage="adult"
/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"

ORIGIN
Query Match 8.1%; Score 336.4; DB 5; Length 567;
Best Local Similarity 76.6%; Pred. No. 3.3e-64;
Matches 412; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

```

```

1727 TGCCCGCTTACTCCATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCCGCGCAGG 1786
Db TAGCCGCTTACTCCATTGCGCAGCCCTGCAAGATATATACACTTCTTACCCGGAAGAG 89
QY 1787 GCATCTTTGCAACGAGATCTTGCGAGATATTAATAAAGTTGAGGCTTGCGAGTCTCTCA 1846
Db 90 GGCTTTTACCAACGAGGCTCTGTGAGACATCAAGAAGTTTGGAGGCTTGCGAGTCTCTGA 149
QY 1847 ACCATCTGTGATCTGAAGTTTACCAACAGATGGTGGAGGTTGACTTTGACGATC 1906
Db 150 AACACCTAGGCACCTGAATTTTACCAACATGCGGAGGAGGAGTGACCTTCGATGAGT 209
QY 1907 AAGTGACCTCAAGGGGAATCAACATTTATCAACTGGCAGTCTTCCGAGAGGATGAAT 1966
Db 210 GGGGTGACCTGTGGGGAATCACTCCATCATCAACTGGCACCTCTCCGAGAGGAGCGGT 269
QY 1967 CGGTGTGTTCCATGAGTGGCAACTACAAACGCTTACGCTAAGCCGAGTGAACGACTCA 2026
Db 270 CCATTGTGTTCAAGGAAGTTGGGTACTCAATGTGTATGCCAAGAGGAGAAAGACTGT 329
QY 2027 ACATCAACGAAAGAAATCTCTGAGTGGCTTCTCCAAAGTGTCTTCTTCTCCAAT 2086
Db 330 TCATCAATGAGGGAGAGATCTTGTGGAGTGGTCTCCAGAGAGGTGCGCTTCTCCAAT 389
QY 2087 CGNATCGAGACTGTGTCGGGACACAGGAAGGGAGATCATCGAGGGAGGCCACTGCT 2146
Db 390 GCAGCCGGGACTGTTCAGGAGGAGGACAGGAAGGGATCATTTGAGGAGAGGCCACTGCT 449
QY 2147 GCTTTCAATGCGATGCGATGTCAGAGGAGGAGAGTTCAGTGAATCAAAACGATGCAAGTGGT 2206
Db 450 GTTTTGAAGTGTGGAGTGTCTGACGGGAGTACAGTGGTGAGACAGATGCGAGTGGCT 509
QY 2207 GTACAAAGTGGCGGAATGATTTCTGTCGAATGAGAACACACAGTCTGTCGATGCGCAA 2264
Db 510 GTGACAAAGTGGCGGATGATCTTGTGTCGAATGAGAACACACACTTCTGTCGATGCGCAA 567

```

```

RESULT 14
LOCUS CK483622
DEFINITION AGENCOURT_17636458 NIH_MGC_235 Rattus norvegicus cDNA clone
IMAGE:7109300 5', mRNA sequence.
ACCESSION CK483622
VERSION CK483622.1 GI:40827970
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 776)
NIH-MGC http://mgi.mcg.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999).
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLW14574 row: j column: 18
High quality sequence stop: 590.
Location/Qualifiers
1..776
/organism="Rattus norvegicus"
/mol_type="mRNA"

```

```

/db xref="taxon:10116"
/clone="IMAGE:7109300"
/tissue_type="kidney, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_235"
/notes="Organ: kidney; Vector: pExpress-1; Site: 1: EcoRV;
Site_2: NotI; RNA obtained from pooled kidney tissue from
a mix of male and female animals at 8 wk old. Tissues were
snap-frozen before RNA extraction and purification
(Tri-reagent method). cDNA was primed using oligo-dT
primer: 5'-pGACTAGTTCTAGATCGGAGCGGCCCT(T)25-3' and
cloned into the EcoRV/NotI sites of pExpress-1.
Size-selection >1.4kb resulted in an average insert size
of 2.2 kb. This primary library is non-normalized
(normalized primary library is NIH_MGC_236) and was
constructed by Express Genomics (Frederick, MD). Note:
this is a NIH_MGC library."

```

ORIGIN

```

Query Match 8.0%; Score 329.8; DB 7; Length 776;
Best Local Similarity 68.0%; Pred. No. 1.1e-62;
Matches 524; Conservative 0; Mismatches 232; Indels 15; Gaps 4;

QY 1012 CCCAATGATCAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAAAC 1071
Db 1 CCCAATGATCAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAAAC 60
QY 1072 TGGGTGGAAACCCCTGGCAGCCGATGACTATGCGCCGCCAGGCAATGACAAAGTTCCGG 1131
Db 61 TGGGTGGCAACAATTCGAGCTGATGACGACTATGGCAGACCTGGCATTGAGAAGTTCCGA 120
QY 1132 GAGGAGCCCTTAAGAGGAGACATCTGATTGACTTCAGTGAGATGATCTCTCAGTACTAC 1191
Db 121 GAGGAGCCGAAAGAGAGGATATCTGATTTGATTGAGAGCTCATCTCCAGTACTCT 180
QY 1192 ACCCAGAGCAGTTGGAGTTTCATCGCCGAGCTCATCCAGAACTCTTCGCCAAGTCAATC 1251
Db 181 GACGAGGAGAGATCCAGCAGAGTGGTGAAGTGATCCAAAACCTCTACGCCAAGGTCAAT 240
QY 1252 GTGGTCTTCCAAATGGCCCGGACCTGGAGCCGCTCATCCAGGAGATAGTTCCGGGAAC 1311
Db 241 GTGGTCTTCCAAATGGCCCGGACCTGGAGCCGCTCATCCAGGAGATAGTTCCGGCGGTAAC 300
QY 1312 ATCACCAGATCGGATCTGGCTGGCCAGGAGCTTGGCCAGAGTCTTCGGTCTATTGGCAAG 1371
Db 301 ATCAGAGGAGGATCTGGCTGGCTAGGAGGCTGGCCAGTCTTCGCTGATTTGCTATG 360
QY 1372 CCAGAGTACTTCCAGTGGTGGCGGACCATCGGCTTCGCTCTAGGGGGGGGGGCTATC 1431
Db 361 CCTGAGTATTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 1432 CCAGGTTCAACAAGTTCTGAGAGGAGTCCACCCAGCAGGTCCTCGGACATGGGTTT 1491
Db 421 CCAGGTTCTCGAGAAATTCCTAGAGAAAGTTCTCTTAGAAGTCTCTCCACATGTTTT 480
QY 1492 GTCAAGGAGTTCTGGAGGAGACCTTCAACTGTTACTTCAACGAGAAAGACCTTCAGCGAG 1551
Db 481 GCCAAAGAGTTTGGGAAGAAACTTTTAAATTTGCCAC--CTCCAAAGAGGCGCAAAAGGAC 538
QY 1552 CTGAAGAAATTCGAAGTGGCTTCGACGAGGACCGCGGCTCAAGGGGACCGCTCCAGGGG 1611
Db 539 CTTTACTCTGGACACCTTCGTGAGAG--TCACGAAGAGGTGGCAACAG 588
QY 1612 GGGAACTCCAGAGCGAGACCTTACGCCACCCCTGCACTGGGGAGGAGAACATCAACAGC 1671
Db 589 TTACTCAATAGCTCTACTGCTTCCGACCCCTCTGACAGGGGATGAGAATCAACAGT 648
QY 1672 GTGAGAGCCCTTACTGATGATATACACCTGAGGATCTCTACATGATATACGTGGCC 1731
Db 649 GTGGAG--CCCTTATCATGTTTACGAAACATTTACGGATAT--CTACAATGTGTACTTAGCC 705
QY 1732 GTCTACTCTCATTTGCTCACGCCCTGCAAGAGACATCTCTTTGCAAAACCCCGC 1782

```

FEATURES
source

Db 706 GCTACTCTTTGGCATGCCACAGATATACCCCTGCTACCGGAGAGGC 756

RESULT 15
LOCUS BB615658
DEFINITION BB615658 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 4930542118 5', mRNA sequence.
ACCESSION BB615658
VERSION BB615658.1
KEYWORDS GI:16455904
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 653)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, K. I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
Location/Qualifiers
1. .653
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="4930542118"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="SOL3"
/clone_lib="RIKEN full-length enriched, adult male testis"
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

ORIGIN

Query Match 7.6%; Score 313.8; DB 2; Length 653;
Best Local Similarity 69.3%; Pred. No. 4e-59;
Matches 461; Conservative 0; Mismatches 192; Indels 12; Gaps 2;

Qy 1339 GAGGCTTGGCCAGCTCTTCGCTCATTCGACGAGAGTCTTCCACGTGGTGGCGGC 1398
Db 1 GAGGCTTGGCCAGCTCTTCGCTCATTCGACGAGAGTCTTCCACGTGGTGGCGGC 60

Qy 1399 ACCATGGCTTCGCTCTCAGGGGGGGGGTATCCAGGGTTCACCAAGTTCTCTGAAGGAG 1458
Db 61 ACCATGGGTTGGTTCGCTCTGAAGGCTGGCAGATTCAGGGTTCGAGAAATTCCTACAGAA 120

Qy 1459 GTCCACCCAGCAGGTCCTCGGACAAATGGGTTTGTCAAGAGTTCTGGAGGAGACCTTC 1518
Db 121 GTCCATCCAGGAAGTCTGTCCACAATGGTTTGGCAAGAGTTTGGGAAGAACAATTT 180

Qy 1519 AACTGCTACTTACCCGAGAGACCTTCGACGAGCTGAAGAAATTCCAAGTGGCCCTCGCAC 1578
Db 181 AATTGC-----CACCTGCAAGCGGGCGGCAACAGGTTACTCAATAGCTCCACTGCCTTCGTA 235

Qy 1579 GGACCGCGGCTCAAGGGGACGGCTCCAGGGGGGAACTCCAGACGGGACAGCCCTACGC 1638
Db 236 GAA-----GTCAAGGAGGAGCGGCAACAGGTTACTCAATAGCTCCACTGCCTTCGTA 288

Qy 1639 CACCCCTGACTGGGAGGAGACATCCAGCGTGGAGACCCCTACCTGGATTATACA 1698
Db 289 CCCTCTGCACGGGGATGAAACATCAATAGTGTGAGACCCCTTACATGGACTACGAA 348

Qy 1699 CACTGAGGATCTCTACCAATGTATAGTGGCGGTCTACTCTCATTTGTCACGCCCTGCAC 1758
Db 349 CATTACGGATATCTTACACGCTGTACTAGCCGTCTACTCTCATTTGGCAGCCCTGCAC 408

Qy 1759 GACATCCACTTTTGCAAAACCCGCGCAGGGCATCTTTTGCAAAACGGATCTTGTGAGATAT 1818
Db 409 GATATATACACCTGCTTACCCGGAAGAGGGCTTTTCAACCAACGGGCTCTGTGAGACATC 468

Qy 1819 AABAAGTTGAGCCCTGGCAGGTCCTCAACCATCTGCTGATCTGAAGTTTACCAACAGC 1878
Db 469 AAGAAGTTGAGCCCTGGCAGGTCCTGAAACACCTACGGCACCTGAATTTACCAACAC 528

Qy 1879 ATGGGTGAGCAGGTTGACCTTTGACGATCAAGGTGACCTCAAGGGGAACTACACATTATC 1938
Db 529 ATGGGGAGCAGGTGACCTTCGATGATGCGGTGACCTGTGGGGAACTACTCCATCATC 588

Qy 1939 AACTGGCAGCTCTCCGAGGAGATGATCGGTGTTGTTCCATGAGTGGGCACTACAC 1998
Db 589 AACTGGCAGCTCTCCGAGGAGATGATCGGTGTTGTTCCATGAGTGGGCACTACAC 648

Qy 1999 GCCTA 2003
Db 649 GTGTA 653

Search completed: November 17, 2004, 06:55:13
Job time : 11890 secs

FEATURES
source

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 06:55:29 ; Search time 297 Seconds
(without alignments)
1240.455 Million cell updates/sec

Title: US-10-016-496-2
Perfect score: 5410
Sequence: 1 MAQLHCQLFLGTLQSYN.....KGTLESPGSKERTTMEET 1027

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_23Sep04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5410	100.0	1027	AAU76004	Aau76004 Shark kid
2	5410	100.0	1027	ABH78761	Abh78761 Dogfish s
3	5410	100.0	1027	ADH10917	Adh10917 Shark pol
4	5410	100.0	1027	ABW02706	Abw02706 Dogfish s
5	5410	100.0	1027	ADI19970	Adi19970 Dogfish s
6	5251.5	97.1	1026	AAW32059	Aaw32059 Dogfish s
7	4106.5	75.9	1059	AAU00508	Aau00508 Chicken c
8	4055.5	75.0	1078	AAU02195	Aau02195 Cynomolgo
9	4044.5	74.8	1078	AAU70325	Aay70325 Human wil
10	4044.5	74.8	1078	ADD48571	Add48571 Human pro
11	4044.5	74.8	1078	AD62143	Ad62143 Human pro
12	4044.5	74.8	1078	AD62147	Ad62147 Human pro
13	4044.5	74.8	1078	ADH10955	Adh10955 Human par
14	4044.5	74.8	1078	ADJ68365	Adj68365 Human hea
15	4044.5	74.8	1078	ADI41014	Adi41014 Human GPC
16	4044.5	74.8	1078	ADI40962	Adi40962 Human GPC
17	4044.5	74.8	1078	ADO29211	Ado29211 Human GPC
18	4039.5	74.7	1078	ADJ93192	Adj93192 Human ext
19	4039.5	74.7	1078	ABG72193	Abg72193 Human cal
20	4037.5	74.6	1078	AAW11889	Aaw11889 Parathyro
21	4037.5	74.6	1078	AAW54846	Aaw54846 Human par
22	4037.5	74.6	1078	AAW38274	Aaw38274 Human par
23	4037.5	74.6	1078	AAW38274	Aaw38274 Human par
24	4037.5	74.6	1078	AAW38274	Aaw38274 Human par
25	4037.5	74.6	1078	AAW38274	Aaw38274 Human par

26	4037.5	74.6	1078	3	AAV51827	Aay51827 Human cal
27	4037.5	74.6	1078	4	AAW74391	Aab74391 Protein e
28	4037.5	74.6	1078	5	AAW7822	Abw7822 HuCar4.0.
29	4037.5	74.6	1078	6	ABP91817	Abp91817 Human cal
30	4029.5	74.5	1088	2	AAW11888	Aaw11888 Parathyro
31	4029.5	74.5	1088	2	AAW54845	Aaw54845 Human par
32	4029.5	74.5	1088	2	AAW41779	Aay41779 Human par
33	4029.5	74.5	1088	2	AAW89564	Aaw89564 Human par
34	4029.5	74.5	1088	3	AAW51826	Aay51826 Human cal
35	4029.5	74.5	1088	4	AAW74390	Aab74390 Protein s
36	4029.5	74.5	1088	5	AAW7821	Abw7821 HuPCARS.2
37	4029.5	74.5	1088	8	ADW47114	Adw47114 Human cal
38	4029.5	74.5	1089	7	ADW48589	Adw48589 Human pro
39	4022.5	74.4	1088	2	AAW38273	Aaw38273 Human par
40	3999.5	73.9	1085	2	AAW54844	Aaw54844 Bovine pa
41	3999.5	73.9	1085	2	AAW38272	Aaw38272 Bovine pa
42	3999.5	73.9	1085	2	AAW41778	Aay41778 Bovine pa
43	3999.5	73.9	1085	2	AAW89563	Aaw89563 Bovine pa
44	3999.5	73.9	1085	3	AAW51825	Aay51825 Bovine ca
45	3999.5	73.9	1085	5	AAW47820	Aab47820 BOPCAR1.

ALIGNMENTS

RESULT 1
AAU76004
ID AAU76004 standard; protein; 1027 AA.
XX AC AAU76004;
XX DT 07-AUG-2003 (revised)
DT 08-MAY-2002 (first entry)
XX DE Shark kidney calcium receptor related protein-1 (SKCar-RP-1).
XX KW Shark kidney calcium receptor related protein-1; SKCar-RP-1;
KW polyvalent cation-sensing receptor protein; PVCR; fish; flounder;
KW salinity tolerance; fat content; protein content; weight;
KW fish maturation; fish development; spiny dogfish.
XX OS Squalus acanthias.
XX FN US6337391-B1.
XX PD 08-JAN-2002.
XX PF 28-SEP-1998; 98US-00162021.
XX PR 27-MAR-1996; 96US-00622738.
XX PR 27-MAR-1997; 97WO-US005031.
XX PA (BCHM) BRIGHAM & WOMENS HOSPITAL.
XX PI Harris HW, Brown EM, Hebert SC;
XX WI; 2002-163246/21.
XX DR N-PSDB; ABK14910.
XX PT New nucleic acid molecule encoding polyvalent cation-sensing receptor
protein, useful for regulating adaptation of fish e.g. flounder to marine
and fresh water environments, and to alter tissue or meat/muscle
composition.
XX PS Claim 4; Fig 5A-E; 83pp; English.
XX CC The invention describes an isolated nucleic acid sequence (I) encoding a
polyvalent cation-sensing receptor protein (PVCR), especially Shark
Kidney calcium receptor related protein-I (SKCar-RP-I) that allows fish
to sense ion concentrations. The aquatic PVCR allows the successful
adaptation of fish, such as flounder, to marine and fresh water
environments, and controls maturation and developmental stages in marine
species. Modulating the expression of PVCR activates or inhibits PVCR

CC mediated ion transport and endocrine changes that permit fish to adapt to
 CC fresh or salt water. Activating pVCR in epithelial cells increases or
 CC decreases salinity tolerance in aquatic species. Regulating salinity
 CC tolerance is useful to develop new species of marine fish that are easily
 CC adaptable to fresh water aqua culture. The methods are useful for
 CC altering body composition e.g. fat content, protein content, weight,
 CC thickness, moisture and taste. The species can be maintained in both
 CC environments, consecutively to reduce parasites, bacteria and
 CC contaminants. This is the amino acid sequence of the shark kidney calcium
 CC receptor related protein-1 (SKCaR-pp-1), described in the method of the
 CC invention. (Updated on 07-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 1027 AA;

Query Match 100.0%; Score 5410; DB 5; Length 1027;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHCQLLFGFTLLQSNVSGYGNPQRAQKKGDIILGGLFPIHFGVAAKQDQLKSRPE 60
 DB 1 MAQLHCQLLFGFTLLQSNVSGYGNPQRAQKKGDIILGGLFPIHFGVAAKQDQLKSRPE 60

QY 61 ATKCIYNPRGRWLOAMIFATEEINNSMTFLPNITLGVRIPTDCTNTVSKALEATLSFVA 120
 DB 61 ATKCIYNPRGRWLOAMIFATEEINNSMTFLPNITLGVRIPTDCTNTVSKALEATLSFVA 120

QY 121 QNKIDSLNLDLFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180
 DB 121 QNKIDSLNLDLFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180

QY 181 KNEYKAFIETINDEQOATAMAEIIEHPQWNVWGLAADDDYGRGIDKPFEEAVKRDIC 240
 DB 181 KNEYKAFIETINDEQOATAMAEIIEHPQWNVWGLAADDDYGRGIDKPFEEAVKRDIC 240

QY 241 IDPSEMISQYTKOLEFTADVIQNSSAKVIVFNSGPDLEPLIOEIVRMITRDIWLAS 300
 DB 241 IDPSEMISQYTKOLEFTADVIQNSSAKVIVFNSGPDLEPLIOEIVRMITRDIWLAS 300

QY 301 EAWASSLIAKPEYFHVGGTIGFALRAGRIFGFNKFLKEVHPSSSDNGFVKEPWEETF 360
 DB 301 EAWASSLIAKPEYFHVGGTIGFALRAGRIFGFNKFLKEVHPSSSDNGFVKEPWEETF 360

QY 361 NCYFTEKTLTQKNSKVPBGHPAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420
 DB 361 NCYFTEKTLTQKNSKVPBGHPAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420

QY 421 HLRISYNVVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLHLKFTNS 480
 DB 421 HLRISYNVVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLHLKFTNS 480

QY 481 MGEQVDFDDQGLKGNYYIINWOLSADESVLFHEVGNNAYAKPSDRNLNNEKILMSG 540
 DB 481 MGEQVDFDDQGLKGNYYIINWOLSADESVLFHEVGNNAYAKPSDRNLNNEKILMSG 540

QY 541 FSKVVPFNSCRDPCVPGTRKGIIEGPTCCFECMACAEGFSDENDASACTKCPNDFWSN 600
 DB 541 FSKVVPFNSCRDPCVPGTRKGIIEGPTCCFECMACAEGFSDENDASACTKCPNDFWSN 600

QY 601 ENHTSCIAKEIYLSWTEPFGIALTIFAVLGLITTSFVLGVIFKPRNPPIVKATNRELVS 660
 DB 601 ENHTSCIAKEIYLSWTEPFGIALTIFAVLGLITTSFVLGVIFKPRNPPIVKATNRELVS 660

QY 661 LLLFSLICCFSSSLFIQEPBPDWTCRLQPAFGISFVLCISILVKNRVLVFEAKIPT 720
 DB 661 LLLFSLICCFSSSLFIQEPBPDWTCRLQPAFGISFVLCISILVKNRVLVFEAKIPT 720

QY 721 SLHRKWVGNLQFLVFLCILQVITCIWLVTAPPSSYRNHLEDEVFITCDEGSLMA 780
 DB 721 SLHRKWVGNLQFLVFLCILQVITCIWLVTAPPSSYRNHLEDEVFITCDEGSLMA 780

QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFTTFSMLIFFIWIWISFIPAYSTYKGF 840
 DB 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFTTFSMLIFFIWIWISFIPAYSTYKGF 840

QY 841 VSAVEVIAILASSFGLLGCIYFNKCVIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
 DB 841 VSAVEVIAILASSFGLLGCIYFNKCVIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900

QY 901 AASRKSSSICGSTITSSPASSTCGPLTMMQRCSTQKVSFGSGTIVTSLSFEETGRYAT 960
 DB 901 AASRKSSSICGSTITSSPASSTCGPLTMMQRCSTQKVSFGSGTIVTSLSFEETGRYAT 960

QY 961 LSTASRSNADGRSGDDLPSSRHDDGPPQKCEPOPANDARYKAAPTKGTLSPPGSKER 1020
 DB 961 LSTASRSNADGRSGDDLPSSRHDDGPPQKCEPOPANDARYKAAPTKGTLSPPGSKER 1020

QY 1021 PTTMEET 1027
 DB 1021 PTTMEET 1027

RESULT 2
 ABB78761
 ID ABB78761 standard; protein; 1027 AA.
 XX AC ABB78761;
 XX DT 23-JUL-2002 (first entry)
 XX DE Dogfish shark kidney cation receptor (SKCaR) protein SEQ ID NO:18.
 XX KW Fish; polyvalent cation sensing receptor; pVCR; anadromous fish;
 XX KM polyvalent cation sensing receptor modulator; pVCR modulator; feed;
 XX KW atlantic salmon; arctic char; rainbow trout.
 XX OS Squalus acanthias.
 XX FN WO200230182-A2.
 XX PD 18-APR-2002.
 XX PF 11-OCT-2001; 2001WO-US031562.
 XX PR 12-OCT-2000; 2000US-00687372.
 XX PR 12-OCT-2000; 2000US-00687476.
 XX PR 12-OCT-2000; 2000US-00687477.
 XX PA (AQUA-) AQUABIO PROD SCI LLC.
 XX PI Harris WH, Russell DR, Nearing J, Betka M;
 XX WPI; 2002-416815/44.
 XX DR N-PSDB; ABL59964.
 XX PS
 XX CC Improving the raising of pre-adult anadromous fish e.g. salmon involves
 CC adding polyvalent cation sensing receptor modulator and a feed containing
 CC an agent that increases level of modulator in serum of fish.
 CC
 CC Example 1; Fig 28; 201pp; English.
 CC The present invention describes a method for improving the raising of pre
 CC -adult anadromous fish maintained in fresh water prior to transfer to
 CC seawater. The method involves: (a) adding at least one polyvalent cation
 CC sensing receptor (pVCR) modulator to the fresh water; and (b) adding a
 CC feed containing an agent that increases the level of pVCR modulator in
 CC the serum of fish. The pVCR modulator has anabolic activity. The method
 CC can be used for improving the raising of pre-adult anadromous fish e.g.
 CC salmon, char and trout, maintained in fresh water prior to transfer to
 CC seawater. The present sequence represents dogfish shark kidney cation
 CC receptor (SKCaR), which is relative to the pVCRs from salmon, char and
 CC trout
 XX SQ Sequence 1027 AA;

Query Match 100.0%; Score 5410; DB 5; Length 1027;
 Best Local Similarity 100.0%; Pred. No. 0;

		Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MAQHCOLLFLGFTLLQSYNVSGYGNORAKKGDIIILGGLFPIHFGVAAKQDLSRPE	60		
Db	1	MAQHCOLLFLGFTLLQSYNVSGYGNORAKKGDIIILGGLFPIHFGVAAKQDLSRPE	60		
Qy	61	ATKCIYRNFGRFRLQAMIFAEEINNSMTFLPNIITLGYRIFDTCNTVSKALEATLSFVA	120		
Db	61	ATKCIYRNFGRFRLQAMIFAEEINNSMTFLPNIITLGYRIFDTCNTVSKALEATLSFVA	120		
Qy	121	QNKIDSLNLDLDFNCSDHIPSTIAVVGATGGISTAVANLLGLFYIPQVSYASSSRLSN	180		
Db	121	QNKIDSLNLDLDFNCSDHIPSTIAVVGATGGISTAVANLLGLFYIPQVSYASSSRLSN	180		
Qy	181	KNEYKAFRLTIPNDEQQATAMAEIIEHFQWNWVGTAAADDYGRPGIDKFREEAVKRDIC	240		
Db	181	KNEYKAFRLTIPNDEQQATAMAEIIEHFQWNWVGTAAADDYGRPGIDKFREEAVKRDIC	240		
Qy	241	IDFSEMIQYTTQKLEFIADVIQNSSAKVIVFNSNGFDLEPLIQEIVRRNITDRIWLAS	300		
Db	241	IDFSEMIQYTTQKLEFIADVIQNSSAKVIVFNSNGFDLEPLIQEIVRRNITDRIWLAS	300		
Qy	301	EAWASSSLIAKPEYHVHVGTTIGFALRAGRTPGNKELKEVHPSRSSDNGFVKEFWBETP	360		
Db	301	EAWASSSLIAKPEYHVHVGTTIGFALRAGRTPGNKELKEVHPSRSSDNGFVKEFWBETP	360		
Qy	361	NCYFTEKTLTQIKNSKVPESHGPAAGDGSKAGNSRRRTALRHPCCTGEENITSVETPYLDYT	420		
Db	361	NCYFTEKTLTQIKNSKVPESHGPAAGDGSKAGNSRRRTALRHPCCTGEENITSVETPYLDYT	420		
Qy	421	HLRISYNYVAVYSIAHALQDIHSCKPGTGFANGSCADIIKKVAMQVNLHLLKFTNS	480		
Db	421	HLRISYNYVAVYSIAHALQDIHSCKPGTGFANGSCADIIKKVAMQVNLHLLKFTNS	480		
Qy	481	MGEQVDFDDGDLKGNYYTIINWQLSAEDSVLFEHVGNYNAYAKPSRLNINEKKILWSG	540		
Db	481	MGEQVDFDDGDLKGNYYTIINWQLSAEDSVLFEHVGNYNAYAKPSRLNINEKKILWSG	540		
Qy	541	FSKVVPFNSCRDVCVGRKGIIEGEPTCCFEACAEDEFSNDASACTKCPNDFWSN	600		
Db	541	FSKVVPFNSCRDVCVGRKGIIEGEPTCCFEACAEDEFSNDASACTKCPNDFWSN	600		
Qy	601	ENHSCIAKEIYLSWTFPGFALTIIPAVLGILITSFVLGVFIKFRNTPIVKAATNRELSY	660		
Db	601	ENHSCIAKEIYLSWTFPGFALTIIPAVLGILITSFVLGVFIKFRNTPIVKAATNRELSY	660		
Qy	661	LLLFSLICCFSSSLIFICEPRDWTCLRLQPAFGISFVLCISCLVKNRVLLVFEAKIPT	720		
Db	661	LLLFSLICCFSSSLIFICEPRDWTCLRLQPAFGISFVLCISCLVKNRVLLVFEAKIPT	720		
Qy	721	SLHRKWGVLNQFLVFLCIIIVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDEGSLMA	780		
Db	721	SLHRKWGVLNQFLVFLCIIIVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDEGSLMA	780		
Qy	781	LGFLIGYTCLLAAICFFFAFKSRKLPENFNKAPRTTFSMILFFFIWISFIPAYVSTYCKF	840		
Db	781	LGFLIGYTCLLAAICFFFAFKSRKLPENFNKAPRTTFSMILFFFIWISFIPAYVSTYCKF	840		
Qy	841	VSAVEVIAIASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS	900		
Db	841	VSAVEVIAIASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS	900		
Qy	901	AASRRSSLCGSTISSPASSTCGPLTMEQRCSTQKVSFGSGVTLSLFEETGRYAT	960		
Db	901	AASRRSSLCGSTISSPASSTCGPLTMEQRCSTQKVSFGSGVTLSLFEETGRYAT	960		
Qy	961	LSRTARSNSADGRSGDDLPSRHHPDQPPQKCEPOPANDARYKAAPTKGTLESFGGSKER	1020		
Db	961	LSRTARSNSADGRSGDDLPSRHHPDQPPQKCEPOPANDARYKAAPTKGTLESFGGSKER	1020		
Qy	1021	PTTMEET 1027			
Db	1021	PTTMEET 1027			

RESULT 3
ADHI0917

ID ADHI0917 standard; protein; 1027 AA.

XX ADHI0917;

XX AC (first entry)

DT 11-MAR-2004

XX Shark polyvalent cation sensing receptor (PVCr)-related protein.

DE polyvalent cation sensing receptor; PVCr; shark; growth increase;

XX mortality reduction.

KW Unidentified.

OS WO2003087331-A2.

XX 23-OCT-2003.

XX 09-APR-2003; 2003WO-US011188.

XX 11-APR-2002; 2002US-00121441.

PR 18-APR-2002; 2002US-00125772.

PR 18-APR-2002; 2002US-00125778.

PR 18-APR-2002; 2002US-00125792.

XX (MARI-) MARICAL INC.

PA Harris HW, Nearing J, Betka M;

XX WPI; 2003-845319/78.

XX N-PSDB; ADHI0916.

XX New Atlantic salmon polyvalent cation-sensing receptor, PVCr,

PT polypeptides useful in commercial raising of salmon and restoration of

PT wild Atlantic salmon populations especially in transfer from freshwater

PT to seawater.

XX Example 1; SEQ ID NO 2; 269pp; English.

XX The invention comprises the amino acid and coding sequences of polyvalent

XX cation sensing receptor (PVCr) proteins from Atlantic salmon. The DNA and

XX protein sequences of the invention are useful in the commercial raising

XX of Atlantic salmon and the restoration of wild Atlantic salmon

XX populations, especially in the transfer from freshwater to seawater with

XX increased growth and reduced mortality. The present amino acid sequence

XX represents a shark PVCr-related protein.

XX SQ Sequence 1027 AA;

Query Match 100.0%; Score 5410; DB 7; Length 1027;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQHCOLLFLGFTLLQSYNVSGYGNORAKKGDIIILGGLFPIHFGVAAKQDLSRPE 60

Db 1 MAQHCOLLFLGFTLLQSYNVSGYGNORAKKGDIIILGGLFPIHFGVAAKQDLSRPE 60

Qy 61 ATKCIYRNFGRFRLQAMIFAEEINNSMTFLPNIITLGYRIFDTCNTVSKALEATLSFVA 120

Db 61 ATKCIYRNFGRFRLQAMIFAEEINNSMTFLPNIITLGYRIFDTCNTVSKALEATLSFVA 120

Qy 121 QNKIDSLNLDLDFNCSDHIPSTIAVVGATGGISTAVANLLGLFYIPQVSYASSSRLSN 180

Db 121 QNKIDSLNLDLDFNCSDHIPSTIAVVGATGGISTAVANLLGLFYIPQVSYASSSRLSN 180

Qy 181 KNEYKAFRLTIPNDEQQATAMAEIIEHFQWNWVGTAAADDYGRPGIDKFREEAVKRDIC 240

Db 181 KNEYKAFRLTIPNDEQQATAMAEIIEHFQWNWVGTAAADDYGRPGIDKFREEAVKRDIC 240

Qy 241 IDFSEMIQYTTQKLEFIADVIQNSSAKVIVFNSNGFDLEPLIQEIVRRNITDRIWLAS 300

Db 241 IDPSEMSQYTKQLFEIADVIQNSAKVIVFNSGPDLEPLIOEIVERNITRIWLAS 300
 QY 301 EAWASSSLIAKPEYFHVVGTTGIFALRAGRIIPGFKFLKEVHPSSSDNGFVKFEWETF 360
 Db 301 EAWASSSLIAKPEYFHVVGTTGIFALRAGRIIPGFKFLKEVHPSSSDNGFVKFEWETF 360
 QY 361 NCYFTEKTLTQKNSKVPVSHGPAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
 Db 361 NCYFTEKTLTQKNSKVPVSHGPAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
 QY 421 HLRIISYNNVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLLKFTNS 480
 Db 421 HLRIISYNNVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLLKFTNS 480
 QY 481 MGEQVDFDDGDLKGNYYTIINQLSAEDSVLPFHEVGNVAYAKPSDELNEXKILWSG 540
 Db 481 MGEQVDFDDGDLKGNYYTIINQLSAEDSVLPFHEVGNVAYAKPSDELNEXKILWSG 540
 QY 541 FSKVWPFNSCSDCVPGTRKGIIEGEPCCFECMACAEGFSDENDASACTKCPNDFWSN 600
 Db 541 FSKVWPFNSCSDCVPGTRKGIIEGEPCCFECMACAEGFSDENDASACTKCPNDFWSN 600
 QY 601 ENHTSCIAKEIYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPPIVKATNRELSY 660
 Db 601 ENHTSCIAKEIYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPPIVKATNRELSY 660
 QY 661 LLLFSLICCFSSLLIFIGEPDWTCLRQAPAGISFVLCISCLVKTNRVLLVFEAKIPT 720
 Db 661 LLLFSLICCFSSLLIFIGEPDWTCLRQAPAGISFVLCISCLVKTNRVLLVFEAKIPT 720
 QY 721 SLHRXWVGLNLQFLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDEGLMA 780
 Db 721 SLHRXWVGLNLQFLVFLCILVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDEGLMA 780
 QY 781 LGFLIGYCTLLAICFFFAFKSRKLPENFNEAKFTFMSLIFFIWISFIPAYVSTYCKF 840
 Db 781 LGFLIGYCTLLAICFFFAFKSRKLPENFNEAKFTFMSLIFFIWISFIPAYVSTYCKF 840
 QY 841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNITIEEVRCSSTAHAFAKVAARATLRS 900
 Db 841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNITIEEVRCSSTAHAFAKVAARATLRS 900
 QY 901 AASRRSSSLCGSTISSPASSTCGFLTWEMQRCSTQKVSFGSGTVTLSSLFEBTGRYAT 960
 Db 901 AASRRSSSLCGSTISSPASSTCGFLTWEMQRCSTQKVSFGSGTVTLSSLFEBTGRYAT 960
 QY 961 LSRTARSNSADGRGDDLPSSHHPQGPQKCEPOPANDARYKAAPTGTLESPPGSKER 1020
 Db 961 LSRTARSNSADGRGDDLPSSHHPQGPQKCEPOPANDARYKAAPTGTLESPPGSKER 1020
 QY 1021 PTTMEET 1027
 Db 1021 PTTMEET 1027

RESULT 4
 ID ABW02706 standard; protein; 1027 AA.
 AC ABW02706;
 XX ABW02706;
 XX 11-MAR-2004 (first entry)

DE Dogfish shark kidney calcium receptor related protein-I (SKCaR-RP-I).
 XX Polyvalent cation-sensing receptor; PVCR; anabolic; homeostatic;
 KW shark kidney calcium receptor related protein-I; SKCaR-RP-I;
 KW dogfish shark; SKCaR-I.
 OS Squalus acanthias.
 XX
 PN US2003166908-A1.

XX 04-SEP-2003.
 PD 10-DEC-2001; 2001US-00016496.
 XX 27-MAR-1996; 96US-00622738.
 XX 27-MAR-1997; 97WO-US005031.
 PR 28-SEP-1998; 98US-00162021.
 PR 17-NOV-2000; 2000US-00715538.
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA Harris HW, Brown EM, Hebert SC;
 XX WPI; 2003-874926/81.
 XX N-PSDB; AAD64738.
 DR
 DR
 XX
 PT Fish polyvalent cation-sensing receptor proteins, useful for assisting
 PT fish in adapting to changing ion concentrations by altering water intake
 PT and absorption, urine output or for modulating the fat, protein and
 PT moisture content of muscle.
 XX
 PS Claim 7; SEQ ID NO 2; Opp; English.
 XX
 CC The invention relates to aquatic polyvalent cation-sensing receptor
 CC (PVCR) proteins and methods of regulating PVCR functions in aquatic
 CC species. PVCR is used to screen candidate compounds that may be used to
 CC assist fish in adapting to changing ion concentrations by altering water
 CC intake, water absorption or urine output and/or for modulating the
 CC percentage of total fat, protein and moisture of muscle of the fish. The
 CC present sequence is dogfish shark kidney calcium receptor related protein
 CC -I (SKCaR-RP-I or SKCaR-I). This sequence is used to illustrate the
 CC method of the invention
 XX
 SQ Sequence 1027 AA;

Query Match 100.0%; Score 5410; DB 7; Length 1027;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHQQLFLGFTLLQSYNVSQYGNPQRAQKKGDIILGGLFPIHFGVAAKQDQLKSPE 60
 Db 1 MAQLHQQLFLGFTLLQSYNVSQYGNPQRAQKKGDIILGGLFPIHFGVAAKQDQLKSPE 60

QY 61 ATKICIRNFRGRFWLOAMIFAEIENNSMTFLPNTLGVRIEDTCTNTVSKALEATLSFVA 120
 Db 61 ATKICIRNFRGRFWLOAMIFAEIENNSMTFLPNTLGVRIEDTCTNTVSKALEATLSFVA 120

QY 121 ONKIDSLNLDDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFVPOVSYASSRLLSN 180
 Db 121 ONKIDSLNLDDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFVPOVSYASSRLLSN 180

QY 181 KNEYKAFLETIPNDEQQATAMAEIIIEHFQMNWVGTIAADDDYGRPGIDKFREEAVKRDIC 240
 Db 181 KNEYKAFLETIPNDEQQATAMAEIIIEHFQMNWVGTIAADDDYGRPGIDKFREEAVKRDIC 240

QY 241 IDPSEMSQYTKQLFEIADVIQNSAKVIVFNSGPDLEPLIOEIVERNITRIWLAS 300
 Db 241 IDPSEMSQYTKQLFEIADVIQNSAKVIVFNSGPDLEPLIOEIVERNITRIWLAS 300

QY 301 EAWASSSLIAKPEYFHVVGTTGIFALRAGRIIPGFKFLKEVHPSSSDNGFVKFEWETF 360
 Db 301 EAWASSSLIAKPEYFHVVGTTGIFALRAGRIIPGFKFLKEVHPSSSDNGFVKFEWETF 360

QY 361 NCYFTEKTLTQKNSKVPVSHGPAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
 Db 361 NCYFTEKTLTQKNSKVPVSHGPAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420

QY 421 HLRIISYNNVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLLKFTNS 480
 Db 421 HLRIISYNNVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLLKFTNS 480

QY 481 MGEQVDFDDGDLKGNYYTIINQLSAEDSVLPFHEVGNVAYAKPSDELNEXKILWSG 540

Db 481 MGEQVDFDDGDLKGNVYIIINWQLSAEDSVLFHEVGNVYAKPSDELININEKILWSG 540
Qy 541 FSKVVPFNSGRDCVPGTRKGIIEGEPTCCPECMACAEGESDENDASACTKCPNDPWSN 600
Db 541 FSKVVPFNSGRDCVPGTRKGIIEGEPTCCPECMACAEGESDENDASACTKCPNDPWSN 600
Qy 601 ENHTSCIAKEIEYLSWTFPGIALTIPAVLGILITISFVLGVFIKFRNTPIVKATNRELSY 660
Db 601 ENHTSCIAKEIEYLSWTFPGIALTIPAVLGILITISFVLGVFIKFRNTPIVKATNRELSY 660
Qy 661 LLLFSLICCFSSSLIFIGEPRDWTCLRPQAFGISFVLCISCLVKTNRVLLVFEAKIPT 720
Db 661 LLLFSLICCFSSSLIFIGEPRDWTCLRPQAFGISFVLCISCLVKTNRVLLVFEAKIPT 720
Qy 721 SLHRKWGLNQFLVFLVLCILVQIVTCIIWLYTAPSSYRNHELEDEVIFITCDEGSLMA 780
Db 721 SLHRKWGLNQFLVFLVLCILVQIVTCIIWLYTAPSSYRNHELEDEVIFITCDEGSLMA 780
Qy 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNENAKTTFMSLIIFFIIVWISFIPAYVSTYCKF 840
Db 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNENAKTTFMSLIIFFIIVWISFIPAYVSTYCKF 840
Qy 841 VSAVEVIAILASSFGLLCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
Db 841 VSAVEVIAILASSFGLLCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
Qy 901 AASRRSSSLCGSTISSPASSTCGPLTWEMQRCSTQKVSFGSGTVTLSLSFETGRYAT 960
Db 901 AASRRSSSLCGSTISSPASSTCGPLTWEMQRCSTQKVSFGSGTVTLSLSFETGRYAT 960
Qy 961 LSRTARSNSADGRGDDLPGRHHDQGPQKCEPOPANDARYKAAPTKGTLESFGGSKER 1020
Db 961 LSRTARSNSADGRGDDLPGRHHDQGPQKCEPOPANDARYKAAPTKGTLESFGGSKER 1020
Qy 1021 PTWMEET 1027
Db 1021 PTWMEET 1027

RESULT 5
ADI19970
ID ADI19970 standard; protein; 1027 AA.
XX ADI19970;
AC ADI19970;
DT 15-APR-2004 (first entry)
XX Dogfish shark kidney cation receptor (SKCar) protein.
DE Pre-adult anadromous fish; polyvalent cation sensing receptor; PVCR;
KW stress; dogfish shark; receptor.
XX Squalus acanthias.
OS US2003230247-A1.
XX 18-DEC-2003.
XX 09-APR-2003; 2003US-00410872.
XX 12-OCT-2000; 2000US-00687372.
XX 12-OCT-2000; 2000US-00687476.
XX 12-OCT-2000; 2000US-00687477.
XX 11-OCT-2001; 2001US-00975553.
XX 11-OCT-2001; 2001WO-US031562.
XX (MARI-) MARICAL INC.
XX Harris HW, Russell DR, Nearing J, Betka M;
XX WPI; 2004-061122/06.
XX N-PSDB; ADI19962.

XX Growing pre-adult anadromous fish in freshwater comprises adding feed
PT containing an amount of NaCl for fish consumption to the freshwater to
PT increase the level of the Polyvalent Cation Sensing Receptor modulator in
XX serum of the fish.
PS Example 19; Fig 28; 109pp; English.
XX The present invention relates to methods for improving the raising of pre
CC -adult anadromous fish or preparing these fish for transfer to seawater
CC by modulating expression of a receptor referred to as the Polyvalent
CC Cation Sensing Receptor (PVCR). The invention is useful in increasing
CC survival and growth and reduce stress of the fish that have been
CC transferred to seawater. The present sequence is a dogfish shark cation
CC receptor (SKCar) protein.
XX Sequence 1027 AA;
SQ Query Match 100.0%; Score 5410; DB 8; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQLHCOLLPLGFTLLQSYNVSGYGNQRAQKGDIIILGGLPIHFGVAAKQDQDKSRPE 60
Db 1 MAQLHCOLLPLGFTLLQSYNVSGYGNQRAQKGDIIILGGLPIHFGVAAKQDQDKSRPE 60
Qy 61 ATKCIYRNFGRFRLQAMIFAEIEINNSMTFLPNITLGYRIEDTCTNVSKALEATLSFVA 120
Db 61 ATKCIYRNFGRFRLQAMIFAEIEINNSMTFLPNITLGYRIEDTCTNVSKALEATLSFVA 120
Qy 121 QNKIDSLNLDNFCNCDHIPSTIYVVGATGSGISTAVANLLGLFYIPOVSYASSSLLSN 180
Db 121 QNKIDSLNLDNFCNCDHIPSTIYVVGATGSGISTAVANLLGLFYIPOVSYASSSLLSN 180
Qy 181 KNEYKAFRLTIPNDEQOATAMABIEHFQWNWVGTAAADDDYGRPGIDKFREAEVAKRDIC 240
Db 181 KNEYKAFRLTIPNDEQOATAMABIEHFQWNWVGTAAADDDYGRPGIDKFREAEVAKRDIC 240
Qy 241 IDSEMIQYITOKLEFIADVIQNSAKVIVVFSNGPDLELIQIQRNITDRIWLAS 300
Db 241 IDSEMIQYITOKLEFIADVIQNSAKVIVVFSNGPDLELIQIQRNITDRIWLAS 300
Qy 301 EAWSSSLIAKPEYFHVVGTTIGFALRAGRIPOGFKLKEVHPSRSSDNGFVKFEWEET 360
Db 301 EAWSSSLIAKPEYFHVVGTTIGFALRAGRIPOGFKLKEVHPSRSSDNGFVKFEWEET 360
Qy 361 NCYFTEKTLTQLXNSKVPSPHGAQDGGKAGNSRRRTALRHPCGTGENITSVETPYLDYT 420
Db 361 NCYFTEKTLTQLXNSKVPSPHGAQDGGKAGNSRRRTALRHPCGTGENITSVETPYLDYT 420
Qy 421 HLRISYVYVAVYSIAHALQDHSCKPGTGI FANGSCADIKKVEAQVNLHLHLKFTNS 480
Db 421 HLRISYVYVAVYSIAHALQDHSCKPGTGI FANGSCADIKKVEAQVNLHLHLKFTNS 480
Qy 481 MGEQVDFDDGDLKGNVYIIINWQLSAEDSVLFHEVGNVYAKPSDRJNINEKILWSG 540
Db 481 MGEQVDFDDGDLKGNVYIIINWQLSAEDSVLFHEVGNVYAKPSDRJNINEKILWSG 540
Qy 541 FSKVVPFNSGRDCVPGTRKGIIEGEPTCCPECMACAEGESDENDASACTKCPNDPWSN 600
Db 541 FSKVVPFNSGRDCVPGTRKGIIEGEPTCCPECMACAEGESDENDASACTKCPNDPWSN 600
Qy 601 ENHTSCIAKEIEYLSWTFPGIALTIPAVLGILITISFVLGVFIKFRNTPIVKATNRELSY 660
Db 601 ENHTSCIAKEIEYLSWTFPGIALTIPAVLGILITISFVLGVFIKFRNTPIVKATNRELSY 660
Qy 661 LLLFSLICCFSSSLIFIGEPRDWTCLRPQAFGISFVLCISCLVKTNRVLLVFEAKIPT 720
Db 661 LLLFSLICCFSSSLIFIGEPRDWTCLRPQAFGISFVLCISCLVKTNRVLLVFEAKIPT 720
Qy 721 SLHRKWGLNQFLVFLVLCILVQIVTCIIWLYTAPSSYRNHELEDEVIFITCDEGSLMA 780
Db 721 SLHRKWGLNQFLVFLVLCILVQIVTCIIWLYTAPSSYRNHELEDEVIFITCDEGSLMA 780

QY 781 LGFLIGYTCLLAACFFFAFKSRKLPENFNEAKPTTFMSMLFFIWIWIFIPAYVSTYQKF 840
 DB 781 LGFLIGYTCLLAACFFFAFKSRKLPENFNEAKPTTFMSMLFFIWIWIFIPAYVSTYQKF 840
 QY 841 VSAVEVIALASSFGLGCIYFNKCYIILFKPCRTNIEEVRCSAAHAFKVAARATLRRS 900
 DB 841 VSAVEVIALASSFGLGCIYFNKCYIILFKPCRTNIEEVRCSAAHAFKVAARATLRRS 900
 QY 901 AASRKRSSSLCGSTISSPASTCGPLTWEMQRCSTQKVSFGSGVTVLISLFEETGRYAT 960
 DB 901 AASRKRSSSLCGSTISSPASTCGPLTWEMQRCSTQKVSFGSGVTVLISLFEETGRYAT 960
 QY 961 LSRTARSNSADGRSGDDLPSRHHDGPPQKCEPOPANDARYKAAPTKGTLESPPGSKER 1020
 DB 961 LSRTARSNSADGRSGDDLPSRHHDGPPQKCEPOPANDARYKAAPTKGTLESPPGSKER 1020
 QY 1021 PTTMEET 1027
 DB 1021 PTTMEET 1027

RESULT 6
 AAW32059
 ID AAW32059 standard; protein; 1026 AA.
 AC AAW32059;
 DT 27-MAR-1998 (first entry)
 XX
 DE Dogfish shark kidney calcium receptor related protein (SKCar-RP).
 XX
 KW Calcium receptor related protein; Car-RP; dogfish shark; SKCar-RP;
 KW polycation-sensing receptor; aquaculture; fish farming;
 KW salinity tolerance.
 XX
 OS Squalus acanthias.
 XX
 FH Key Location/Qualifiers
 FT Region 351..395
 FT /note= "region in extracellular domain that is highly
 FT divergent from mammalian pVCR"
 FT 870
 FT Region
 FT /note= "region in C-terminal domain that is highly
 FT divergent from mammalian pVCR"
 XX
 PN WO9735977-A1.
 XX
 PD 02-OCT-1997.
 XX
 PF 27-MAR-1997; 97WO-US005031.
 XX
 PR 27-MAR-1996; 96US-00622738.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Harris HW, Brown E, Hebert S;
 DR WPI; 1997-489640/45.
 DR N-PSDB; AAT89290.
 XX
 PT New isolated Aquatic polyvalent cation-sensing receptor - used to develop
 PT products for increasing or decreasing the salinity tolerance of fish for
 PT use in aquaculture.
 XX
 PS Claim 9; Fig 5A-B; 57pp; English.
 XX
 CC This protein comprises dogfish shark kidney calcium receptor related
 CC protein (SKCar-RP), an aquatic polyvalent cation-sensing receptor (pVCR).
 CC Its amino acid sequence was deduced from a kidney cDNA clone (see
 CC AAT89290). It shows 74% homology to rat kidney pVCR and bovine
 CC parathyroid pVCR and possesses general features that are homologous to
 CC pVCR proteins, including a large extracellular domain, 7 transmembrane

CC domains and a cytoplasmic C-terminal domain. Also claimed are: an
 CC isolated pVCR present in the plasma membranes of aquatic species,
 CC especially on the apical membrane of epithelial cells of elasmobranch
 CC fish, particularly from cells found in the collecting duct or late distal
 CC tubule in the kidney, intestine, gill, rectal gland, gonad or brain; an
 CC antibody that specifically binds to a pVCR; and a method of screening for
 CC aquatic pVCR agonists and antagonists. Modulation of the expression of
 CC the aquatic pVCR activates or inhibits aquatic pVCR mediated ion
 CC transport and endocrine changes that permit fish to adapt to fresh or
 CC salt water. The method facilitates the aquaculture of marine fish and can
 CC provide for the development of marine fish that are easily adaptable to
 CC fresh water aquaculture
 XX
 SQ Sequence 1026 AA;
 Query Match 97.1%; Score 5251.5; DB 2; Length 1026;
 Best Local Similarity 97.2%; Pred. No. 0;
 Matches 1006; Conservative 1; Mismatches 11; Indels 17; Gaps 2;
 QY 1 MAQLHCQLLFLGFTLLQSYNVSGYGNQRAQKGDIIILGGLPFIHFGVAAKQDLKSRPE 60
 DB 1 MAQLHCQLLFLGFTLLQSYNVSGYGNQRAQKGDIIILGGLPFIHFGVAAKQDLKSRPE 60
 QY 61 ATCIRYNFRGFRWLQAMIFAEIEINNSMTFLPNTITLGYRIFTDCTNTVSKALEATLSFYA 120
 DB 61 ATCIRYNFRGFRWLQAMIFAEIEINNSMTFLPNTITLGYRIFTDCTNTVSKALEATLSFYA 120
 QY 121 QNKIDSINLDEFCNCSHIPSTIAVVGATSGISTAVANLLGLFYIPOVSYASSRSLSN 180
 DB 121 QNKIDSINLDEFCNCSHIPSTIAVVGATSGISTAVANLLGLFYIPOVSYASSRSLSN 180
 QY 181 KNEYKAFRLTIPNDEQOATAMAEIIIEHFQWNVVGTLLAADDYGRGIDKFREEAVKRDIC 240
 DB 181 KNEYKAFRLTIPNDEQOATAMAEIIIEHFQWNVVGTLLAADDYGRGIDKFREEAVKRDIC 240
 QY 241 IDFSEMIQYITQKOLEFIADVIQNSAKVIVFVNSGPDLEPLIOEIVARNITDRIWLAS 300
 DB 241 IDFSEMIQYITQKOLEFIADVIQNSAKVIVFVNSGPDLEPLIOEIVARNITDRIWLAS 300
 QY 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIIPGNKFLKEVHP-----SRSDNGFV 352
 DB 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIIPGNKFLKEVHPAGRTWGLSRSSG---- 356
 QY 353 KEFWSTFNCFYTEKTLTQIKNSKVPSPHGAQGDGSKAGNSRRTALRHPCTGEENITSV 412
 DB 357 -----RRLQLLHREDLTQIKNSKVPSHGAQGDGSKAGNSRRTALRHPCTGEENITSV 411
 QY 413 ETPYLDYTHLRISYVNVVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAWQVLNHL 472
 DB 412 ETPYLDYTHLRISYVNVVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAWQVLNHL 471
 QY 473 LHLKFTNSMGEQVDFDDQDGLKGNVTIINWQSADESVLFHEVGNYNAYAKPSRLNIN 532
 DB 472 LHLKFTNSMGEQVDFDDQDGLKGNVTIINWQSADESVLFHEVGNYNAYAKPSRLNIN 531
 QY 533 EKKILWSGSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAGFSDSDNASACTK 592
 DB 532 EKKILWSGSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAGFSDSDNASACTK 591
 QY 593 CPNDFWSNENHTSCIAKEIEYLSWTEPPFGIALTITFAVLGILITSFVLGVFIKFRNTPIVK 652
 DB 592 CPNDFWSNENHTSCIAKEIEYLSWTEPPFGIALTITFAVLGILITSFVLGVFIKFRNTPIVK 651
 QY 653 ATNRELSYLLLSLICCFSSSLIFIGEPDRDWTCLRQAPAFGISFVLICISLIIVKNNRVL 712
 DB 652 ATNRELSYLLLSLICCFSSSLIFIGEPDRDWTCLRQAPAFGISFVLICISLIIVKNNRVL 711
 QY 713 VFEAKIPTSLHRKWGLNLOFLVFLICILVQIVTICIIWLYTAPPSSYRNHELEDEVIPT 772
 DB 712 VFEAKIPTSLHRKWGLNLOFLVFLICILVQIVTICIIWLYTAPPSSYRNHELEDEVIPT 771
 QY 773 CDGSGSMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKPTTFMSMLFFIWIWIFIP 832

Db	772	CDEGSLMALGFLIGVTCILAAICFFAFKSRKLPENFNEAKFITFMSLIFVWISFIPA	831
Qy	833	YVSTYGVKFSVAEVIALLASSFGLLGCIYFNKCVIILFKPCRNIEEVRCSAAHAFKVA	892
Db	832	YVSTYGVKFSVAEVIALLASSFGLLGCIYFNKCVIILFKPCRNIEEVRCSAAHAFKVA	891
Qy	893	ARATLRRSAASRRSSSLCGSTISSPASSTCGPGLTMMQRCSTQKVSFGSGVTLSLSP	952
Db	892	ARATLRRSAASRRSSSLCGSTISSPASSTCGPGLTMMQRCSTQKVSFGSGVTLSLSP	951
Qy	953	EETGRYATLSRTARSNSADGRSGDDLPSSRHHDQGPQKCEPQANDARYKAAPTGTLE	1012
Db	952	EETGRYATLSRTARSNSADGRSGDDLPSSRHHDQGPQKCEPQANDARYKAAPTGTLE	1011
Qy	1013	SPGSKERPTTMEET	1027
Db	1012	SPGSKERPTTMEET	1026
RESULT 7			
ID	AAU00508	standard; protein; 1059 AA.	
XX	AAU00508		
DT	29-AUG-2001	(first entry)	
DE	Chicken calcium-sensitive receptor (CaR) protein.		
XX			
KW	Avian; chicken; calcium-sensing receptor; CaR; clone C1D;		
KW	extracellular calcium homeostasis; parathyroid hormone; PTH;		
KW	serum calcium regulator; bone deposition.		
OS	Gallus sp.		
XX			
Key	Location/Qualifiers		
Domain	1..611	/label= Extracellular domain	
FT	/note= "Amino-terminal predominantly hydrophilic domain"		
FT	1..19	/label= Signal peptide	
FT	20..1059	/label= Mature_CaR_protein	
FT	136..165	/note= "Hydrophobic region characteristic of calcium-sensing receptors and metabotropic glutamate receptors"	
FT	612..861	/note= "Hydrophobic core comprising helical transmembrane domains"	
FT	862..1059	/note= "Carboxy-terminal hydrophilic domain"	
XX	US6210964-B1.		
PN	03-APR-2001.		
PD	14-AUG-1998;	98US-00134513.	
XX	18-AUG-1997;	97US-0058095P.	
XX	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.		
PA	Brown EM, Diaz R, Bai M, Quinn SJ;		
PI	WPI; 2001-289636/30.		
DR	N-PSDB; AAS01709.		
XX	New avian calcium-sensing receptor polynucleotide and encoded receptor		
PT	protein, useful for regulating serum concentration of calcium animals,		
PT	particularly in chickens.		
XX	Claim 1; Fig 2A-2D; 43pp; English.		
PS			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			
XX			

QY 781 LGFLIGVTCLLAAICFFFAKPKRKLNFENAKFIITFSLIPIFVWISFIPAYSTYKGF 840
 DB 772 LGFLIGVTCLLAAICFFFAKPKRKLNFENAKFIITFSLIPIFVWISFIPAYSTYKGF 831
 QY 841 VSAVEVIALASSGILLGCIYENKCVIILFKPCENTIEVRCSSTAAHAFKVAARATLRS 900
 DB 832 VSAVEVIALAAGFGLACIFENKCVIILFKPCENTIEVRCSSTAAHAFKVAARATLRS 891
 QY 901 AASRKRSLSLGGSTISSPASSTCGPG-----LTMORCSTQKVSFGSGTWT 947
 DB 892 NVSRKRSLSLGGSTGTPSSISSSKSNHEDPPPLPASAERQRCQKQKVSFGSGTWT 951
 QY 948 LSLSPETGRYATLSRTASRSNADSGDDPLPSRHDDGPPKCEPQANDARYKAAPT 1007
 DB 952 LSLSPETGRYATLSRTASRSNADSGDDPLPSRHDDGPPKCEPQANDARYKAAPT 1007
 QY 1008 KGTLESPGGSKE 1019
 DB 1005 FQTASSPETSSQ 1016

RESULT 8
 ID AAU02195
 XX AAU02195 standard; protein; 1078 AA.
 AC AAU02195;
 XX
 DT 26-SEP-2001 (first entry)
 DE
 XX Cynomolgous monkey calcium-sensing receptor.
 XX
 KW Monkey; calcium-sensing receptor; bacteria; fungus; protozoa; viral;
 KW infection; HIV-1; HIV-2; human immunodeficiency virus; pain; cancer;
 KW diabetes; obesity; anorexia; bulimia; Parkinson's disease; stroke;
 KW acute heart failure; hypotension; hypertension; urinary retention;
 KW osteoporosis; angina pectoris; myocardial infarction; ulcer; asthma;
 KW allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic;
 KW neurological disorder; anxiety; schizophrenia; manic depression;
 KW depression; delirium; dementia; severe mental retardation; dyskinesia;
 KW Huntington's disease; Gilles de la Tourette's syndrome; vaccine.
 XX
 OS Macaca cynomolgus.
 XX
 PN WO200140252-A1.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US032864.
 XX
 PR 01-DEC-1999; 99US-0168342P.
 PR 30-NOV-2000; 2000US-00727205.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX
 PI Ellis CE;
 XX
 DR WPI; 2001-408275/43.
 DR N-PSDB; AAS06331.
 XX
 PT Novel Cynomolgous Monkey Calcium-Sensing Receptor polypeptides are useful
 PT for treating infections, pain, cancer, diabetes, obesity, asthma,
 PT schizophrenia, hypertension, urinary retention, Parkinson's disease and
 PT stroke.
 XX
 PS Claim 2; page 28; 38pp; English.
 XX
 CC The sequence represents the amino acid sequence of Cynomolgous monkey
 CC calcium-sensing receptor. The calcium-sensing receptor nucleic acid and
 CC polypeptide are useful for treating bacterial, fungal, protozoan and
 CC viral infections, particularly infections caused by HIV-1 or HIV-2, pain,
 CC cancer, diabetes, obesity, anorexia, bulimia, Parkinson's disease, acute

CC heart failure, hypotension, hypertension, urinary retention,
 CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers,
 CC asthma, allergies, benign prostatic hypertrophy, migraine, vomiting,
 CC psychotic and neurological disorders including anxiety, schizophrenia,
 CC manic depression, depression, delirium, dementia and severe mental
 CC retardation, and dyskinesias, such as Huntington's disease or Gilles de
 CC la Tourette's syndrome. The polypeptide is useful for structure-based
 CC design of agonist, antagonist or inhibitor of the calcium-sensing
 CC receptor. The DNA sequence is useful for chromosome localisation studies.
 CC The polypeptide and nucleic acid are also useful as vaccines
 XX
 SQ Sequence 1078 AA;

Query Match 75.0%; Score 4055.5; DB 4; Length 1078;
 Best Local Similarity 74.3%; Pred. No. 0;
 Matches 785; Conservative 85; Mismatches 136; Indels 51; Gaps 7;

QY 1 MAQLHCOLLFLGFTLLQSYNVGYNQRAQKGGDIILGGLFPIHFGVAAKODLKS RPE 60
 DB 1 MAFYCCFWLLALT-----WTSAYGDPQRAQKGGDIILGGLFPIHFGVAAKODLKS RPE 56
 QY 61 ATKCI RY NFRGFWLQAMIFAEIEINNSMTFLPNITLGYRIFDTCTNTVSKALEATLSFVA 120
 DB 57 SVECI RY NFRGFWLQAMIFAEIEINNSMTFLPNITLGYRIFDTCTNTVSKALEATLSFVA 116
 QY 121 QNKIDSINLDEFNCSDHIPSTIAVVGATGSGTAVANLLGLFYIPQVSYASSSLLSN 180
 DB 117 QNKIDSINLDEFNCSEHIPSTIAVVGATGSGTAVANLLGLFYIPQVSYASSSLLSN 176
 QY 181 KNEYKAFRLTIPNDEQATAMAEIIEHFQWNVVGTTLAADDYCRPGIDKFRFEAVKRDIC 240
 DB 177 KNQFKSFLRTPNDEHQATAMADIIEYFRNVVGTTLAADDYCRPGIEKFRFEAEERDIC 236
 QY 241 IDSEMI SYYTQKOLEFIADVIQNSSAKVIIVFSGPDLEPLIQEIVRNTITDINLAS 300
 DB 237 IDSEMI SYYTQKOLEFIADVIQNSSAKVIIVFSGPDLEPLIQEIVRNTITDINLAS 296
 QY 301 EAWASSLLAKPYFHVVGTTGFALRAGRIQFNKFLXVHPSSSDNGFVKEWEETFF 360
 DB 297 EAWASSLLAMPYFHVVGTTGFALRAGRIQFNKFLXVHPSSSDNGFVKEWEETFF 356
 QY 361 NCVFTKXTLTQLKNSKVPSSGHPAAQGGKAGNSRRALRHPTGEBENTTSVETPYDVT 420
 DB 357 NCHLQEGAKGPL---PVDTFLRGHEESGGRFNS-STAFRPLCTGDNISSETPYDVT 412
 QY 421 HLRISYNVVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVAQVNLHLHLKFTNS 480
 DB 413 HLRISYNVVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVAQVNLHLHLKFTNS 472
 QY 481 MGEQVDFDQGLKGNVTIINWQSADESVLFEHVGNYNAYAKPSDRLININEKILMSG 540
 DB 473 MGEQVDFDQGLKGNVTIINWQSADESVLFEHVGNYNAYAKPSDRLININEKILMSG 532
 QY 541 FSKVVPFNSCRDVPGRKGIIEGPCTCCFCMACAECEPDSNDASACTCPDPSN 600
 DB 533 FSKVVPFNSCRDVPGRKGIIEGPCTCCFCMACAECEPDSNDASACTCPDPSN 592
 QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLIGLITSFVLGVFIKFRNTPIVKATNRELSY 660
 DB 593 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLIGLITSFVLGVFIKFRNTPIVKATNRELSY 652
 QY 661 LLLFSLICFSSSLPIGEPDRWTCRLRQAPAGISFVLICISILVKTNRVLLVFAKPIPT 720
 DB 653 LLLFSLICFSSSLPIGEPDRWTCRLRQAPAGISFVLICISILVKTNRVLLVFAKPIPT 712
 QY 721 SLHRKRWGLNLOFLVFLCILVQIVTCIITWLTAPPSSYRNHELEDEVIFITCDGSLMA 780
 DB 713 SLHRKRWGLNLOFLVFLCILVQIVTCIITWLTAPPSSYRNHELEDEVIFITCDGSLMA 772
 QY 781 LGFLIGVTCLLAAICFFFAKPKRKLNFENAKFIITFSLIPIFVWISFIPAYSTYKGF 840
 DB 773 LGFLIGVTCLLAAICFFFAKPKRKLNFENAKFIITFSLIPIFVWISFIPAYSTYKGF 832

QY 841 VSAVEVIAIASSFGLGCIYENKCVIILFKPCRNTIEBEVRCSTAAHAFKVAARATLRRS 900
DB 833 VSAVEVIAIASSFGLGCIYENKCVIILFKPCRNTIEBEVRCSTAAHAFKVAARATLRRS 892
QY 901 AASRRSSSLCGSTISSPASSSTCGPG-----LTMEM 931
DB 893 NVSRKRSSSLGGSTGTSSTSSSSKSNGBDPPQPERKQKQOPLALTOEQEQOQPLTLFQ 952
QY 932 Q-----RCSTQKVSFGSGVTLSISPEETGRYATLSRTARSNSADGRSGDDLPSRHH 984
DB 953 QOCSQQQPRCK-QKVFSGSVTFSLSDPEPKNAHNRNSTHONSLEAKSSDTLRRH- 1010
QY 985 DQGPQKCEPOPANDARYKAAPTKGTLESPPGSKERP 1021
DB 1011 -----QALLPLQCGEADSLSVQETGLQGVGGDHRP 1042

RESULT 9
ID AAY70325
XX AAY70325 standard; protein; 1078 AA.
AC AAY70325;
XX 20-JUN-2000 (first entry)
DT Human wild type calcium sensing receptor, CasR.
DE
XX
XX Calcium Sensing Receptor; CasR; human; calcium level; modulator;
KW hypotensive; osteopathic; receptor activity; hyperparathyroidism;
KW osteoporosis; Paget's disease; treatment; hypercalcaemia malignancy;
KW hypertension; gene therapy.
XX
XX Homo sapiens.
XX WO200006601-A1.
XX 10-FEB-2000.
XX 28-JUL-1999; 99WO-US017116.
XX 30-JUL-1998; 98US-0094702P.
XX (AVET) AVENTIS PHARM PROD INC.
XX Yu KT, Labaudiniere RF, Thrower LW;
PI WPI; 2000-195263/17.
DR N-PSDB; AA251398.
XX
PT Nucleic acids encoding isoforms of human calcium sensing receptor for
PT treating, e.g. hyperparathyroidism or osteoporosis.
PS Claim 19; Page 76-80; Sipp; English.
XX
XX The present amino acid sequence is the wild type human calcium sensing
XX receptor CasR, expressed in the kidney. There are multiple alternatively
XX spliced isoforms of CasR, that arise from partial deletion of residues
XX from this wild type sequence. The CasR isoforms have hypotensive and
XX osteopathic activity. The isoforms can be used to identify agonists and
XX antagonists that modulate the receptor activity and calcium levels. These
XX modulators are useful for treating hyperparathyroidism or osteoporosis.
XX Paget's disease, hypercalcaemia malignancy or hypertension. The DNA
XX sequence is also useful for altering the CasR activity and in gene
XX therapy
XX
SQ Sequence 1078 AA;
Query Match 74.8%; Score 4044.5; DB 3; Length 1078;
Best Local Similarity 74.0%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

QY 1 MAQLHCQLLFLGFTLLQSVNVSQGNQRAQKKGDIILGGLFPIHFQVAAKDDLSRPE 60

DB 1 MAFVSCCWWLLALT---WHTSAYQDQRAQKKGDIILGGLFPIHFQVAAKDDLSRPE 56
QY 61 ATKIRVNFSGRWLQAMIFAEIENNSMTFLENITLGYRIFTCNTVSKALEATISFVA 120
DB 57 SVECIRNFGFRWLQAMIFAEIENNSPALLENITLGYRIFTCNTVSKALEATISFVA 116
QY 121 QNKIDSNLNDFCNCSHPSTIAVVGATGSG-STAVANLLGLFYIPQVSYASSSLLSN 180
DB 117 QNKIDSNLNDFCNCSHPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSSLLSN 176
QY 181 KNEYKAFRLRIPNDECOATAMABIEHFQWNTVGTAAADDDYGRPGIDFEREEAVRDC 240
DB 177 KNQFKSLRTIPNDEHQATAMADIIYFRWNWVGTTAADDYGRPGIEKPREAEERDC 236
QY 241 IDFSEMISQYTKQLEFIADVIQNSAKIVVVSNGPDLEPLIQIQRNINIDRIWLAS 300
DB 237 IDFSELISQYSDSEEBIOHVVEVIONSTAKIVVVSNGPDLEPLIKVIRENITKGIWLAS 296
QY 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPOGFNFKLKVHPSRSDNGFVKFEWEET 360
DB 297 EAWASSSLIAKPEYFHVVGTTIGFALKAGQIPGREFLKKVHPSRSDNGFVKFEWEET 356
QY 361 NCYFTEKTLTQLNKSNKVPESHGPAAGDQSGKAGNSRRTALRHPCTGEBNITSVETPYLDYT 420
DB 357 NCHLQEGAKGPL---PVDTELRGHEBSGDRFSNS-STAFPLCTGDNISSEVETPIDYT 412
QY 421 HLRISYVYVAVYSIAHALQDIHSCKPGTGIPIANGSCADIKKVEAMQVNLHLHLKPTNS 480
DB 413 HLRISYVYVAVYSIAHALQDITCLPGRGLFTNGSCADIKKVEAMQVNLHLHLKPTNS 472
QY 481 MGEQVDDDDGDLKGNVTIINWOLSAEDSVLFEYGNVYAKPSDRNLNINEKILLWSG 540
DB 473 MGEQVDFECCDGLVGNYSIINWHLSPEDGSIIVFEYGNVYAKPSDRNLNINEKILLWSG 532
QY 541 PSKVVPFNSGSRDCVPCGRKGIIEGPTCCFECMACAEFSDSDENASACTKCPNDFWSN 600
DB 533 PSREVPSNCSRDCLAGTRKGIIEGPTCCFECVCEPDGEYSDETDASACNKPDDFWSN 592
QY 601 ENHTSCIAKIEVLSWTEPFGIALITPAVLGILITFVLGVFKFRTPIVKATNRELSY 660
DB 593 ENHTSCIAKIEVLSWTEPFGIALITPAVLGILITFVLGVFKFRTPIVKATNRELSY 652
QY 661 LLLFSLICCFSSSLIFIGEPDWTCLRQAPAGISFVLCISCLVKNRVLVFEAKIPT 720
DB 653 LLLFSLICCFSSSLIFIGEPDWTCLRQAPAGISFVLCISCLVKNRVLVFEAKIPT 712
QY 721 SLHRKWVGLNLQFLVLCILVQIVTCIIWLYTAPPSSYNHLEDEVIPTCEGSLMA 780
DB 713 SFHRKMWGLNLQFLVLCILVQIVTCIIWLYTAPPSSYNHLEDEVIPTCEGSLMA 772
QY 781 LGFLIGYTCLLAALCEPFAKSKLLENFNEAKFITFSMLIFRIVMTSFTPAYVSTYVKF 840
DB 773 LGFLIGYTCLLAALCEPFAKSKLLENFNEAKFITFSMLIFRIVMTSFTPAYVSTYVKF 832
QY 841 VSAVEVIAIASSFGLGCIYFNKCVIILFKPCRNTIEBEVRCSTAAHAFKVAARATLRRS 900
DB 833 VSAVEVIAIASSFGLGCIYFNKCVIILFKPCRNTIEBEVRCSTAAHAFKVAARATLRRS 892
QY 901 AASRRSSSLCGSTISSPASSSTCGPG-----LTMEM 931
DB 893 NVSRKRSSSLGGSTGTSSTSSSSKSNGBDPPQPERKQKQOPLALTOEQEQOQPLTLFQ 952
QY 932 Q-----RCSTQKVSFGSGVTLSISPEETGRYATLSRTARSNSADGRSGDDLPSRHH 984
DB 953 QOCSQQQPRCK-QKVFSGSVTFSLSDPEPKNAHNRNSTHONSLEAKSSDTLRRH- 1010
QY 985 DQGPQKCEPOPANDARYKAAPTKGTLESPPGSKERP 1021
DB 1011 -----QALLPLQCGEADSLSVQETGLQGVGGDHRP 1042

RESULT 10
ADD48571

ID	ADE62143 standard; protein; 1078 AA.	Db	1	MAFYSCWVLLALT---	WHTSAYGPDQRAQKGDIIILGGLPFIHFGVAAKDDLSRPE	56
XX	AC	Qy	61	ATKCIYNERGFRWLQAMIFABEINNSMTF	PNITLGYRIFDTCNTVSKALEATLSFVA	120
XX	XX	Db	57	SVECIYNERGFRWLQAMIFABEINNSPALL	PNLTGLYRIFDTCNTVSKALEATLSFVA	116
DT	29-JAN-2004 (first entry)					
XX	Human Protein P41180, SEQ ID NO 8072.	Qy	121	QNKIDSLNDEFNCSDHIPSTIATVVGATSG	SGISTAVANLLGLFYIPOVSYASSSLLSN	180
XX	Human; pain; neuronal tissue; gene therapy;	Db	117	QNKIDSLNDEFNCSEHIPSTIATVVGATSG	SVTAVANLLGLFYIPOVSYASSSLLSN	176
KW	spinal segmental nerve injury; chronic constriction injury; CCI;	Qy	181	KNEYKAPLRTIPNDEQATAMABEIIHFWNW	VGTIAADDDYGRPGIDKFRBEEAVRDC	240
KW	spared nerve injury; SNI; Chung.	Db	177	KNOFKSFLRTIPNDEHQATAMADIIIFRNW	VGTIAADDDYGRPGIEFREAEERDC	236
XX	Homo sapiens.	Qy	241	IDFSEMIQYTKOLEFIADVIQNSAKVIVV	FSNGPDLPLIQIBIVRNITDRILAS	300
XX	WO2003016475-A2.	Db	237	IDFSELIQSYDEEIQHVVEVIQNSTAKVIV	VVFSNGPDLPLIKIIVRNITKILAS	296
PD	27-FEB-2003.					
XX	14-AUG-2002; 2002WO-US025765.	Qy	301	EAWASSLIAKPEYFHVVGTTIGFALRAGRI	PGFNKFLKEVHPSRSDNGFVKEFEET	360
XX	14-AUG-2001; 2001US-0312147P.	Db	297	EAWASSLIAKPEYFHVVGTTIGFALRAGRI	PGFRFLKKVHPSRSDNGFVKEFEET	356
PR	01-NOV-2001; 2001US-0346382P.					
PR	26-NOV-2001; 2001US-0333347P.					
XX	(GHEO) GEN HOSPITAL CORP.	Qy	361	NCVTEKTLTQLNKSKVPESHGPAAGDGG	KAGNSRRTALRHPCTGEBNITSVETPYD	420
PA	(FARB) BAYER AG.	Db	357	NCHLQEGAKGPL---	PVDIFLRGHEBSGDRFNS -STAFRPLCT	412
XX	Woolf C, D'urso D, Befort K, Costigan M;	Qy	421	HLRISYVYVAVYSIAHALQDIHSCKPGTGI	FANGSCADIKKVEAQVNLHLHLKFTNS	480
XX	WPI: 2003-268312/26.	Db	413	HLRISYVYVAVYSIAHALQDIHSCKPGTGI	FANGSCADIKKVEAQVNLHLHLKFTNN	472
DR	GENBANK; P41180.					
XX	New composition comprising two or more isolated polypeptides, useful for	Qy	481	MGEQVDFDQDGLKGNVTIINWOLSAEDSV	LKPNVPHYGNVAYAKPSDRNLNKKILMSG	540
PT	preparing a medicament for treating pain in an animal.	Db	473	MGEQVDFDQDGLKGNVTIINWOLSAEDSV	LKPNVPHYGNVAYAKPSDRNLNKKILMSG	532
PT	Claim 1; Page; 1017pp; English.	Qy	541	FSKVPFNSCRDCVPTRKGIIEGBPTCCFEC	MACAEGEFSDENDASACTKCPNDFWSN	600
PS		Db	533	FSREVPFNSCRDCVTRKGIIEGBPTCCFEC	MACAEGEFSDENDASACTKCPNDFWSN	592
XX	The invention discloses a composition comprising two or more isolated rat	Qy	601	ENHTSCIATKIEVLSWTEPGIATITFVNLG	ILITTSVLGVTFKFNTPVKTATNELSY	660
CC	or human polynucleotides or a polynucleotide which represents a fragment,	Db	593	ENHTSCIATKIEVLSWTEPGIATITFVNLG	ILITTSVLGVTFKFNTPVKTATNELSY	652
CC	derivative or allelic variation of the nucleic acid sequence. Also	Qy	661	LLFLPSITCCPSSSIIIFGEPRDWTCLRQ	PAFGISFVLCISILVKNRVLLVFEAKIPT	720
CC	claimed are a vector comprising the novel polynucleotide, a host cell	Db	653	LLFLPSITCCPSSSIIIFGEPRDWTCLRQ	PAFGISFVLCISILVKNRVLLVFEAKIPT	712
CC	comprising the vector, a method for identifying a nucleotide sequence	Qy	721	SLHRKWNGLNQFLVFLCIVLVOITCIWLYT	APSSYRNHLEDEVIFITCDEGSLMA	780
CC	which is differentially regulated in an animal subjected to pain and a	Db	713	SFHRKWNGLNQFLVFLCIVLVOITCIWLYT	APSSYRNHLEDEVIFITCDEGSLMA	772
CC	kit to perform the method, an array, a method for identifying an agent	Qy	781	LGFLIGVTCLLAALCFEFAFKSKLPENFNE	AKFITFMSLIFPIVWISFIPAVSYGKF	840
CC	that increases or decreases the expression of the polynucleotide sequence	Db	773	LGFLIGVTCLLAALCFEFAFKSKLPENFNE	AKFITFMSLIFPIVWISFIPAVSYGKF	832
CC	that is differentially expressed in neuronal tissue of a first animal	Qy	841	VSAVEVIAILASSFGLLGCITYPNKCVIIL	FKPCRNITIEVRCSTAAHAFKVAARATLRS	900
CC	subjected to pain, a method for identifying a compound which regulates	Db	833	VSAVEVIAILASSFGLLGCITYPNKCVIIL	FKPCRNITIEVRCSTAAHAFKVAARATLRS	892
CC	the expression of a polynucleotide sequence which is differentially	Qy	901	AASRKRSSSLCGSTISSPASSTCGPG---	-----LTJMEM	931
CC	expressed in an animal subjected to pain, a method for identifying a	Db	893	NVRKKSSSLGSGTGTSPSSISKNSNEDP	FPQPERKQOQPLATQEQOQQOPLTPQ	952
CC	compound that regulates the activity of one or more of the	Qy	932	Q-----RCSTOKVFGSGTIVTSLSFET	GYATLSRTARSNADGRSGDPLSRHH	984
CC	polynucleotides, a method for producing a pharmaceutical composition, a	Db	953	QORSQQQPRCK-QKVIFGSGTIVTSLSF	EDBPQKNAMAHNRNTHQNSLEAKSSDTL	1010
CC	method for identifying a compound or small molecule that regulates the	Qy	985	DQGPPOKCEFPQANDARYKAAPTKGTLES	PGGSKERP	1021
CC	activity in an animal of one or more of the polypeptides given in the	Db	1011	-----QPLLPLOCGTDLTLTVQET	GLQGPVGDDQRP	1042
CC	specification, a method for identifying a compound useful in treating					
CC	pain and a pharmaceutical composition comprising the one or more					
CC	polypeptides or their antibodies. The polynucleotide or the compound that					
CC	modulates its activity is useful for preparing a medicament for treating					
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction					
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene					
CC	therapy). The sequence presented is a human protein (shown in Table 2 of					
CC	the specification) which is differentially expressed during pain. Note:					
CC	The sequence data for this patent did not form part of the printed					
CC	specification, but was obtained in electronic form directly from WIPO at					
CC	ftp.wipo.int/pub/published_pct_sequences.					
XX	Sequence 1078 AA;					
SQ						

Query Match 74.8%; Score 4044.5; DB 7; Length 1078;
Best Local Similarity 74.0%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

Qy 1 MAQLHCQLLFLGFTLLQSNVSGYGNQRAQKGDIIILGGLPFIHFGVAAKDDLSRPE 60

RESULT 12
ADE62147

ID ADH10955 standard; protein; 1078 AA.
 XX ADH10955;
 AC 11-MAR-2004 (first entry)
 DT Human parathyroid calcium receptor (HupCar) protein.
 XX polyvalent cation sensing receptor; pVCR; Atlantic salmon;
 DE growth increase; mortality reduction; human;
 KW parathyroid calcium receptor; HupCar.
 XX Homo sapiens.
 OS WO2003087331-A2.
 XX 23-OCT-2003.
 PD 09-APR-2003; 2003WO-US011188.
 PF 11-APR-2002; 2002US-00121441.
 PR 18-APR-2002; 2002US-00125772.
 PR 18-APR-2002; 2002US-00125778.
 PR 18-APR-2002; 2002US-00125792.
 XX (MARI-) MARICAL INC.
 PA Harris HW, Nearing J, Betka M;
 PI WPI; 2003-845319/78.
 DR New Atlantic salmon polyvalent cation-sensing receptor, pVCR,
 XX polypeptides useful in commercial raising of salmon and restoration of
 PT wild Atlantic salmon populations especially in transfer from freshwater
 PT to seawater.
 XX Disclosure; SEQ ID NO 30; 269pp; English.
 PS The invention comprises the amino acid and coding sequences of polyvalent
 CC cation sensing receptor (pVCR) proteins from Atlantic salmon. The DNA and
 CC protein sequences of the invention are useful in the commercial raising
 CC of Atlantic salmon and the restoration of wild Atlantic salmon
 CC populations, especially in the transfer from freshwater to seawater with
 CC increased growth and reduced mortality. The present amino acid sequence
 CC represents the human parathyroid calcium receptor (HupCar) protein.
 XX Sequence 1078 AA;
 SQ
 Query Match 74.8%; Score 4044.5; DB 7; Length 1078;
 Best Local Similarity 74.0%; Pred. No. 0;
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;
 QY 1 MAQLHCQLLFLGFTLLQSYNVSYGPNQRAQKKGDIILGGLFPIHFGVAAXDQDLKSRPE 60
 Db 1 MAFYSCWLLALT---WHTSAYGPDQRAQKKGDIILGGLFPIHFGVAAXDQDLKSRPE 56
 QY 61 ATKCYRNPGRFRWLOAMIFAEENNSMTFLPNTLGYRIFDTCNTVSKALEATLSFVA 120
 Db 57 SVCEYRNPGRFRWLOAMIFAEENNSMTFLPNTLGYRIFDTCNTVSKALEATLSFVA 116
 QY 121 QNKIDSLNLDLFCNCSHPISTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 180
 Db 117 QNKIDSLNLDLFCNCSHPISTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSN 176
 QY 181 KNEYKAFRTTINDSQQATAMAEIIEHFOWNVWGTAAADDDYGRGIDKIFREEAVKRDIC 240
 Db 177 KNQKSFRTTINDSQQATAMAEIIEHFOWNVWGTAAADDDYGRGIDKIFREEAVKRDIC 236
 QY 241 IDFSEMSIQYVTKOLEFTADYVIONSSAKVIIVFSGNPDLEPLIEIVERNITDRIMLAS 300
 Db 237 IDFSEMSIQYVTKOLEFTADYVIONSSAKVIIVFSGNPDLEPLIEIVERNITDRIMLAS 296
 QY 301 EAWASSSLTAKPEYFHVVGTTIGFALRAGRIFGNKFLKEVHPSRSSDNGFVKFEWETTF 360

Db 297 EAWASSSLTAMPQYFHVVGTTIGFALRAGQIPGFREFLKKVHPKSVHNGFAKEFEWETTF 356
 QY 361 NCYFTEKTLTQKNSKVPSPHGAQDQSGKAGNSRRTALRHPCTGBENITSVETPLDYT 420
 Db 357 NCHLQEGAGKPL---PVDTFLRGHEESGDRFNS-STAPRLCTGDNISSETPIYDT 412
 QY 421 HLRISYNYVAVYSIAHALQDIHSCKPXTGTFANGSCADIKKVEAWQVJNLHLKLTNS 480
 Db 413 HLRISYNYVAVYSIAHALQDIYTCPLGRGLFNGSCADIKKVEAWQVJNLHLNLTNN 472
 QY 481 MGEQVDFDQDGLKGNYYIINWLSAEDSVLFHEVGNVYAKPSDRNLNINEKILKSG 540
 Db 473 MGEQVTFDECDGLVGNYSIINWLSPEDGSIIVFKEVGYNYVYAKGERLFINBEKILKSG 532
 QY 541 FSKVVPFNSCRDVPCTKGIIEGPTCCFECMACAEGEPDENDASACTKCPNDPWSN 600
 Db 533 FSEVFPFNSCRDCLAGTRKGIIEGPTCCFECVECPDGEYDETDASACNCPDPSN 592
 QY 601 ENHTSCIAKEIEYLSWTFPGIATITFAVLGILITSTFVLGVFIKFRNTPIVATNRELSY 660
 Db 593 ENHTSCIAKEIEFLSWTFPGIATITFAVLGILITSTFVLGVFIKFRNTPIVATNRELSY 652
 QY 661 LLLFSLICCFSSSLIFIGPRDWTCLROPAGISFVLICILVKTNRVLLVFEAKIPT 720
 Db 653 LLLFSLICCFSSSLIFIGPRDWTCLROPAGISFVLICILVKTNRVLLVFEAKIPT 712
 QY 721 SLHRKWVGLNLQFLVFLCLIVTCIILWLYTAPSSYRNHELEDEVIITCDEGSLMA 780
 Db 713 SFHRKWVGLNLQFLVFLCLIVTCIILWLYTAPSSYRNHELEDEVIITCDEGSLMA 772
 QY 781 LGFLIGYTCLLAAICFFFAFKSKLPENNEAKFITFSMLIPIVWISIPAVSVYKXF 840
 Db 773 LGFLIGYTCLLAAICFFFAFKSKLPENNEAKFITFSMLIPIVWISIPAVSVYKXF 832
 QY 841 VSAVEVITAILASSFGLLGCIYFNKCVIILFKPCRNITIEVRCSTAAHAFKVAARATLRS 900
 Db 833 VSAVEVITAILASSFGLLGCIYFNKCVIILFKPCRNITIEVRCSTAAHAFKVAARATLRS 892
 QY 901 AASRKSSSLCGSTIISPSASTCGPG-----LTMEM 931
 Db 893 NVSRKSSSLCGSTIISPSASTCGPG-----LTMEM 922
 QY 932 Q-----RCSTOKVSFGSTVTLSTFEEETGYATLSRTARSNSADGRSGDDPLSRHH 984
 Db 953 QRSQQPCK-QRVFGSTVTLSTFEEETGYATLSRTARSNSADGRSGDDPLSRHH 1010
 QY 985 DQPPKCEPQANDARYKAAPTKGTLESFGGSKERP 1021
 Db 1011 -----QPLLPQCGETDLDLTVQETGLQGVGDQRP 1042
 RESULT 14
 ADJ68365
 ID ADJ68365 standard; protein; 1078 AA.
 XX ADJ68365;
 AC 06-MAY-2004 (first entry)
 XX Human heat mitochondrial protein as a therapeutic target SeqID171.
 DT Mitochondrial; human; screening assay; diabetes mellitus;
 DE Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 OS Homo sapiens.
 XX WO2003087768-A2.

XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM,
XX PI Warnock DE;
XX DR WPI; 2003-845369/78.
XX PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX PS Claim 1; SEQ ID NO 171; 180pp; English.
XX CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC cephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological, and
CC cytoskeletal activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX SQ Sequence 1078 AA;
Query Match 74.8%; Score 4044.5; DB 7; Length 1078;
Best Local Similarity 74.0%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;
1 MAQLHCQLLFLGFTLLQSNVSGYGNQRAQKGGDILGGLFPIHFGVAAKDQDLKSRPE 60
1 MAFYSCCWVLLALT---WHTSAYGPDQRAQKGGDILGGLFPIHFGVAAKDQDLKSRPE 56
61 ATKCRYNFRGRFWLQAMFAIEEINNSMTFLPNTLGYRIFDTCNTYSKALEATLSFVA 120
57 SVECRYNFRGRFWLQAMFAIEEINNSPALPNTLGYRIFDTCNTYSKALEATLSFVA 116
121 QNKIDSLNDFPCNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSSRLLSN 180
117 QNKIDSLNDFPCNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSSRLLSN 176
181 KNEYAFRTINDQCATAMAEIIEHPQWNVGTALADDYGRPIDKFEAEVAKRDIC 240
177 KNQKSFRTIENDEHQATAMAEIIEYFRWNVGTALADDYGRPIDKFEAEVAKRDIC 236
241 IDFSMSISQYTKOLEFTADYQNSAKVIVFRSGDPLRLPQLQEIYVRNITDRIMLAS 300
237 IDFSMSISQYDEEIQHVVEVQNSTAKVIVFRSGDPLRLPQLQEIYVRNITDRIMLAS 296
301 EAWASSLSIAKPEYFHVVGTTGFPALRAGRIPGKNFLKEVHPGRSSDNGFKFWEETP 360
297 EAWASSLSIAKPEYFHVVGTTGFPALRAGRIPGKNFLKEVHPGRSSDNGFKFWEETP 356
361 NCYFTTEKTLTKNSKVPSHGPAAGDQSKAGNSRTRALRPHCTGEENITSVETPYLDYT 420
357 NCHLQEGAKGPL---PVDTFLRGHEESGDRFNS--STAFLPLCTGDENISSVETPYLDYT 412

QY 421 HLRISNVYVAVYSIAHALODIHSCKPGTGI FANGSCADIKKVEAQVNLHLHLKFTNS 480
DB 413 HLRISNVYVAVYSIAHALODIYITCLPGRGLFNGSCADIKKVEAQVNLHLHLNFTNN 472
QY 481 MGEQVDFDDQDLKGNYYTIINWQLSAEDSVLPHFVEGNTYNAKAPSDRLNINEKKILWSG 540
DB 473 MGEQVTFDECGDLVGNYSIINWHLSPEDGSI VFEKGVYNNVYAKGERLFINBEKILWSG 532
QY 541 FSKVVPFNSCRDVCPTGRKGIIEGPTCCFECMACAEGEFSDENDASACTPCPNDFSN 600
DB 533 FSEVPFNSCRDCLAGTRKGIIEGPTCCFECVCEPDGEYSDETASACNCKPCPDFSN 592
QY 601 ENHTSCIATKIEIYLSWTEPFGIALTIFAVLIGLITITFVLGVFIKFRNTPIVKATNRELSY 660
DB 593 ENHTSCIATKIEIYLSWTEPFGIALTIFAVLIGLITITFVLGVFIKFRNTPIVKATNRELSY 652
QY 661 LLLFSLICCFSSSLIFIGEPDWTCKLRQAPAFISFVLICISILVKNRVLVFEAKIPT 720
DB 653 LLLFSLICCFSSSLIFIGEPDWTCKLRQAPAFISFVLICISILVKNRVLVFEAKIPT 712
QY 721 SLHRKVVGLNLQFLVFLCIVLVOITCIWLYTAPPSSYRNHELEDEVIFITCDEGLMA 780
DB 713 SFRKRWGLNLQFLVFLCIVLVOITCIWLYTAPPSSYRNHELEDEVIFITCDEGLMA 772
QY 781 LGFLIGYTCLLAAICFFFAFKSKRLPENFNEAKFITFSMLIFIVWISFIPAVSYGKF 840
DB 773 LGFLIGYTCLLAAICFFFAFKSKRLPENFNEAKFITFSMLIFIVWISFIPAVSYGKF 832
QY 841 VSAVEVITAILASSFGLGCIYENKCVIILFKPCNTIEEVRCTAAHAFKVAARATLRS 900
DB 833 VSAVEVITAILASSFGLGCIYENKCVIILFKPCNTIEEVRCTAAHAFKVAARATLRS 892
QY 901 AASRKSSSLCGSTISSPASSTCGP-----LITMEM 931
DB 893 NVSEKSSSLGGSTGTSTPSSISSKNSDPPQPERQKQOPLALTQEQQQOPLTLPO 952
QY 932 Q-----RCSTOKVSGFGTIVLSFETGRYATLSTARSNSADGRSGDDLPFSRH 984
DB 953 QRSQQQPRCK-QKVFISGTVTFSLSFDEPQKVAHNSHTQNSLEAKQSDTLTRH- 1010
QY 985 DQGPPOKCEPOPANDARYKAAPTKGTLESPPGSGKRP 1021
DB 1011 -----QPLLPQCGETDLDLTWQETGLQGVGDQRP 1042
RESULT 15
ADI41014
ID ADI41014 standard; protein; 1078 AA.
XX AC ADI41014;
XX DT 22-APR-2004 (first entry)
XX DE Human GPCR CASR #2.
XX KW Receptor; GPCR; G protein-coupled receptor; reproductive disorder;
XX KW testicular disorder; vas deferens disorder; spermatogenesis; infertility;
XX KW XX male; epididymitis; cryptorchidism; sperm transport disorder;
XX KW testicular cancer; testicular germ cell tumour; male hormone disorder;
XX KW premature puberty; Kallman syndrome; Cushing's syndrome; immune disorder;
XX KW leukaemia; arthritis; asthma; AIDS; rheumatoid arthritis;
XX KW inflammatory bowel disease; sepsis; T-cell mediated cytotoxicity;
XX KW graft-versus-host disease; autoimmunity disorder;
XX KW systemic lupus erythematosus; drug induced haemolytic anaemia;
XX KW Sjogren's disease; T-cell maturation disorder;
XX KW B-cell maturation disorder; vascular disorder; stroke; ischaemia;
XX KW myocardial infarction; atherosclerosis; gastrointestinal disorder; ulcer;
XX KW pulmonary disorder; brain disorder; endocrine disorder; cancer;
XX KW gene therapy.
XX OS Homo sapiens.
XX XX

PN	US2004018976-A1.	Best Local Similarity 74.0%; Pred. No. 0;			
XX		Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;			
PD	29-JAN-2004.				
XX					
XX	13-MAY-2003; 2003US-00436715.				
XX					
PR	14-MAY-2002; 2002US-0380336P.				
XX					
PA	(FEDE/) FEDER J N.				
PA	(MINT/) MINTIER G.				
PA	(RAMA/) RAMANATHAN C S.				
XX					
PI	Feder JN, Mintier G, Ramanathan CS;				
XX					
DR	WPI; 2004-122081/12.				
XX					
PT	New human G-protein coupled receptor polypeptide and polynucleotide,				
PT	useful for diagnosing, preventing, treating or ameliorating a medical				
PT	condition, e.g. reproductive disorder, immunodeficiency disease or				
PT	testicular cancer.				
XX					
PS	Disclosure; SEQ ID NO 74; 290pp; English.				
XX					
CC	The invention relates to an isolated human G protein-coupled receptor				
CC	polypeptide and its encoding polynucleotide, including the full length				
CC	proteins minus the start methionine (and the region of the polynucleotide				
CC	encoding this protein region). The proteins are designated HGPBMX30-1,				
CC	HGPBMX30-2, HGPBMX30-3, HGPBMX41-1, HGPBMX41-2, HGPBMX41-3, and				
CC	HGPBMX42, HGPBMX42-1, HGPBMX43 and HGPBMX44. Also included are				
CC	expression vectors, host cells, antibodies, preventing (treating or				
CC	ameliorating) a medical condition comprising administering to a mammalian				
CC	subject the polypeptide or its modulator and diagnosing a pathological				
CC	condition or a susceptibility to a pathological condition in a subject				
CC	(comprising determining the presence or absence of a mutation in the				
CC	polynucleotide, or the presence or amount of expression of the				
CC	polypeptide in a biological sample and diagnosing a pathological				
CC	condition or a susceptibility to a pathological condition based on the				
CC	presence or absence of the mutation, or the presence or amount of				
CC	expression of the polypeptide). The human G-protein coupled receptor				
CC	polypeptide or polynucleotide can be used for diagnosing a pathological				
CC	condition or a susceptibility to a pathological condition in a subject,				
CC	and for preventing, treating or ameliorating a medical condition, such as				
CC	a disorder related to aberrant G-protein coupled receptor activity, a				
CC	disorder related to aberrant signal transduction, a reproductive disorder				
CC	; a male reproductive disorder, a testicular disorder, a vas deferens				
CC	disorder, spermatogenesis, infertility, Klinefelter's syndrome, XX male,				
CC	epididymitis, genital warts, germinal cell aplasia, cryptorchidism,				
CC	varicocele, immotile cilia syndrome, viral orchitis, sperm transport				
CC	disorders, testicular cancer, choriocarcinoma, non-seminoma, seminoma,				
CC	testicular germ cell tumors, male hormone disorders, premature puberty,				
CC	incomplete puberty, Kallman syndrome, Cushing's syndrome, an immune				
CC	disorder, a proliferative immune disorder, leukaemia, arthritis, asthma,				
CC	immunodeficiency diseases such as AIDS, rheumatoid arthritis,				
CC	granulomatous disease, inflammatory bowel disease, sepsis, acne,				
CC	neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell				
CC	mediated cytotoxicity, immune reactions to transplanted organs and				
CC	tissues, such as host-versus-graft and graft-versus-host diseases, or				
CC	autoimmunity disorders, such as autoimmune infertility, demyelination,				
CC	systemic lupus erythematosus, drug induced haemolytic anaemia, Sjogren's				
CC	disease, scleroderma, T-cell maturation disorders, B-cell maturation				
CC	disorders, vascular disorders, stroke, ischaemia, myocardial infarction,				
CC	atherosclerosis, embolisms, thrombosis, gastrointestinal disorders,				
CC	irritable bowel syndrome, ulcers, pulmonary disorders, brain disorders,				
CC	endocrine disorders, or ovarian, stomach, colon or kidney cancer or its				
CC	related proliferative condition (many other diseases and disorders are				
CC	listed in the specification). The antibodies may be used to purify,				
CC	detect and target the G-protein coupled receptor polypeptides. The				
CC	polynucleotides are also useful in gene therapy. The present sequence				
CC	represents a species homologue of a novel GPCR of the invention.				
XX					
SQ	Sequence 1078 AA;				

Query Match 74.6%; Score 4044.5; DB 8; Length 1078;

Thu Nov 18 06:53:34 2004

us-10-016-496-2.rag

Page 16

Db 1011 -----QPLLPLOGETDLDLTQETGLQGPVGGDQRP 1042

Search completed: November 17, 2004, 11:50:12
Job time : 308 secs

Db 301 EAWASSLLAKPEYFHVVGTTIGFALRAGRIIPGFKFLKEVHPSSRSDNGFVKFEWEETF 360
QY 361 NCYFTEKTLTQKNSKVPBGHGAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
Db 361 NCYFTEKTLTQKNSKVPBGHGAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
QY 421 HLRISNVVAVYSIAHALQDIHSCKPGTGIIFANGSCADIKKVEAWQVNLHLKFTNS 480
Db 421 HLRISNVVAVYSIAHALQDIHSCKPGTGIIFANGSCADIKKVEAWQVNLHLKFTNS 480
QY 481 MGEQVDFDQDGLKGNYYTIIINQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILWSG 540
Db 481 MGEQVDFDQDGLKGNYYTIIINQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILWSG 540
QY 541 FSKVWPFNSCRDCVPGTRKGIIIEGPTCCFECMACAGEFSDENDASACTKCPNDFWSN 600
Db 541 FSKVWPFNSCRDCVPGTRKGIIIEGPTCCFECMACAGEFSDENDASACTKCPNDFWSN 600
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVPFKRNTPIVKATNRELSY 660
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVPFKRNTPIVKATNRELSY 660
QY 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQPAFGISFVLICISILVKTNRVLLVFEAKIPT 720
Db 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQPAFGISFVLICISILVKTNRVLLVFEAKIPT 720
QY 721 SLHRKWVGNLQFLVFLCILVQIVTCIIWLVTAPPSSYRNHELEDEVIFITCDEGSLMA 780
Db 721 SLHRKWVGNLQFLVFLCILVQIVTCIIWLVTAPPSSYRNHELEDEVIFITCDEGSLMA 780
QY 781 LGFLIGYTCLLAACIFFFAFKSRKLPENFEAKFTTFSMLIPFIWISFIPAYVSTYKGF 840
Db 781 LGFLIGYTCLLAACIFFFAFKSRKLPENFEAKFTTFSMLIPFIWISFIPAYVSTYKGF 840
QY 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
Db 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
QY 901 AASRKSSSLCGSTISSPASSTCGPLTMEMORCSTQKVSFGSGVTUJLSFEETGRYAT 960
Db 901 AASRKSSSLCGSTISSPASSTCGPLTMEMORCSTQKVSFGSGVTUJLSFEETGRYAT 960
QY 961 LGRTARSNSADGRSGDDLPSRHHQGPQKCEPOPANDARYKAAPTCKGTLESFGGSKER 1020
Db 961 LGRTARSNSADGRSGDDLPSRHHQGPQKCEPOPANDARYKAAPTCKGTLESFGGSKER 1020
QY 1021 PTTMEET 1027
Db 1021 PTTMEET 1027

RESULT 2

US-10-268-051-8
; Sequence 8, Application US/10268051
; Patent No. 6748900
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jury, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A
; APPLICANT: Betka, Marlies
; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213.2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8

LENGTH: 1027

TYPE: PRT

ORGANISM: Squalus acanthias

US-10-268-051-8

Query Match 100.0%; Score 5410; DB 4; Length 1027;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHCOLLFLGFTLLQSNVSGVGNQRAOKGDIILGGLFPIHFGVAAKQDLKSRPE 60
Db 1 MAQLHCOLLFLGFTLLQSNVSGVGNQRAOKGDIILGGLFPIHFGVAAKQDLKSRPE 60
QY 61 ATKIRYNFRGFWLQAMIFABEINNMTFLPNITLGYRIFDTCTNTVSKALEATLSFVA 120
Db 61 ATKIRYNFRGFWLQAMIFABEINNMTFLPNITLGYRIFDTCTNTVSKALEATLSFVA 120
QY 121 ONKIDSLNLDERCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSLLSN 180
Db 121 ONKIDSLNLDERCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSLLSN 180
QY 181 KNEYKAFRLTIPNDEQOATAMAEIIEHFQWNWVGTLLAADDYGRPGIDKFREEAVKRDIC 240
Db 181 KNEYKAFRLTIPNDEQOATAMAEIIEHFQWNWVGTLLAADDYGRPGIDKFREEAVKRDIC 240
QY 241 IDESEMIQYITOKOLEFTADVIONSSAKVIVVFSNGPDLEPLIQEIVERNITDRIWLAS 300
Db 241 IDESEMIQYITOKOLEFTADVIONSSAKVIVVFSNGPDLEPLIQEIVERNITDRIWLAS 300
QY 301 EAWASSLLAKPEYFHVVGTTIGFALRAGRIIPGFKFLKEVHPSSRSDNGFVKFEWEETF 360
Db 301 EAWASSLLAKPEYFHVVGTTIGFALRAGRIIPGFKFLKEVHPSSRSDNGFVKFEWEETF 360
QY 361 NCYFTEKTLTQKNSKVPBGHGAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
Db 361 NCYFTEKTLTQKNSKVPBGHGAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
QY 421 HLRISNVVAVYSIAHALQDIHSCKPGTGIIFANGSCADIKKVEAWQVNLHLKFTNS 480
Db 421 HLRISNVVAVYSIAHALQDIHSCKPGTGIIFANGSCADIKKVEAWQVNLHLKFTNS 480
QY 481 MGEQVDFDQDGLKGNYYTIIINQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILWSG 540
Db 481 MGEQVDFDQDGLKGNYYTIIINQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILWSG 540
QY 541 FSKVWPFNSCRDCVPGTRKGIIIEGPTCCFECMACAGEFSDENDASACTKCPNDFWSN 600
Db 541 FSKVWPFNSCRDCVPGTRKGIIIEGPTCCFECMACAGEFSDENDASACTKCPNDFWSN 600
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVPFKRNTPIVKATNRELSY 660
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVPFKRNTPIVKATNRELSY 660
QY 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQPAFGISFVLICISILVKTNRVLLVFEAKIPT 720
Db 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQPAFGISFVLICISILVKTNRVLLVFEAKIPT 720
QY 721 SLHRKWVGNLQFLVFLCILVQIVTCIIWLVTAPPSSYRNHELEDEVIFITCDEGSLMA 780
Db 721 SLHRKWVGNLQFLVFLCILVQIVTCIIWLVTAPPSSYRNHELEDEVIFITCDEGSLMA 780
QY 781 LGFLIGYTCLLAACIFFFAFKSRKLPENFEAKFTTFSMLIPFIWISFIPAYVSTYKGF 840
Db 781 LGFLIGYTCLLAACIFFFAFKSRKLPENFEAKFTTFSMLIPFIWISFIPAYVSTYKGF 840
QY 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
Db 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
QY 901 AASRKSSSLCGSTISSPASSTCGPLTMEMORCSTQKVSFGSGVTUJLSFEETGRYAT 960
Db 901 AASRKSSSLCGSTISSPASSTCGPLTMEMORCSTQKVSFGSGVTUJLSFEETGRYAT 960

```

QY 961 LSRARSNSADGRSGDDLPSRHHDDQPPKCEPQANDARYKAAPTGTLESPPGSKER 1020
DB 961 LSRARSNSADGRSGDDLPSRHHDDQPPKCEPQANDARYKAAPTGTLESPPGSKER 1020
QY 1021 PTTMEET 1027
DB 1021 PTTMEET 1027

RESULT 3
US-09-134-513-2
; Sequence 2, Application US/09134513
; Patent No. 6210964
; GENERAL INFORMATION:
; APPLICANT: Brown, Edward M.
; APPLICANT: Diaz, Ruben
; APPLICANT: Bai, Mei
; APPLICANT: Quinn, Stephen J.
; TITLE OF INVENTION: The Avian Extracellular Calcium-Sensing
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Vinson & Elkins L.L.P.
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004-1008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,513
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: BR1331/13003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-134-513-2

Query Match 75.9%; Score 4106.5; DB 3; Length 1059;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 788; Conservative 85; Mismatches 130; Indels 29; Gaps 5;

QY 1 MAQLHCOLLFLGFTLLQLSNVSGYGNQRAQKGGDIIILGGLFPIHFGVAADQDLKSPE 60
DB 1 MLYSCCLILLFT-----WNTRYGNQRAQKGGDIIILGGLFPIHFGVAADQDLKSPE 56
QY 61 ATKIRYNPRGRFWLQAMTFAIEEINNSMTFLPNITLGYRIPDTCNTVSKALEATLSFA 120
DB 57 SVECIYNPRGRFWLQAMTFAIEEINNSMTFLPNITLGYRIPDTCNTVSKALEATLSFA 116
QY 121 QNKIDSLNDEFNCSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180
DB 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 176
QY 181 KNEYKAFRLTIENDEQATAMAEIIIEHFQWNVVGTLLAADDDYGRFGIDKFREEAVKRDIC 240
DB 177 KNOFKSFLRTIENDEHQAAMADIIIEYFQWNVVGTLLAADDDYGRFGIDKFREEABERDIC 236

```

```

QY 241 IDSEMIQYTKQLEFIADYIQTSSAKVIVVFSNGDPLEPLIOEIVRNTITDRILWAS 300
DB 237 IDSEMIQSDEBEEIQQVVEVIQNSTARVIVVSSGDPLEPLIKEIVRNTITGKIWLAS 296
QY 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIIFGFKFLKEVHPSRSDNGFVKPEWETF 360
DB 297 EAWASSSLIAMPEFFRVIGSTIGFALKAGQIPGFRFLOKVHPKPGANNFAKEPWEETF 356
QY 361 NCYFTEKTLTQLNKSKVPBGHPAAQDGGKAGNSRRTALRHPTGENTITSVETPYLDYT 420
DB 357 NCYLPSES-----KNSPASASFHKAHEGLGAGNG-TAAFRPPCTGENTITSVETPYMDFT 411
QY 421 HLRISYNYVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAMQVNLHLHLFTNS 480
DB 412 HLRISYNYVAVYSIAHALQDIYTCYTGKGLFNGSCADIKKVEAMQVNLHLHLFTNS 471
QY 481 MGEQVDPDQDGLKGNYYIINWOLSAEDBSVUFHEVGNYNAYAKPDRNINEKILLWSG 540
DB 472 MGEQVDPDEFGLVGNYSIINWHLSPEDGVSVPVEVGHYNVYAKGERLFINENKILLWSG 531
QY 541 FSKVVPSCNSRDCVPTGKGIIEGPTCCFECMACAEGEBSFSDENASACTKCPDNFSN 600
DB 532 FSKEVPSCNSRDLCPGTRKGIIEGPTCCFECVDCPDGEYSDETDAACDKCPEYWSN 591
QY 601 ENHTSCIAKEIYLSWTEPFGIALTIFAVLIGILITSFVLGVFIKFRNTPIVKATNRELSY 660
DB 592 ENHTSCIPKQIEFLSWTEPFGIALTIFAVLIGIFLTSFVLGVFTKFRNTPIVKATNRELSY 651
QY 661 LLLFSLICPSSSLIFIGEPDWTCLRQPAFGISFVLCSILYKTNRVLLVFEAKIPT 720
DB 652 LLLFSLICPSSSLIFIGEPQNTCLRQPAFGISFVLCSILYKTNRVLLVFEAKIPT 711
QY 721 SLHRKVMGLNLQFLVFLCIVLVOITWLYTAPSSYRNHELEDEVIPTCDEGSLMA 780
DB 712 SLHRKVMGLNLQFLVFLCIVLVOITWLYTAPSSYRNHELEDEVIPTCDEGSLMA 771
QY 781 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKFITFSMLIFIVWISPIPAVSYTGKF 840
DB 772 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKFITFSMLIFIVWISPIPAVSYTGKF 831
QY 841 VSAVEVTAIILASSFGLLGCYENKCVIILPKCRNTIEEVRCTAAHAFKVAARATLRS 900
DB 832 VSAVEVTAIILASSFGLLGCYENKCVIILPKCRNTIEEVRCTAAHAFKVAARATLRS 891
QY 901 AASRKSSSLCGSTISSPASTCGPG-----LTMEMQRCSTQKVSFGSGTGT 947
DB 892 NVSRKRSNLSGGSTGTFSSSISSKNHEDPPFLPASAEQRQQRQCKQKVSFGSGTGT 951
QY 948 LSLSPETGRYATLSRTARSNSADGRSGDDLPSRHHDDQPPKCEPQANDARYKAAPT 1007
DB 952 LSLSPETGRYATLSRTARSNSADGRSGDDLPSRHHDDQPPKCEPQANDARYKAAPT 1004
QY 1008 KGTLESPPGSGKE 1019
DB 1005 FQTASSPETSSQ 1016

RESULT 4
US-08-485-588-7
; Sequence 7, Application US/08485588
; Patent No. 5688938
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center

```

STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
FILING APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 74.6%; Score 4037.5; DB 1; Length 1078;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

QY 1 MAQLHCGLFLGFTLLQSNVSGYGNORAKKGIILGGLFPFHFGVAAKQDLKSRPE 60
DB 1 MAFYSCCVLLALT-----WHTSAYGPDQAKKGIILGGLFPFHFGVAAKQDLKSRPE 56
QY 61 ATKCIYRNGRGRWLQAMIFAEIEINNSMTFLPNTILGYRIFDTCNTVSKALEATLSFVA 120
DB 57 SVECIYRNGRGRWLQAMIFAEIEINNSPALLPNTILGYRIFDTCNTVSKALEATLSFVA 116
QY 121 QNKIDSLNDFECNSDHPSTIAVVGATGSGISTAVANLLGLFIPQVSVASSRLLSN 180
DB 117 QNKIDSLNDFECNSDHPSTIAVVGATGSGISTAVANLLGLFIPQVSVASSRLLSN 176
QY 181 KNEYKAFRTIPNDEQQAAMAEIIEHFQWNVWGTAAADDDYGRPGIDKFFREAEVXRDC 240
DB 177 KNQFKSFLRTIPNDEHQATAMADIEYFRWNVWGTIAADDDYGRPGIEKFFREAEERDIC 236
QY 241 IDPSEWISQYVTKQLEPTADVIQNSSAKVIVVFNFGPDLEPLQEIIVRNITDRIWLAS 300

DB 237 IDFSELISQYSDDEEIQHVVEVQNSTAKVIVVFNFGPDLEPLQEIIVRNITDRIWLAS 296
QY 301 EAWASSSLIAKPEYFHVVGTTIGFALNAGRIPOGKFKLKEVHPSRSDNGFVKEFEETFF 360
DB 297 EAWASSSLIAKPEYFHVVGTTIGFALNAGRIPOGKFKLKEVHPSRSDNGFVKEFEETFF 356
QY 361 NCYFTEKTLTQLKNSKVPSPGAPAAQDGGKAGNSRRATLRHPCTGBENTISVETPVDLT 420
DB 357 NCHLOGKAGPL---PVDTLRGHESGDRFNS-STARFPLCTGDNSSVETPVDLT 412
QY 421 HLRISYVYVAVYSIAHALODIHSCKPGTGI FANGSCADIKKVEAWQVNLHLHLKFTNS 480
DB 413 HLRISYVYVAVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAWQVNLHLHLFTNN 472
QY 481 MGEQVDFDDGDLKGNVTIINWOLSAEDBSVLPHVEGYNVAYAKPSDRNLNINEKILWSG 540
DB 473 MGEQVTFDECDLVGNYSIINWHLSPEDGSI VFKVGYVNVYAKGERLFINEKILWSG 532
QY 541 FSKVVPFNSCRDVCVPTGRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPDNFWSN 600
DB 533 FSREVPFNSCRDCLAGTRKGIIEGPTCCFECVCEPDGEYSDETDASACNKPDPFWSN 592
QY 601 ENHTSCIATKEIEYLSWTEPFGIALTTFVILGILITSVLGVFKFKPNTPIVKTATNRELSY 660
DB 593 ENHTSCIATKEIEFLSWTEPFGIALTTFVILGILITSVLGVFKFKPNTPIVKTATNRELSY 652
QY 661 LLLFSLTCCFSSSLIFIGPRDWTCLROPAPFGISFVLCISILVKTNRVLLVFEAKIPT 720
DB 653 LLLFSLTCCFSSSLIFIGPRDWTCLROPAPFGISFVLCISILVKTNRVLLVFEAKIPT 712
QY 721 SLHRKVVGLNLQFLVFLCILVQIVTCIWLITAPSSYANHELEDEVI FICDEGSLMA 780
DB 713 SFHRKVVGLNLQFLVFLCFTMQIVICVILWITAPSSYANHELEDEVI FICDEGSLMA 772
QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFVIWISFIPAYVSTYGF 840
DB 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFVIWISFIPAYVSTYGF 832
QY 841 VSAVEVIALASSFGLLGCYFNKCVIILFKPCORNTIEVRCSTAAHAFKVAARATLRS 900
DB 833 VSAVEVIALASSFGLLGCYFNKCVIILFKPCORNTIEVRCSTAAHAFKVAARATLRS 892
QY 901 AASRKSSSLCGSTISSPASSICGPG-----LTWEM 931
DB 893 NVSRKSSSLGGSTGTPSSSSSKNSNEDPPFQPERQKQQPLALTQEQQQQLPLPQ 952
QY 932 Q-----RCSTOKVSFGSTVTLSSFEETGRYATLSRTARSNSADGRSGDDLP SRHH 984
DB 953 QORSQQOPRCK-QKVI FSGT VTFSLSFDBPKQNAHGNSTHONSLEAKQSDDLTRH- 1010
QY 985 DQSPPKCEPQAPANDARYKAAPTKGTLESPPGSKERP 1021
DB 1011 -----QPLLPLOQGTDLTLVQETGLQGPVGQDQRP 1042

RESULT 5
US-08-484-565-7
; Sequence 7, Application US/08/484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James B. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles

STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-565-7

Query Match 74.6%; Score 4037.5; DB 1; Length 1078;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

QY 1 MAOLHCOLLFLGFTLLQSNVSGYGNQRAQKKGDIILGGLFPIHFGVAADQDLKSRPE 60
DB 1 MAFYSCCWVLLALT---WHTSAYGPDQAQKKGDIILGGLFPIHFGVAADQDLKSRPE 56
QY 61 ATKCYRNGRGRWLQAMFAIEEINNSMTFLPNITLGYRIPDTCNTVSKALEATLSFVA 120
DB 57 SVECYRNGRGRWLQAMFAIEEINNSMTFLPNITLGYRIPDTCNTVSKALEATLSFVA 116
QY 121 QNKISLNLDECNCSDHPTSTIAVVGATSGISTAVANLGLFVYPOVSASSRLLSN 180
DB 117 QNKISLNLDECNCSHPTSTIAVVGATSGISTAVANLGLFVYPOVSASSRLLSN 176
QY 181 KNEYKAFRLTIENDEQATAMAEIIEHFQWNVGTLAADDYGRFGIDKFREEAVKRDIC 240
DB 177 KNQKSFRLTIENDEQATAMAEIIEHFQWNVGTLAADDYGRFGIEKFREEAEERDIC 236
QY 241 IDFSEMSIYYTKQLEFADVIQNSAKVIIVFNGPDLEPLIOEIVRRNITDRIWLAS 300
DB 237 IDFSELSIYSDEEIOHVVEIQNSTAKVIIVFSSGPDLEPLIKEIVRRNITGKIWLAS 296

QY 301 EAWASSLLIAKPEYFHVVGTTIGFALRAGRI PGFNKFLKEVHPSRSSDNGFVKFEWEETF 360
DB 297 EAWASSLLIAKPEYFHVVGTTIGFALRAGRI PGFRFLKAVHPRKSVHNGFAKFEWEETF 356
QY 361 NCYFTEKTLTQKNKVPSHGPAAGDQSGKAGNSRRALTARHPCTGBENITSVETPYDYT 420
DB 357 NCHLQEGAKGPL---PVDTFLRGHEESGDRFNS-STAFLPLCTGDENISSVETPYDYT 412
QY 421 HLRISYNNVAVYSIAHALQDIHSCKPGTGI FANGSCADI KKVAAQVNLHLLHLKFTNS 480
DB 413 HLRISYNNVAVYSIAHALQDIYTCUPGRGLFTNGSCADI KKVAAQVNLHLLHLNFTNN 472
QY 481 MGEQVDFDQGDLLKGNYYTIINWOLSAEDSVLFHEVGYNNAYAKPSDRININEKILWSG 540
DB 473 MGEQVDFDECGDLVGNYSIINWHLSPEDGSI VFEKVGYYNVYAKKGERLFINEEKILWSG 532
QY 541 FSKVPFNSCSDRCVPGTRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWN 600
DB 533 FSREVPFNSCSDRCLAGTRKGIIEGPTCCFECVCEPDGEYDETDASACNCPDDFWN 592
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGLITISFVLGVPIKFRNTPIVKATNRELSY 660
DB 593 ENHTSCIAKEIEFLSWTEPFGIALTIFAVLGLITIFAVLGVPIKFRNTPIVKATNRELSY 652
QY 661 LLLFSLICPSSSLIFIGPRDWTCLROPAGISVLCISCLLVKTNRVLLVFEAKIPT 720
DB 653 LLLFSLICCFSSSLFFIGEPQDWTCLROPAGISVLCISCLLVKTNRVLLVFEAKIPT 712
QY 721 SLHRKMWGLNLQFLVFLCIILOVITCIITWLYTAPSSYRNHELEDEVIFITCEGSLMA 780
DB 713 SFHRKMWGLNLQFLVFLCIILOVITCIITWLYTAPSSYRNHELEDEVIFITCEGSLMA 772
QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFMSLIFPIVWISFIPAYVSTYKGF 840
DB 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFMSLIFPIVWISFIPAYVSTYKGF 832
QY 841 VSAVEVIAILASSFGLLGCITYFNKCVIILPKPCNTEIEVRCSTAAHAFKVAARATLRS 900
DB 833 VSAVEVIAILASSFGLLGCITYFNKCVIILPKPCNTEIEVRCSTAAHAFKVAARATLRS 892
QY 901 AASRKSSSLCGSTISSPASSTCGPG-----LTMEM 931
DB 893 NVSRKSSSLGGSTGTFPSSSISSKNSNEDFPQPERQKQOQPLALTQOQOQPLTPQ 952
QY 932 Q-----RCSTOKVSFGSGTWTLSFBEHTGYATLSRTARNSADGRSGDLSRHH 984
DB 953 QORSQOQPRCK-QKVI FSGTWTLSFBEHTGYATLSRTARNSADGRSGDLSRHH- 1010
QY 985 DQPPKCEPQANDARYKAAPT KGTLESFGGSKERP 1021
DB 1011 -----QPLLPLQCGEITDLDTVQETGLQGPVGGQRP 1042

RESULT 6
US-08-480-751-7
Sequence 7, Application US/08480751
Patent No. 585684
GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California


```

; SOFTWARE: FastSeq for Windows Version 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,719B
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Douglas C. Murock
; REGISTRATION NUMBER: 37,549
; REFERENCE/DOCKET NUMBER: 213/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-719B-7

```

```

Query Match 74.6%; Score 4037.5; DB 3; Length 1078;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

```

```

QY 1 MAQLHCQLLFLGFTLLQSVNGVGNQRAQKGDIIILGGLPPIHFGVAAKDQDKSRPE 60
DB 1 MAFYSCCWVLLALT---WHTSAYGPDQRAQKGDIIILGGLPPIHFGVAAKDQDKSRPE 56
QY 61 ATKCIYRNGRFRWLQAMIFATEEINNSMTPLPNTTLGVRIFDTCNTVSKALEATLSVA 120
DB 57 SVECIYRNGRFRWLQAMIFATEEINNSFPALLPNTTLGVRIFDTCNTVSKALEATLSVA 116
QY 121 QNKIDSLNLDLFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180
DB 117 QNKIDSLNLDLFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSVASSRLLSN 176
QY 181 KNEYKAFRTIENDSQQTAMAEIIEHQQWVWGLAADDYGRPIDKPEEAVKRDIC 240
DB 177 QNKQSFRTIENDSQQTAMAEIIEHQQWVWGLAADDYGRPIDKPEEAEERDIC 236
QY 241 IDFSEMSIQYTKOLEFIADYQNSAKVIIVFSGNPDLEPLIOEIVRRNITDRILAS 300
DB 237 IDFSELSIQSDEEIQHVVEIQNSTAKVIIVFSSGPDLEPLIKEIVRRNITGKIWLAS 296
QY 301 EAWASSLIAPYEHVHVGGTIGFALRAGRIPGKFKLKEVHPSSSSNGFVKFWETTF 360
DB 297 EAWASSLIAMPQYHVHVGGTIGFALKAGQIPGFRFLKKVHPKSVHNGFAKEFWETTF 356
QY 361 NCYFTEKTLTOLKNSKVPESHGPAAGDGSKAGNSRRRTALRHPCTGEENITGVETPYLDYT 420
DB 357 NCHLQEGAKGPL---PVDTFLRGHEESGDRSNS-STAFRLCTGDENISSVEIPYIDYT 412

```

```

RESULT 10
US-08-484-159-7
; Sequence 7, Application US/08484159
; Patent No. 6313146
; GENERAL INFORMATION:
; APPLICANT: Bradford C. Van Wagenen
; APPLICANT: Manuel F. Balandrin
; APPLICANT: Eric G. Del Mar
; APPLICANT: Edward F. Nemeth
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,159

```

```

421 HLRIYNNVYVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWQVNLHLHLKFTNS 480
413 HLRIYNNVYVAVYSIAHALQDIYVCLPGRGLFTNGSCADIKKVEAWQVNLHLHLKFTNN 472
481 MGEQVDFDDQDGLKGNHTIINWOLSAEDSVLPFHEVGNVYAKPSDRNLNINEKILMSG 540
473 MGEQVDFDECDLVGNYSIINWHLSPEDGSIIVFKEVGNVYAKGERLFINNEKILMSG 532
541 FSKVVPFNSCNRDCVPTGRKGIIEGEPTECCFECMACAEGEFSDENDASACTKCPDNDFWN 600
533 FSREVFPNSCNRDCLAGTRKGIIEGEPTECCFECVECPDGEYSDETDASACNKPDPFWSN 592
601 ENHTSCIAKEIEYLSWTEPPGIALTIIPAVLIGLITSVLGVFIFKFRNTPIVKATNEELSY 660
593 ENHTSCIAKEIEYLSWTEPPGIALTIIPAVLIGLITSVLGVFIFKFRNTPIVKATNEELSY 652
661 LLLFSLICCPSSSLIFIGBRDWTCLROPAGISFVLICISILVKTNRVLLVFEAKIPT 720
653 LLLFSLICCPSSSLIFIGBRDWTCLROPAGISFVLICISILVKTNRVLLVFEAKIPT 712
721 SLHRKWGLNLQFLVFLCIVITCIILYTPAPSSYRNHELEDEVIFITCDEGLMA 780
713 SPHRKWGLNLQFLVFLCIVITCIILYTPAPSSYRNHELEDEVIFITCDEGLMA 772
781 LGSLIGYVTCLLAAICFFFAKSKLPENNEAKFITFMSLIPFIVATISFIPAVSYGKF 840
773 LGSLIGYVTCLLAAICFFFAKSKLPENNEAKFITFMSLIPFIVATISFIPAVSYGKF 832
841 VSAVEVIAILASSFGLIGCIYFNKCIILFKPCNTEIEEVRCSAAHAFKVAARATLRRS 900
833 VSAVEVIAILASSFGLIGCIYFNKCIILFKPCNTEIEEVRCSAAHAFKVAARATLRRS 892
901 AASRKSSSLCGSTISSPASSTCGPG-----LTMEM 931
893 NVSRKSSSLGSGTSTPSSSISSKNSNEDPPQPERKQKQPLATQEQOQPLTLPO 952
932 Q-----RCSTQKVSFGSTVLSLSFETGYATLSRTARSRNSADGRSGDDLPSSRH 984
953 QORSQQPRCK-QKVFSGSTVLSLSFETGYATLSRTARSRNSADGRSGDDLPSSRH 984
985 DQGPQKCEPQANDARYKAAPTKGTLESFGSGSKERP 1021
1011 -----QPLLPQCGETDLDLTVOETGLQGPVGGDQRP 1042

```

DB	413	HLRISYNTVAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEANQVLKHLRLHFTNN	472
QY	481	MGEQVDFDDQDGLKGNYYTIINWQLSADESVLPHEVGNYNAYAKPSDRLNINKKILWSG	540
DB	473	MGEQVTFDECDGLVGNYSIIINWHLSPEDGIVFKEVGYNNVYAKKGERLFINKEKILWSG	532
QY	541	FSKVVPRFNSCRDVCVPGTRKGIIEGERTCCFECMACAEGRFSDENASACTCPNDFWSN	600
DB	533	FSREVPFNSCRDCLAGTRKGIIEGERTCCFECVCEPDGYSYDETDASACNKCPCDFWSN	592
QY	601	ENHTSCIAKEIEYLSWTEPPFGIALTIIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY	660
DB	593	ENHTSCIAKEIEFLSWTEPPFGIALTLFAVLGIFLTAFLVGVFIKFRNTPIVKATNRELSY	652
QY	661	LLFLSLICPSSSLIFIGEPDWTCLRQAPAGISFVLCISLIVKTNRVLLVFEAKIPT	720
DB	653	LLFLSLICPSSSLIFIGEPDWTCLRQAPAGISFVLCISLIVKTNRVLLVFEAKIPT	712
QY	721	SLHRKWGVLNQFLVFLICILVQIVTCIIMLYTAPSSYRNHELEDEVIITCDEGLMA	780
DB	713	SPHRKWGVLNQFLVFLICILVQIVTCIIMLYTAPSSYRNHELEDEVIITCDEGLMA	772
QY	781	LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKITFSMLIFIVWISFIPAYVSTYKGF	840
DB	773	LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKITFSMLIFIVWISFIPAYVSTYKGF	832
QY	841	VSAREVIAILASSPGLLCGYFKNKYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS	900
DB	833	VSAREVIAILASSPGLLCGYFKNKYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS	892
QY	901	AASRRKSSSLCGSTISSPASSTCGPG-----ITMEM	931
DB	893	NVSRKRSSSLCGSTGTPSSSISSKNSDEPFPQPERKQKQPLALTQBPQQQPLTFQ	952
QY	932	Q-----RCSTOKVSVSGGVTLVLSFETGRVATLRTARSRNSADGRSGDPLSRHH	984
DB	953	QORSOQQPRCK-QKVFSGGVTFSLFDEPQKNMAHGNSTHNSLEAQKSSDTLTH-	1010
QY	985	DQGPQKCEPQFANDARYKAAPTGTLESPPGSKERP	1021
DB	1011	-----QLEPLQCCGETDLTLVQBTGLQPGVGGDORP	1042
RESULT 11			
US-08-485-588-6			
; Sequence 6, Application US/08485588			
; Patent No. 5688938			
; GENERAL INFORMATION:			
; APPLICANT: Edward M. Brown			
; APPLICANT: Steven C. Hebert			
; APPLICANT: Forrest H. Fuller			
; APPLICANT: James E. Garrett, Jr.			
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE			
; TITLE OF INVENTION: MOLECULES			
; NUMBER OF SEQUENCES: 20			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Lyon & Lyon			
; STREET: First Interstate World Center			
; STREET: Suite 4700			
; CITY: Los Angeles			
; STATE: California			
; COUNTRY: USA			
; ZIP: 90071			
; COMPUTER READABLE FORM:			
; Sequence 6, Application US/08485588			
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: FASTSEQ			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/485,588			
; FILING DATE: 7 June, 1995			
; CLASSIFICATION: 435			

```

; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon C.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1088 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-588-6

Query Match 74.5%; Score 4029.5; DB 1; Length 1088;
Best Local Similarity 73.3%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

QY 1 MAQLHCQLFLGFTLQSYNGYGPORAKKGGDIILGGLPHHFGVAAKQDQLKSRPE 60
DB 1 MAFYSCCVLLALT----WHTSAYGQDQRAKKGGDIILGGLPHHFGVAAKQDQLKSRPE 56
QY 61 ATKIRYNFRGRFWLQAMFAIEENNSMTPLNITLGYRIFDTCNTVSKALEATLSFVA 120
DB 57 SVEICRYNFRGRFWLQAMFAIEENNSFPALLPNITLGYRIFDTCNTVSKALEATLSFVA 116
QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYPOVSASSRLLSN 180
DB 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYPOVSASSRLLSN 176
QY 181 KNEYKAFRTIENDEQQTAMAEIIEHFQWNVWGLAADDYGRPGIDKPREBAVKRDIC 240
DB 177 KNQKFSFLRTIENDEHQATAMADIIIEYFNWNVGIIAADDYGRPGIEKFRBEEAERDIC 236
QY 241 IDSEMSISQYTKOLEFIADYIONSAAKVIIVFNSGPDLEPLIOEIVRRNITPRIMLAS 300
DB 237 IDFSELISQYSDDEEIQHVVEIQNSTAKVIIVFSSGPDLEPLIKEIVRRNITGKIWLAS 296
QY 301 EAWASSLIAKPEYHVVGTTGFPALRAGRIKPKFKLKVHPSSSDNGFVKPEWETTF 360
DB 297 EAWASSSLIAMPQYHVVGTTGFPALKAGQIPGREFLKVKHPKSVHNGFAKFEWETTF 356
QY 361 NCYFTEKTLTQLKNGKVPSPHGAQDGSKAGNSRRTALRHPCTGEEINITSVETPYLDYT 420
DB 357 NCHLQEGAGKPL---PVDTFLEHRESGDRFNS--STAFRLCTGDNISVETPYIDYT 412
QY 421 HLRIYNVAVYSIAHAHQDTHSCPKPGTIFANGSCADIKKVEAWQVNLHLHLKFTNS 480
DB 413 HLRIYNVAVYSIAHAHQDIYITCLPGRGLFTNGSCADIKKVEAWQVNLHLHLNFTN 472

```

```

; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon C.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1088 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-588-6

RESULT 12
US-08-484-565-6
; Sequence 6, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James R. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9

```

```

QY 481 MGEQVDFDDGDLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRLINEKILWSG 540
DB 473 MGEQVTFDECGDLVGNYSIINWHLSPEDGSIYFKEVGYNNYAKGERLFINEKILWSG 532
QY 541 FSK-----VVPFNSCSRDVPGTRKGIIEBETCCCFECMACAEGEFSDENDASAC 590
DB 533 FSREPLTFVLSVLQVPFNSCSRDCLAGTRKGIIEBETCCCFECVCEPCDGEYDETDASAC 592
QY 591 TKCPNDFNSNENHTSCIAKEIEYLSWTEPFGALTIFAVLGLITSFVLGVFIKPRNTPI 650
DB 593 NKCPDDFWSNENHTSCIAKEIEBLSWTEPFGALTIFAVLGLITFAVJGVFIKFRNTPI 652
QY 651 VKATNEELSYLLFLSLICCFSSSLPIFGPRDWTCLRQPAFGISFVLCISILVKTNRV 710
DB 653 VKATNEELSYLLFLSLICCFSSSLPIFGPDWTCLRQPAFGISFVLCISILVKTNRV 712
QY 711 LNVFEAKIPTSLSHRKQWGLNQLPFLVLCILVQIVTCIILWLTAPPSSYRNHELEDEVIF 770
DB 713 LNVFEAKIPTSPHRKQWGLNQLPFLVLCITFMQIVICVILWLTAPPSSYRNQOELEDEIF 772
QY 771 ITCDEGLMALGFLICYTCLLAAICFFFAFKGRKLPENEFNEAKFITFSMLIFFIVWISFI 830
DB 773 ITCHEGLMALGFLICYTCLLAAICFFFAFKGRKLPENEFNEAKFITFSMLIFFIVWISFI 832
QY 831 PAYVSTYGFVSAAVEVIAILASFGLLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 890
DB 833 PAYASTYGFVSAAVEVIAILASFGLLGCIYFNKCYIILFKPSRNTIEEVRCTAAHAFK 892
QY 891 VAARATLRSAASRKSSSLCGSTISSPASSICGPG----- 926
DB 893 VAARATLRSENVSRRKSSSLGSGTSPSSSSISSKNSNSDDPPRPRKQOQPLALTOQE 952
QY 927 -----LTMEMQ-----RCSTQKVSFGSGTTLSTLSFEETGRYATLSRTARSNSADGR 974
DB 953 QCOQPLTLPOORSQOQPRCK-QKVI-FSGTGTVTSLSFDEPKQNAHNRNSTHONSLEAQ 1011
QY 975 SGDDLPSRHHDQGPPOKCEFPQANDARYKAAPTKGTLESPPGSGKERP 1021
DB 1012 KSSDTLTRH-----QPLPLQCGETDLDTVOETGLQGPVGGDQRP 1052

```



```

APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1088 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-565-6

```

```

Query Match 74.5%; Score 4029.5; DB 1; Length 1088;
Best Local Similarity 73.3%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches 136; Indels 61; Gaps 8;

```

```

QY 1 MAQLHCOLLFLGFTLQSVNGYGNORAKKGGIILGGLFPIHFGVAAKQDLKSRPE 60
DB 1 MAFYSCWVLLALT---WHTSAYGDQRAKKGDIILGGLFPIHFGVAAKQDLKSRPE 56
QY 61 ATKCRYNPRGRWLOAMIFAEIENNSMTPLNITLGYRFDTCNTVSKALEATLSFVA 120
DB 57 SVECIYNFRGRWLOAMIFAEIENNSPALLNLTGYRFDTCNTVSKALEATLSFVA 116
QY 121 QNKIDSLNDFCNGSDHIPSTIAVVGATGSGISTAVANLGLFYIPOVSVASSRLLSN 180
DB 117 QNKIDSLNDFCNGSEHPISTIAVVGATGSGVSTAVANLGLFYIPOVSVASSRLLSN 176
QY 181 KNEYKAFRTIENDSQQATMAEIIIEHFQWNVGTLAADDYGRPGIDKPREBAVKRDC 240
DB 177 KNQFKSFLRTIENDSQQATMAEIIIEFQWNVGTLAADDYGRPGIDKPREBAVKRDC 236
QY 241 IDFSEMIQYTKQKLEFIADYQNSAKVIVFNSGPDLEPLIOEIVRRNITRIWLAS 300
DB 237 IDFSELIQYDEEBIQHVEIQNSAKVIVFNSGPDLEPLIOEIVRRNITRIWLAS 296
QY 301 EAWASSLIAPYEHYVVGTTGIFALRAGRIPGKFLKEVHPSSSDNGFVKFWEETP 360
DB 297 EAWASSLIAPYEHYVVGTTGIFALRAGRIPGKFLKEVHPSSSDNGFVKFWEETP 356
QY 361 NCYFTEKTLTQKNSKVPSPHGAAGDGSKAGNSRRRTALRHPCTEENITSVETPYLDY 420
DB 357 NCHLOEAGKGL- --PVDTELRGHEESGDRFNS- STAFRLCTGDNISVETPYIDYT 412
QY 421 HLRISYNTVAVYSTAHALQDIHCKPGTGIKANGSCADIKKVEAWQVNLHLKLTNS 480
DB 413 HLRISYNTVAVYSTAHALQDIHCKPGTGIKANGSCADIKKVEAWQVNLHLKLTNS 472
QY 481 MGEQVDFDQDGLKNGYTIINWLSAEDSVLFHEVGNYNAYAKPSRLNINEKKILWSG 540
DB 473 MGEQVTFDECGLDGVNYSIINWLSAEDSVLFHEVGNYNAYAKPSRLNINEKKILWSG 532

```

```

QY 541 FSK-----VVPFNSCRDVPGRTRKGIIEGPTCCFECMACABEGFSDENDASAC 590
DB 533 FSREPLTFVLSVLQVFNCSRDCLAGTRKGIIEGPTCCFECVBCPDGEYDEIDASAC 592
QY 591 TKCPNDFWNSNHTSCIAKEIEYLSWTEPFGIALTIIPAVLGLITISFVLGVPIKFRNTPI 650
DB 593 NKCPDDFWNSNHTSCIAKEIEYLSWTEPFGIALTIIPAVLGLITISFVLGVPIKFRNTPI 652
QY 651 VKATNRELSYLLLFSLICCFSSSLIFIGPRDWTCLROPAFGISVLCISILVKTNEV 710
DB 653 VKATNRELSYLLLFSLICCFSSSLIFIGPRDWTCLROPAFGISVLCISILVKTNEV 712
QY 711 LLVFEAKIPTSRLHRKMWGLNLQFLVFLCIVLQVITCIILVYTAPESSYRNHELEDEVIF 770
DB 713 LLVFEAKIPTSRLHRKMWGLNLQFLVFLCIVLQVITCIILVYTAPESSYRNHELEDEVIF 772
QY 771 ITCEGSLNALGFLIGYTCILAAICFFFAFKSRKIPENENEAKEFTFSLIFIVWISFI 830
DB 773 ITCEGSLNALGFLIGYTCILAAICFFFAFKSRKIPENENEAKEFTFSLIFIVWISFI 832
QY 831 PAYVSTYGRFVSAVEVIAILASSFGLLGCIFYNKCXYIILFKPCRNTEIEVRCSTAAHAFK 890
DB 833 PAYVSTYGRFVSAVEVIAILASSFGLLGCIFYNKCXYIILFKPCRNTEIEVRCSTAAHAFK 892
QY 891 VAARATLRRSAASRKRSSSLCGSTTSSPASSTCGPG----- 926
DB 893 VAARATLRRSNVSRKRSSSLCGSTTSSPASSTCGPG----- 952
QY 927 -----LTMEMQ-----RCSTQKVSFGSGTIVLSLFEETGRVATLSRTASRNSADCR 974
DB 953 QQQQJTLPLQQQSRQQQPRCK-QKVFSGSTVFSLSFDEPKQNAHNSHTQNSLEAQ 1011
QY 975 SGDDLPSRHHDOGPQKCEPQANDARYKAAPTKGTLESPPGSGKERP 1021
DB 1012 KSSDUTLRH-----QPLLPQCGTDLTLVQETGLQGPVGDDQRP 1052

```

```

RESULT 13
US-08-480-751-6
; Sequence 6, Application US/08480751
; Patent No. 5858684
; GENERAL INFORMATION:
; APPLICANT: Edward F. Nemeth
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,751
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784

```

FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1088 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-751-6

Query Match 74.5%; Score 4029.5; DB 2; Length 1088;
Best Local Similarity 73.3%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

1 MAQLHCQLLFLFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKXQDLKSRPE 60
1 MAFYSCWVLLALT---WHTSAYGPDQRAQKGGDIILGGLFPIHFGVAAKXQDLKSRPE 56
61 ATKTRYNFRGRWLOAMFAIEEINNSMTFLPNTLTGRIPTDNTVSKALEATLSVA 120
57 SVECIYRFRGRWLOAMFAIEEINNSPALLPNTLTGRIPTDNTVSKALEATLSVA 116
121 QNKIDSLNLDPCNCSHPISTAVVATGSGISTAVANLLGLFIPQVSVASSRLLSN 180
117 QNKIDSLNLDPCNCSHPISTAVVATGSGISTAVANLLGLFIPQVSVASSRLLSN 176
181 KNEYKAFLETIPNDEQQAAMAEIIEHFQWVWVGTAAADDDYGRPGIDKFRBAVVRDIC 240
177 KNQKSFRTIPNDEHQATAMADIIEYFRWVWVGTAAADDDYGRPGIEKFRBAEERDIC 236
241 IDESEMSIYYTQKLEFADVTQNSSAKVIVFVSGNPDLEPLIOEIVRBNITDRILAS 300
237 IDFSELSIQSYDEEIEQHVVVEIQNSTAKVIVFVSGNPDLEPLIEIVRBNITDRILAS 296
301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIEFGNFKLKEVHPFSRSDNGFVKEFEETP 360
297 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIEFGNFKLKEVHPFSRSDNGFVKEFEETP 356
361 NCYFTEKTITOLKNKVPBGHPAAGDQSGKAGNSRTALRHCTGEENITSVETPYDLYT 420
357 NCHLQEGAKGPL---PVDITFLRGHEESGDRFNS--STAFRPLCTGDNISSEVETPYDIT 412
421 HURISYVAVYVSIHAHQDIHSCKPGTGIFANGSCADIKKEVAVQVNLHLLHKLFTNS 480
413 HURISYVAVYVSIHAHQDIHSCKPGTGIFANGSCADIKKEVAVQVNLHLLHKLFTNS 472
481 MGEQVDFDQDGLKGNYYTINWQLSAEDSVIFHEVGNVYNAKSDRLNINEKILWSG 540
473 MGEQVDFDQDGLKGNYYTINWQLSAEDSVIFHEVGNVYNAKSDRLNINEKILWSG 532

541 FSK-----VVPFNSCRDVCVPTGRKGIIEGPTCCFECMACAEGBFSDNDASAC 590
533 FSREPLTFVLVULQVFPNSCRDCLAGTRKGIIEGPTCCFECVCEPCDEYSDETDASAC 592
591 TKCPNDFWNSNHTSCIAKEIEFYSWTEPFGIALTIFAVLGLITISFVLGVPIKPNFTPI 650
593 NKCPDDFWNSNHTSCIAKEIEFYSWTEPFGIALTIFAVLGLITISFVLGVPIKPNFTPI 652
651 VKATNRELSVLLLFSLICCFSSSLIFIGEPDWTCLROPAGFISFVLCISILVKTNRV 710
653 VKATNRELSVLLLFSLICCFSSSLIFIGEPDWTCLROPAGFISFVLCISILVKTNRV 712
711 LLVFEAKIPTSLHRKWVGNLQFLVFLCILVQIVTCIILWLTAPSSVYRNEHEDEVIF 770
713 LNVFEAKIPTSLHRKWVGNLQFLVFLCILVQIVTCIILWLTAPSSVYRNEHEDEVIF 772
771 ITCDGSLMALGELIGYTCLLAACFFPAKSKRLPENNEAKFITFSMLIPIVWISL 830
773 ITCDGSLMALGELIGYTCLLAACFFPAKSKRLPENNEAKFITFSMLIPIVWISL 832
831 PAYVSTYGVKFSVAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 890
833 PAYASTYGVKFSVAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 892
891 VAARATLRNSVSRKSSSLGSGTSPSSSISSKNSDPPFRPERKQKQPLALTQOE 952
893 VAARATLRNSVSRKSSSLGSGTSPSSSISSKNSDPPFRPERKQKQPLALTQOE 952
927 -----LTMEMQ-----RCSTOKVSFGSGTSLISFEETGRYATLSRTARSNGADGR 974
953 QQQOPLTLPOQSRQQPRCK-OKVIFGSGTIVFSLFDEPQKNVAHNSHTQNSLEAQ 1011
975 SGDDLFSRHHDOGPQKCEPQANDARYKAAPTKGTLESPPGSGKERP 1021
1012 KSSDTLTRH-----QPLLPLOQGETDLDLTQVQETGLQGFVGGDQRP 1052

RESULT 14
US-08-943-986-6
Sequence 6, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994

FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 209/069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1088 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-784-6

Query Match 74.5%; Score 4029.5; DB 3; Length 1088;
Best Local Similarity 73.3%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

Qy 1 MAQLHCQLLFLGFTLLQSNVSGYGNQRAQKGGIILGLFPFIHFGVAADQDLKSPE 60
Db 1 MAFYSCCWVLLALT---WHTSAYGDQRAQKGGIILGLFPFIHFGVAADQDLKSPE 56

Qy 61 ATKCRYNRGRFRWLQAMIFALEEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA 120
Db 57 SVECRYNRGRFRWLQAMIFALEEINNSPALNLTGLYRIFDTCNTVSKALEATLSFVA 116

Qy 121 QNKISLNLDFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
Db 117 QNKISLNLDFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPOVSYASSRLLSN 176

Qy 181 KNEYKAFRTIENDSQQTAMAEIIEHPQNNVGTAAADDDYGRPIDKFRFEAAVKRDIC 240
Db 177 KNQKSFRTIENDEHQATMAEIIIEYFAWNVGTIIAADDDYGRPIDKFRFEAAVKRDIC 236

Qy 241 IDFSEMSQYTTQKLEFIADYIQNSAKVIYVFSNGPDLEPLIQEIVRNRITDRILWAS 300
Db 237 IDFSELSQYSDEEBIQHVVEIQNSTAKVIYVFSNGPDLEPLIKRIVRNRITGKIWAS 296

Qy 301 EAWASSLIATKPEYFHVVGTTGFALRAGRIIPGNKFLKEVHPSSSDNGFVKFEWETF 360
Db 297 EAWASSLIAMPQYFHVVGTTGFALKAGQIPGFREFLKKVHPKSVHNGFAKEWETF 356

Qy 361 NCVFTEKTLTQKNKVPSPGHGPAAGDGSKAGNSRRTRLRHPCTGEENITSVETPYDYT 420
Db 357 NCHLQEGAKPL--PVDTFLRGHEBSGDRFNS-STAFRPLCTGDNISSVETPYDYT 412

Qy 421 HLRISYNTVAVYSTAHALQDTHSCPGTGIIFANGSCADIKKVEAWQVNLHLHLKFTNS 480
Db 413 HLRISYNTVAVYSTAHALQDIYTCPLGRGLFTNGSCADIKKVEAWQVNLHLHLFTNN 472

Qy 481 MGEQVDFDQDGLKGNVTIINWOLSAEDSVLFHEVGNVNAVAKPDSRLNINEKKILWSG 540
Db 473 MGEQVTFDECGDLVGNYSIINWHLSPEDSGSIYFKEVGYNYVAKGERLFINEEKILWSG 532

Qy 541 FSK-----VVPFNSCRDCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASAC 590
Db 533 FSKREPLTFVLSVLQVFPFNSCRDCLAGTRKGIIEGEPTCCFECVCEPDGEYSDETDASAC 592

Qy 591 TKCPDNDFWSENHTSCIAKIEIYLSWTEPFGIALTFVAVLGILITSFVLGVFIKERNTP 650
Db 591 TKCPDNDFWSENHTSCIAKIEIYLSWTEPFGIALTFVAVLGILITSFVLGVFIKERNTP 650

Search completed: November 17, 2004, 12:00:51
Job time : 131 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 11:57:34 ; Search time 513 Seconds
(without alignments)
708.945 Million cell updates/sec

Title: US-10-016-496-2

Perfect score: 5410
Sequence: 1 MAQLHCOLLFLGLTLLQSYN.....KGTLESFGSGSKERTTWEET 1027

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5410	100.0	1027	14	US-10-125-792-2
2	5410	100.0	1027	14	US-10-125-778-2
3	5410	100.0	1027	14	US-10-268-051-8
4	5410	100.0	1027	14	US-10-125-772-2
5	5410	100.0	1027	14	US-10-016-496-2
6	5410	100.0	1027	14	US-10-410-885-2
7	4055.5	75.0	1078	9	US-09-727-205-2
8	4044.5	74.8	1078	14	US-10-159-339-8
9	4044.5	74.8	1078	15	US-10-436-715-22
10	4044.5	74.8	1078	15	US-10-436-715-74
11	4044.5	74.8	1078	15	US-10-416-588-3
12	4044.5	74.8	1078	16	US-10-408-755A-171
13	4039.5	74.7	1078	13	US-10-002-854-2

14	4037.5	74.6	1078	14	US-10-225-567A-118
15	4029.5	74.5	1088	15	US-10-673-888-1
16	3999.5	73.9	1085	14	US-10-159-339-10
17	3999.5	73.9	1085	15	US-10-041-615-108
18	3999.5	73.9	1085	15	US-10-436-715-21
19	3999.5	73.9	1085	15	US-10-436-715-75
20	3996	73.9	1079	14	US-10-159-339-9
21	3996	73.9	1079	15	US-10-436-715-24
22	3996	73.9	1079	15	US-10-436-715-73
23	3996	73.9	1079	15	US-10-673-888-2
24	3976.5	73.5	1079	15	US-10-436-715-23
25	3976.5	73.5	1079	15	US-10-436-715-72
26	3946.5	72.9	1078	14	US-10-125-792-28
27	3946.5	72.9	1078	14	US-10-125-778-28
28	3946.5	72.9	1078	14	US-10-125-772-28
29	3946.5	72.9	1078	14	US-10-410-885-30
30	3769	69.7	867	14	US-10-179-373-19
31	3769	69.7	867	16	US-10-725-103-19
32	3769	69.7	867	16	US-10-725-489-19
33	3769	69.7	867	16	US-10-725-080A-19
34	3769	69.7	867	17	US-10-725-472A-19
35	3728	68.9	941	14	US-10-125-792-8
36	3728	68.9	941	14	US-10-125-778-8
37	3728	68.9	941	14	US-10-125-772-8
38	3728	68.9	941	14	US-10-410-885-8
39	3728	68.9	941	14	US-10-410-885-14
40	3721	68.8	941	14	US-10-125-792-10
41	3721	68.8	941	14	US-10-125-778-10
42	3721	68.8	941	14	US-10-125-772-10
43	3721	68.8	941	14	US-10-410-885-10
44	3705.5	68.5	940	15	US-10-041-615-107
45	3651	67.5	1002	15	US-10-393-347-3

ALIGNMENTS

RESULT 1

US-10-125-792-2
; Sequence 2, Application US/10125792
; Publication No. US20030051269A1
; GENERAL INFORMATION:
; APPLICANT: MariCal
; APPLICANT: Harris, H. William
; APPLICANT: Betka, Marlies
; APPLICANT: Nearing, Jacqueline A.
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-007
; CURRENT APPLICATION NUMBER: US/10/125,792
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 1027

TYPE: PRT

ORGANISM: Squalus acanthias

US-10-125-792-2

Query Match 100.0%; Score 5410; DB 14; Length 1027;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQLHCOLLFLGLTLLQSYNVSQGNQAKKGDIIILGLFPIHFVAAKDQDKSRPE 60

Db 1 MAQLHCOLLFLGLTLLQSYNVSQGNQAKKGDIIILGLFPIHFVAAKDQDKSRPE 60

```

QY 61 ATCIRYNFRGFWLQAMIFAEIEINNSMTFLPNITLGYRIEDTNTVSKALEATLSFVA 120
Db 61 ATCIRYNFRGFWLQAMIFAEIEINNSMTFLPNITLGYRIEDTNTVSKALEATLSFVA 120
QY 121 QNKIDSLNDFPCNCSHDHPSIAVVGATGSGISTAVANLLGLFPIPOVSYASSRLLSN 180
Db 121 QNKIDSLNDFPCNCSHDHPSIAVVGATGSGISTAVANLLGLFPIPOVSYASSRLLSN 180
QY 181 KNEYKAFRTIPNDEQOATAMAEIIEHFQWNVGTLAADDYGRGIDKFRFEEAVKRDIC 240
Db 181 KNEYKAFRTIPNDEQOATAMAEIIEHFQWNVGTLAADDYGRGIDKFRFEEAVKRDIC 240
QY 241 IDPSEMISQYTKQLEFADVIQNSAKVIVVFNGBDLEPLIOEIVRNITDRILWAS 300
Db 241 IDPSEMISQYTKQLEFADVIQNSAKVIVVFNGBDLEPLIOEIVRNITDRILWAS 300
QY 301 EAWASSLLIAKPEYFHVVGTTIGFALRAGRIIPGNKFLKEVHPSSDNGFVKEFEWETF 360
Db 301 EAWASSLLIAKPEYFHVVGTTIGFALRAGRIIPGNKFLKEVHPSSDNGFVKEFEWETF 360
QY 361 NCYFTEKTLTQLKNSKVPBGHGAQDGSKAGNSRRTALRHPTCTGEENITSVETPYLDYT 420
Db 361 NCYFTEKTLTQLKNSKVPBGHGAQDGSKAGNSRRTALRHPTCTGEENITSVETPYLDYT 420
QY 421 HLRIISYVYVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAVQVNLHLHLKFTNS 480
Db 421 HLRIISYVYVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAVQVNLHLHLKFTNS 480
QY 481 MGEQVDFDQGDILKGNYYIINWQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILWSG 540
Db 481 MGEQVDFDQGDILKGNYYIINWQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILWSG 540
QY 541 FSKVVPFNSCSDCVPGTRKGIIEGPTCCFCMACAEGEFDENDASACTCPNDFWSN 600
Db 541 FSKVVPFNSCSDCVPGTRKGIIEGPTCCFCMACAEGEFDENDASACTCPNDFWSN 600
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGLIITSVFLGVFKRNTPIVKATNRELSY 660
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGLIITSVFLGVFKRNTPIVKATNRELSY 660
QY 661 LLLFSLICCFSSLLIPGPRDWTCLRLQPAFGISFVLCISCLIKVKNRVLVFEAKIPT 720
Db 661 LLLFSLICCFSSLLIPGPRDWTCLRLQPAFGISFVLCISCLIKVKNRVLVFEAKIPT 720
QY 721 SLHRKWGJNLQFLVFLCILVQIVTCIIWLTPAPSSYRNHELEDEVIITCDEGSUMA 780
Db 721 SLHRKWGJNLQFLVFLCILVQIVTCIIWLTPAPSSYRNHELEDEVIITCDEGSUMA 780
QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWIISFIPAYVSTYKGF 840
Db 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWIISFIPAYVSTYKGF 840
QY 841 VSAVEVIAIASSFGLGCIYVNCYIILFKCRNTIEBVCSTAAHAPKVAARATLRS 900
Db 841 VSAVEVIAIASSFGLGCIYVNCYIILFKCRNTIEBVCSTAAHAPKVAARATLRS 900
QY 901 AASRKESLSCGSTITSSPASTCGPGLTWMQRCSTQKVSFGSGTIVTSLSFEEETGRYAT 960
Db 901 AASRKESLSCGSTITSSPASTCGPGLTWMQRCSTQKVSFGSGTIVTSLSFEEETGRYAT 960
QY 961 LSRTARSNSADGRGDDLLPSRHQDQPPQKCEPOPANDARYKAAPTGTLESFGGSKER 1020
Db 961 LSRTARSNSADGRGDDLLPSRHQDQPPQKCEPOPANDARYKAAPTGTLESFGGSKER 1020
QY 1021 PTTMEET 1027
Db 1021 PTTMEET 1027

```

RESULT 2

US-10-125-778-2

Sequence 2, Application US/10125778

```

; Publication No. US20030082574A1
; GENERAL INFORMATION:
; APPLICANT: MariCal
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Becka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-005
; CURRENT APPLICATION NUMBER: US/10/125.778
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121.441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240.392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240.003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Squalus acanthias
US-10-125-778-2

Query Match 100.0%; Score 5410; DB 14; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHCOLLFLGFTLLQSYNVSGYGNQRAQKGDIIILGGLFPIHFGVAAKQDLKSRPE 60
Db 1 MAQLHCOLLFLGFTLLQSYNVSGYGNQRAQKGDIIILGGLFPIHFGVAAKQDLKSRPE 60
QY 61 ATCIRYNFRGFWLQAMIFAEIEINNSMTFLPNITLGYRIEDTNTVSKALEATLSFVA 120
Db 61 ATCIRYNFRGFWLQAMIFAEIEINNSMTFLPNITLGYRIEDTNTVSKALEATLSFVA 120
QY 121 QNKIDSLNDFPCNCSHDHPSIAVVGATGSGISTAVANLLGLFPIPOVSYASSRLLSN 180
Db 121 QNKIDSLNDFPCNCSHDHPSIAVVGATGSGISTAVANLLGLFPIPOVSYASSRLLSN 180
QY 181 KNEYKAFRTIPNDEQOATAMAEIIEHFQWNVGTLAADDYGRGIDKFRFEEAVKRDIC 240
Db 181 KNEYKAFRTIPNDEQOATAMAEIIEHFQWNVGTLAADDYGRGIDKFRFEEAVKRDIC 240
QY 241 IDPSEMISQYTKQLEFADVIQNSAKVIVVFNGBDLEPLIOEIVRNITDRILWAS 300
Db 241 IDPSEMISQYTKQLEFADVIQNSAKVIVVFNGBDLEPLIOEIVRNITDRILWAS 300
QY 301 EAWASSLLIAKPEYFHVVGTTIGFALRAGRIIPGNKFLKEVHPSSDNGFVKEFEWETF 360
Db 301 EAWASSLLIAKPEYFHVVGTTIGFALRAGRIIPGNKFLKEVHPSSDNGFVKEFEWETF 360
QY 361 NCYFTEKTLTQLKNSKVPBGHGAQDGSKAGNSRRTALRHPTCTGEENITSVETPYLDYT 420
Db 361 NCYFTEKTLTQLKNSKVPBGHGAQDGSKAGNSRRTALRHPTCTGEENITSVETPYLDYT 420
QY 421 HLRIISYVYVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAVQVNLHLHLKFTNS 480
Db 421 HLRIISYVYVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAVQVNLHLHLKFTNS 480
QY 481 MGEQVDFDQGDILKGNYYIINWQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILWSG 540
Db 481 MGEQVDFDQGDILKGNYYIINWQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILWSG 540
QY 541 FSKVVPFNSCSDCVPGTRKGIIEGPTCCFCMACAEGEFDENDASACTCPNDFWSN 600
Db 541 FSKVVPFNSCSDCVPGTRKGIIEGPTCCFCMACAEGEFDENDASACTCPNDFWSN 600
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGLIITSVFLGVFKRNTPIVKATNRELSY 660
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGLIITSVFLGVFKRNTPIVKATNRELSY 660

```


661 LLLFSLICCFSSLLIFIGEPDWTCLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720
661 LLLFSLICCFSSLLIFIGEPDWTCLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720
721 SLHRKWGLNLQFLVFLCIIIVQIVTCIIMWTAPSSYRNHELEDEVIPTCDEGSLMA 780
721 SLHRKWGLNLQFLVFLCIIIVQIVTCIIMWTAPSSYRNHELEDEVIPTCDEGSLMA 780
781 LGFLGYTCLLAACICFFPAFKSRKLPENFNEAKETTFPSMLFFIIVWISFIPAYVSTYKGF 840
781 LGFLGYTCLLAACICFFPAFKSRKLPENFNEAKETTFPSMLFFIIVWISFIPAYVSTYKGF 840
841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 900
841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 900
901 AASRRSSLCGSTISSPASSTCGGLTWMORCSTQKVSFGSGVTLSLSPFEETGRYAT 960
901 AASRRSSLCGSTISSPASSTCGGLTWMORCSTQKVSFGSGVTLSLSPFEETGRYAT 960
961 LSRTARSNSADGRSGDDLPSRHHDPGPPQKCEPOPANDARYKAAPTKGTLESFGSKER 1020
961 LSRTARSNSADGRSGDDLPSRHHDPGPPQKCEPOPANDARYKAAPTKGTLESFGSKER 1020
1021 PTTMEET 1027
1021 PTTMEET 1027
RESULT 3
US-10-268-051-8
; Sequence 8, Application US/10268051
; Publication No. US20030124090A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jarry, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M.
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213 2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Squalus acanthias
US-10-268-051-8
Query Match 100.0%; Score 5410; DB 14; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQLHCQLLFLGFTLLQSYNVSYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE 60
DB 1 MAQLHCQLLFLGFTLLQSYNVSYGPNQRAQKKGDIILGGLFPIHFGVAAKDQDLKSRPE 60
QY 61 ATKCRYNPRGRWRLOAMIFAEIENNSMTFLPNITLGYRIEDTCTVSKALEATLSFVA 120
DB 61 ATKCRYNPRGRWRLOAMIFAEIENNSMTFLPNITLGYRIEDTCTVSKALEATLSFVA 120
QY 121 QNKIDSLNDEFNCSDHPIPSIAVVGATSGISITAVANLLGLFIPOVSYASSRLLSN 180
DB 121 QNKIDSLNDEFNCSDHPIPSIAVVGATSGISITAVANLLGLFIPOVSYASSRLLSN 180
QY 181 KNEYKAFURTIIPNDEQQATAMAEIIEHFOWNVWGTTLAADDYGRPGIDKFREEAVRDI 240

DB 181 KNEYKAFURTIIPNDEQQATAMAEIIEHFOWNVWGTTLAADDYGRPGIDKFREEAVRDI 240
QY 241 IDSEMIQYTKQLEFADVIQNSAKVIVVFSNGPDLPLIQLIQRNITDRILWLAS 300
DB 241 IDSEMIQYTKQLEFADVIQNSAKVIVVFSNGPDLPLIQLIQRNITDRILWLAS 300
QY 301 EAWASSLIAKPYFHVVGTTIGFALRAGRIIPGNFKFLKEVHPSSDSNGFVKFEWETF 360
DB 301 EAWASSLIAKPYFHVVGTTIGFALRAGRIIPGNFKFLKEVHPSSDSNGFVKFEWETF 360
QY 361 NCYFTEKTLTKNSKVPESHGPAAGDGGKAGNSRRTALRHPCGTGENITSVETPLDYT 420
DB 361 NCYFTEKTLTKNSKVPESHGPAAGDGGKAGNSRRTALRHPCGTGENITSVETPLDYT 420
QY 421 HLRIYNVYVAVYSIAHALQDIHSCCKPGTCTIFANGSCADIKKVEAQVNLHLLHAKFTNS 480
DB 421 HLRIYNVYVAVYSIAHALQDIHSCCKPGTCTIFANGSCADIKKVEAQVNLHLLHAKFTNS 480
QY 481 MGEQVDFDDGGDLKGNVTIINWQLSAEDSVLPHEVGNVYNAKPSDRNLNINEKKILWSG 540
DB 481 MGEQVDFDDGGDLKGNVTIINWQLSAEDSVLPHEVGNVYNAKPSDRNLNINEKKILWSG 540
QY 541 FSKVVPFNSRDCVCPGTRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWSN 600
DB 541 FSKVVPFNSRDCVCPGTRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWSN 600
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIIFAVLGILITISFVLGVFIKFRNTPIVKATNRELSY 660
DB 601 ENHTSCIAKEIEYLSWTEPFGIALTIIFAVLGILITISFVLGVFIKFRNTPIVKATNRELSY 660
QY 661 LLLFSLICCFSSLLIFIGEPDWTCLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720
DB 661 LLLFSLICCFSSLLIFIGEPDWTCLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720
QY 721 SLHRKWGLNLQFLVFLCIIIVQIVTCIIMWTAPSSYRNHELEDEVIPTCDEGSLMA 780
DB 721 SLHRKWGLNLQFLVFLCIIIVQIVTCIIMWTAPSSYRNHELEDEVIPTCDEGSLMA 780
QY 781 LGFLGYTCLLAACICFFPAFKSRKLPENFNEAKETTFPSMLFFIIVWISFIPAYVSTYKGF 840
DB 781 LGFLGYTCLLAACICFFPAFKSRKLPENFNEAKETTFPSMLFFIIVWISFIPAYVSTYKGF 840
QY 841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 900
DB 841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 900
QY 901 AASRRSSLCGSTISSPASSTCGGLTWMORCSTQKVSFGSGVTLSLSPFEETGRYAT 960
DB 901 AASRRSSLCGSTISSPASSTCGGLTWMORCSTQKVSFGSGVTLSLSPFEETGRYAT 960
QY 961 LSRTARSNSADGRSGDDLPSRHHDPGPPQKCEPOPANDARYKAAPTKGTLESFGSKER 1020
DB 961 LSRTARSNSADGRSGDDLPSRHHDPGPPQKCEPOPANDARYKAAPTKGTLESFGSKER 1020
QY 1021 PTTMEET 1027
DB 1021 PTTMEET 1027
RESULT 4
US-10-125-772-2
; Sequence 2, Application US/10125772
; Publication No. US20030124657A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213 1006-006
; CURRENT APPLICATION NUMBER: US/10/125,772
; CURRENT FILING DATE: 2002-08-16

```

; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Squalus acanthias
US-10-125-772-2

Query Match      100.0%; Score 5410; DB 14; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKDQDLKSRE 60
DB 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKDQDLKSRE 60
QY 61 ATKCIYRNFGRFWLQAMIFAEIEINNSMTFLPNITLGYRIEDTCTNTVSKALEATLSFVA 120
DB 61 ATKCIYRNFGRFWLQAMIFAEIEINNSMTFLPNITLGYRIEDTCTNTVSKALEATLSFVA 120
QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
DB 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
DB 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
QY 181 KNEYKAFPLTIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRPGIDKFEAEVKRDI 240
DB 181 KNEYKAFPLTIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRPGIDKFEAEVKRDI 240
QY 241 IDPSEMIQYVTKQLEFIADVIQNSAKVIVVFNNGPDLEPLIQEIVVRNITDRIWLAS 300
DB 241 IDPSEMIQYVTKQLEFIADVIQNSAKVIVVFNNGPDLEPLIQEIVVRNITDRIWLAS 300
QY 301 EAWASSLLAKPEYFHVVGTTIGFALRAGRIEFGNKFKEVHPSSDNGFVKFEWETP 360
DB 301 EAWASSLLAKPEYFHVVGTTIGFALRAGRIEFGNKFKEVHPSSDNGFVKFEWETP 360
QY 361 NCYFTEKTLTQKNSKVPESHGPAAGDQSGKAGNSRRRTALRHPCTGEENITSVETPYLDY 420
DB 361 NCYFTEKTLTQKNSKVPESHGPAAGDQSGKAGNSRRRTALRHPCTGEENITSVETPYLDY 420
QY 421 HLRISYNNVAVYSTAHALODTHSKPGTGIIFANGSCADIKKVEAMQVNLHLLHKFTNS 480
DB 421 HLRISYNNVAVYSTAHALODTHSKPGTGIIFANGSCADIKKVEAMQVNLHLLHKFTNS 480
QY 481 MGEQVDFDQDGLKGNYYTIINQLSAEDSVLFHEVGNVAVAKPSDRNLNINEKKILMSG 540
DB 481 MGEQVDFDQDGLKGNYYTIINQLSAEDSVLFHEVGNVAVAKPSDRNLNINEKKILMSG 540
QY 541 FSKVPFNSCSDVCPGTRKGIIEBPTCCFPCMACAEFGSDENDASACTKCPNDPWSN 600
DB 541 FSKVPFNSCSDVCPGTRKGIIEBPTCCFPCMACAEFGSDENDASACTKCPNDPWSN 600
QY 601 ENHTSCIAKEIEVLSWTEPFGIALTIFAVLGLITISFVLGVIFKRPNTPIVKATNRELSY 660
DB 601 ENHTSCIAKEIEVLSWTEPFGIALTIFAVLGLITISFVLGVIFKRPNTPIVKATNRELSY 660
QY 661 LLLFSLICFSSSLIFIGEPDWTCLRLQPAFGISFVLCISCIILVKNRVLVFEAKIPT 720
DB 661 LLLFSLICFSSSLIFIGEPDWTCLRLQPAFGISFVLCISCIILVKNRVLVFEAKIPT 720
QY 721 SLHRKRWGNLQFLVFLCILVQIVTCIIWLVTAPSSYRNHELEDEVIETCDGSLMA 780
DB 721 SLHRKRWGNLQFLVFLCILVQIVTCIIWLVTAPSSYRNHELEDEVIETCDGSLMA 780
QY 781 LGFLIGYTCLLAACIFFAFKSKRLPENFNEAKFITFSMLPIFYIWIISFIPAYVSTYGF 840

```

```

DB 781 LGFLIGYTCLLAACIFFAFKSKRLPENFNEAKFITFSMLPIFYIWIISFIPAYVSTYGF 840
QY 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCNTIEEVRCTAAHAFKVAARATLRS 900
DB 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCNTIEEVRCTAAHAFKVAARATLRS 900
QY 901 AAKRKSLSLGGSTISSPASSTCGPLTMMQSCSTQKVSFGSGTIVTSLSEETCRYAT 960
DB 901 AAKRKSLSLGGSTISSPASSTCGPLTMMQSCSTQKVSFGSGTIVTSLSEETCRYAT 960
QY 961 LSRTARSNSADGRSGDGLPSRHHQPPQKCPFPQANDARYKAAPTKGTLESPPGSKER 1020
DB 961 LSRTARSNSADGRSGDGLPSRHHQPPQKCPFPQANDARYKAAPTKGTLESPPGSKER 1020
QY 1021 PTTMEET 1027
DB 1021 PTTMEET 1027

RESULT 5
US-10-016-496-2
; Sequence 2, Application US/10016496
; Publication No. US20030166908A1
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use Thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/10/016,496
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US/09/162,021B
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: squalus acanthias
US-10-016-496-2

Query Match      100.0%; Score 5410; DB 14; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKDQDLKSRE 60
DB 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKDQDLKSRE 60
QY 61 ATKCIYRNFGRFWLQAMIFAEIEINNSMTFLPNITLGYRIEDTCTNTVSKALEATLSFVA 120
DB 61 ATKCIYRNFGRFWLQAMIFAEIEINNSMTFLPNITLGYRIEDTCTNTVSKALEATLSFVA 120
QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
DB 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
QY 181 KNEYKAFPLTIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRPGIDKFEAEVKRDI 240
DB 181 KNEYKAFPLTIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRPGIDKFEAEVKRDI 240
QY 241 IDPSEMIQYVTKQLEFIADVIQNSAKVIVVFNNGPDLEPLIQEIVVRNITDRIWLAS 300
DB 241 IDPSEMIQYVTKQLEFIADVIQNSAKVIVVFNNGPDLEPLIQEIVVRNITDRIWLAS 300
QY 301 EAWASSLLAKPEYFHVVGTTIGFALRAGRIEFGNKFKEVHPSSDNGFVKFEWETP 360

```

301 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIPGNKFLKEVHPSSSDNGFVKPWEETF 360
361 NCYFTEKTLTQKNSKVPESHGPAAGDSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420
361 NCYFTEKTLTQKNSKVPESHGPAAGDSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420
421 HLRIYNNVAVYSIAHALQDIHSCPKPTGIFANGSCADIKKVEAWQVNLHLLKFTNS 480
421 HLRIYNNVAVYSIAHALQDIHSCPKPTGIFANGSCADIKKVEAWQVNLHLLKFTNS 480
481 MGEQVDFDDQGLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILWSG 540
481 MGEQVDFDDQGLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILWSG 540
541 FSKVVPFNSCSDCVPGTRKGIIEGPTCCFECMACAEGFSDENDASACTCPNDFWSN 600
541 FSKVVPFNSCSDCVPGTRKGIIEGPTCCFECMACAEGFSDENDASACTCPNDFWSN 600
601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660
601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660
661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLCISCLVKTNRVLLVFEAKIPT 720
661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLCISCLVKTNRVLLVFEAKIPT 720
721 SLHRKWGLNLQFLVFLCIVQITCIIWLVTAPSSVNRNHELEDEVIFITCDEGSLMA 780
721 SLHRKWGLNLQFLVFLCIVQITCIIWLVTAPSSVNRNHELEDEVIFITCDEGSLMA 780
781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKITFMSLPIFVWISFIPAYVSTYCKF 840
781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKITFMSLPIFVWISFIPAYVSTYCKF 840
841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSAAHAFKVAARATLRRS 900
841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSAAHAFKVAARATLRRS 900
901 AASRKRSSSLCSTISSPASSTCGFLTMEMQRCSTQKVSFGSGVTITLSLFEETGRYAT 960
901 AASRKRSSSLCSTISSPASSTCGFLTMEMQRCSTQKVSFGSGVTITLSLFEETGRYAT 960
961 LSRTARSNSADGRSGDDLPSSHQCGPPQKCEPOPANDARYKAAPTKGTLESFGGSKER 1020
961 LSRTARSNSADGRSGDDLPSSHQCGPPQKCEPOPANDARYKAAPTKGTLESFGGSKER 1020
1021 PTTMEET 1027
1021 PTTMEET 1027

RESULT 6

US-10-410-885-2
; Sequence 2, Application US/10410885
; Publication No. US2003023266A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213,1006-008
; CURRENT APPLICATION NUMBER: US/10/410,885
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 10/125,778
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/125,772
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/125,792
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11

; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Squalus acanthias
; US-10-410-885-2

Query Match 100.0%; Score 5410; DB 14; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQLHCOLLFLGTLTLOSYNVSGYGNQRAQKGDIIILGGLPIHFGVAAKQDOLSRPE 60
Db 1 MAQLHCOLLFLGTLTLOSYNVSGYGNQRAQKGDIIILGGLPIHFGVAAKQDOLSRPE 60
Qy 61 ATKIRYNFSGPRWLOAMIFAIEEINNSMTFLFNITLGYRIFDTCTVSKALEATLSFVA 120
Db 61 ATKIRYNFSGPRWLOAMIFAIEEINNSMTFLFNITLGYRIFDTCTVSKALEATLSFVA 120
Qy 121 QNKIDSNLNDEFNCSDHIPSTIIAVVGATSGGISTAVANLLGLFYIPQVSYASSRLLSN 180
Db 121 QNKIDSNLNDEFNCSDHIPSTIIAVVGATSGGISTAVANLLGLFYIPQVSYASSRLLSN 180
Qy 181 KNEYKAFRLRIPNDEQOATAMAEIIEHFQNNWVGTAAADDYGRPGIDKEREAVKEDIC 240
Db 181 KNEYKAFRLRIPNDEQOATAMAEIIEHFQNNWVGTAAADDYGRPGIDKEREAVKEDIC 240
Qy 241 IDFSEMIQYTTQKLEFIADVIQNSAKVIVVFSNGPDLEPIQIEVRENITDRIWLAS 300
Db 241 IDFSEMIQYTTQKLEFIADVIQNSAKVIVVFSNGPDLEPIQIEVRENITDRIWLAS 300
Qy 301 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIPGNKFLKEVHPSSSDNGFVKPWEETF 360
Db 301 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIPGNKFLKEVHPSSSDNGFVKPWEETF 360
Qy 361 NCYFTEKTLTQKNSKVPESHGPAAGDSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420
Db 361 NCYFTEKTLTQKNSKVPESHGPAAGDSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420
Qy 421 HLRIYNNVAVYSIAHALQDIHSCPKPTGIFANGSCADIKKVEAWQVNLHLLKFTNS 480
Db 421 HLRIYNNVAVYSIAHALQDIHSCPKPTGIFANGSCADIKKVEAWQVNLHLLKFTNS 480
Qy 481 MGEQVDFDDQGLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILWSG 540
Db 481 MGEQVDFDDQGLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILWSG 540
Qy 541 FSKVVPFNSCSDCVPGTRKGIIEGPTCCFECMACAEGFSDENDASACTCPNDFWSN 600
Db 541 FSKVVPFNSCSDCVPGTRKGIIEGPTCCFECMACAEGFSDENDASACTCPNDFWSN 600
Qy 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660
Qy 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLCISCLVKTNRVLLVFEAKIPT 720
Db 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLCISCLVKTNRVLLVFEAKIPT 720
Qy 721 SLHRKWGLNLQFLVFLCIVQITCIIWLVTAPSSVNRNHELEDEVIFITCDEGSLMA 780
Db 721 SLHRKWGLNLQFLVFLCIVQITCIIWLVTAPSSVNRNHELEDEVIFITCDEGSLMA 780
Qy 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKITFMSLPIFVWISFIPAYVSTYCKF 840
Db 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKITFMSLPIFVWISFIPAYVSTYCKF 840
Qy 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSAAHAFKVAARATLRRS 900

Db 841 VSAVEVIALASSPGLGCIYFNKCVIIILFKCRNTIEEVRCSTAAHAFKVAARATLRS 900
 QY 901 AASRKSSSLCGSTISSPASSTCGPGLTWEMORCSTQKVSFGSGVTLSLSFEETGRVAT 960
 Db 901 AASRKSSSLCGSTISSPASSTCGPGLTWEMORCSTQKVSFGSGVTLSLSFEETGRVAT 960
 QY 961 LSTARSNSADRSDDLPSRHHDOGPPOKCEPOPANDARYKAAPTGTLESPOGSKER 1020
 Db 961 LSTARSNSADRSDDLPSRHHDOGPPOKCEPOPANDARYKAAPTGTLESPOGSKER 1020
 QY 1021 PTTMEET 1027
 Db 1021 PTTMEET 1027
 RESULT 7
 US-09-727-205-2
 ; Sequence 2, Application US/0977205
 ; Patent No. US20020064813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ELLIS, CATHERINE E.
 ; TITLE OF INVENTION: MONKEY CALCIUM SENSING RECEPTOR
 ; FILE REFERENCE: GP-70665
 ; CURRENT APPLICATION NUMBER: US/09/727, 205
 ; CURRENT FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/168, 342
 ; PRIOR FILING DATE: 1999-12-01
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1078
 ; TYPE: PRT
 ; ORGANISM: MACACA CYNOMOLGUS
 US-09-727-205-2
 Query Match 75.0%; Score 4055.5; DB 9; Length 1078;
 Best Local Similarity 74.3%; Pred. No. 4.2e-307; Indels 51; Gaps 7;
 Matches 785; Conservative 85; Mismatches 136;

QY 1 MAQLHCQLLFLGTLTQSYNVSQYGNPORAQKGGDIILGGLFPIHFGVAAKDDQLKSRE 60
 Db 1 MAFYCCFWLLALT---WHTSAYGPDQQAQKGGDIILGGLFPIHFGVAAKDDQLKSRE 56
 QY 61 ATKIRYNPRGRFWLQAMFAIEEINNSMTFLPNTLGYRIPTDTCNTVSKALEATLSFA 120
 Db 57 SVECIYRNFGRFWLQAMFAIEEINNSMTFLPNTLGYRIPTDTCNTVSKALEATLSFA 116
 QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLGLFYIPQVSVASSRLLSN 180
 Db 117 QNKIDSLNDEFNCSEHPISTIAVVGATGSGVSTAVANLGLFYIPQVSVASSRLLSN 176
 QY 181 KNEYKAFRTIENDSOQATAMAEIEHFWNNWVGTAAADDDYGRPGIDKPREEAVKRDIC 240
 Db 177 KXQKSFRTIENDSOQATAMAEIEHFWNNWVGTAAADDDYGRPGIDKPREEAEERDIC 236
 QY 241 IDPSEMISOYTKOLEFTADVQNSAKVIVVPSNGPDLEPLQIEIVERNITDRIWLAS 300
 Db 237 IDPSELISQISDEEILQHVIVQNSAKVIVVPSNGPDLEPLQIEIVERNITKILWAS 296
 QY 301 EAWASSSLIAPEYFHVVGTTIGFALRAGRIPGFNKFLEKVEHPSRSSDNGFVKFEWETF 360
 Db 297 EAWASSSLIAPEYFHVVGTTIGFALRAGRIPGFNKFLEKVEHPSRSSDNGFVKFEWETF 356
 QY 361 NCYFTEKTIJOLKNSKVPESHGAAQGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420
 Db 357 NCHLOEGAKGPL---PVDITFLGHEESGGRFNS--STAFRLCTGDENISSVETPYIDYT 412
 QY 421 HLRIISYNYVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAQVNLHLHLKFTNS 480
 Db 413 HLRIISYNYVAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAQVNLHLHLFTNN 472
 QY 481 MGEQVDFDQDGLKGNYYTINWQLSABESVLFEHGVNAYAKPSDRNLNEXKILWSG 540

Db 473 MGEQVDFDQDGLVGNYSIINWHLSPEDGSIIVFKEYGVYNNYAKGERLFINEKILWSG 532
 QY 541 FSKVVPFNSCRVCVGTGRKGIIEGEPTCCFCEMACAEGEFSDENDASACTKCPDWFNS 600
 Db 533 FSEVPFNSCRDCLAGTRKGIIEGEPTCCFCEVCEPDGEYSDETASACNCPDWFNS 592
 QY 601 ENHTSCIATKIEIYLSWTEPPGIALTIIFAVLGILITISFVLGFIKFRNTPIVKATNRELSY 660
 Db 593 ENHTSCIATKIEIYLSWTEPPGIALTIIFAVLGIFLTAFLVGVFIKFRNTPIVKATNRELSY 652
 QY 661 LLLFSLICCFSSSLIFIGEPDWTCLROPAPGISFVLICISILVNTNRVLLVFEAKIPT 720
 Db 653 LLLFSLICCFSSSLIFIGEPDWTCLROPAPGISFVLICISILVNTNRVLLVFEAKIPT 712
 QY 721 SLHRKWGLNLQFLVFLCIILOVITCIWLYTAPPSSYRNHELEDEVIITCDEGLMA 780
 Db 713 SPHRKWGLNLQFLVFLCIILOVITCIWLYTAPPSSYRNHELEDEVIITCDEGLMA 772
 QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFPIVWISFIPAVSYTKP 840
 Db 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFPIVWISFIPAVSYTKP 832
 QY 841 VSAVEVIALASSPGLGCIYFNKCVIIILFKCRNTIEEVRCSTAAHAFKVAARATLRS 900
 Db 833 VSAVEVIALASSPGLGCIYFNKCVIIILFKCRNTIEEVRCSTAAHAFKVAARATLRS 892
 QY 901 AASRKSSSLCGSTISSPASSTCGPG-----DTMEM 931
 Db 893 NVSRKSSSLGSGTGTSTPSSISSKNSSEDPPEPQKQOQPLALTQOQOQPLTLQ 952
 QY 932 Q-----RCSTQKVSFGSGVTLSLSFEETGRVATLSRTASRNSADRSDDLPSRHH 984
 Db 953 QQQSQOQPRCK-QKVIFFSGTIVTSLSFDEPQKNAVAHENSTHNSLEAKQSSDTLARH- 1010
 QY 985 DQGPPOKCEPOPANDARYKAAPTGTLESFGGSKERP 1021
 Db 1011 -----QALLPQCGEADSLSVQETGLQGVGDHRP 1042
 RESULT 8
 US-10-159-339-8
 ; Sequence 8, Application US/10159339
 ; Publication No. US20030166540A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; FILE REFERENCE: D0169NP
 ; CURRENT APPLICATION NUMBER: US/10/159,339
 ; CURRENT FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: US 60/294,411
 ; PRIOR FILING DATE: 2001-05-30
 ; NUMBER OF SEQ ID NOS: 94
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 1078
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-159-339-8
 Query Match 74.8%; Score 4044.5; DB 14; Length 1078;
 Best Local Similarity 74.0%; Pred. No. 3e-306;
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

QY 1 MAQLHCQLLFLGTLTQSYNVSQYGNPORAQKGGDIILGGLFPIHFGVAAKDDQLKSRE 60
 Db 1 MAFYCCFWLLALT---WHTSAYGPDQQAQKGGDIILGGLFPIHFGVAAKDDQLKSRE 56
 QY 61 ATKIRYNPRGRFWLQAMFAIEEINNSMTFLPNTLGYRIPTDTCNTVSKALEATLSFA 120
 Db 57 SVECIYRNFGRFWLQAMFAIEEINNSMTFLPNTLGYRIPTDTCNTVSKALEATLSFA 116

QY 841 VSAVEVIALASSPGLGCIYNNKCYIILFKPCRNTEIEVRCSTRAHAFKVAARATLRS 900
 DB 833 VSAVEVIALASSPGLGCIYNNKCYIILFKPCRNTEIEVRCSTRAHAFKVAARATLRS 892
 QY 901 AASRKSSSLGSGTSSPASS*CGPG-----LTWEM 931
 DB 893 NVSRKRSSSLGSGTSSPASS*CGPG-----LTWEM 931
 QY 932 Q-----RCSTQKVSFGSGVTLSLSPFETGRYATLSRTARSNSADGRSGDLPSSHH 984
 DB 953 QQRSSQOPRCK-QKVFSGSGVTLSLSPFETGRYATLSRTARSNSADGRSGDLPSSHH 984
 QY 985 DOGPPQKCEPQANDARYKAAPTGTLSPPGSGKEP 1021
 DB 1011 -----QPLFLQCGTDLTLTVQETGLQGVGGDQRP 1042

RESULT 10
 US-10-436-715-74
 ; Sequence 74, Application US/10436715
 ; Publication No. US20040018976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
 ; AND SPICE VARIANTS THEREOF
 ; FILE REFERENCE: D0262 NP
 ; CURRENT APPLICATION NUMBER: US/10/436,715
 ; PRIOR FILING DATE: 2003-05-13
 ; PRIOR APPLICATION NUMBER: U.S. 60/380,336
 ; PRIOR FILING DATE: 2002-05-14
 ; NUMBER OF SEQ ID NOS: 471
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 74
 ; LENGTH: 1078
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-436-715-74

Query Match 74.8%; Score 4044.5; DB 15; Length 1078;
 Best Local Similarity 74.0%; Pred. No. 3e-306;
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

QY 1 MAQLHCOLLFLGFTLLQSYNVSGYGNQRAQKGGDIILGGLPPIHFGVAAKQDQLKSRE 60
 DB 1 MAFYSCCWLLALT-----WHTSAYGDPQRAQKGGDIILGGLPPIHFGVAAKQDQLKSRE 56
 QY 61 ATKCIYRNFGRFWLQAMIFATEEINNSMTFLPNTLGVRIFDTCNTVSKALEATLSFVA 120
 DB 57 SVEICIRYRNFGRFWLQAMIFATEEINNSMTFLPNTLGVRIFDTCNTVSKALEATLSFVA 116
 QY 121 QNKIDSLNLDDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180
 DB 117 QNKIDSLNLDDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 176
 QY 181 KNEYKAFRTINDSQOATAMAEIIEHQWVWVGLAADDYGRGIDKPEEAVKRDIC 240
 DB 177 KNOFKSFLRTINDSQOATAMAEIIEHQWVWVGLAADDYGRGIDKPEEAVKRDIC 236
 QY 241 IDPSEMISQYTKOLEFIADYQNSAKVIVVFGNGPDLEPLIQEIVERNITRIWLAS 300
 DB 237 IDPSEMISQYTKOLEFIADYQNSAKVIVVFGNGPDLEPLIQEIVERNITRIWLAS 296
 QY 301 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIPGKFKFKEVHPSRSSDNGFKVFEWETF 360
 DB 297 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIPGKFKFKEVHPSRSSDNGFKVFEWETF 356
 QY 361 NCVFETKTUTQLKNSVPKSHGPAAGDGSKAGNSRRTALRHPCTEENITSVETPYLDYT 420
 DB 357 NCHLQEGAKGPL---PVDTFLEHESGDRFNS--STAFRLCTGDNISSEVETPYLDYT 412
 QY 421 HLRIISYNTVAVYSIAHALQDHSCKPGTGFANGSCADIKKVEAQVNLHLHLKFTNS 480
 DB 413 HLRIISYNTVAVYSIAHALQDHSCKPGTGFANGSCADIKKVEAQVNLHLHLKFTNS 472

QY 481 MGSQVDFDQGDLLKGYNTIINWOLSAEDSVLPHEVGNVYNAKPSDRNLNINEKILWSG 540
 DB 473 MGSQVDFDQGDLLKGYNTIINWOLSAEDSVLPHEVGNVYNAKPSDRNLNINEKILWSG 532
 QY 541 FSKVVPFNSCRDVCVGRKGIIEGPTCCFECMACAECEFSDENDASACTKCPNDFWSN 600
 DB 533 FSEVPFNSCRDVCVGRKGIIEGPTCCFECMACAECEFSDENDASACTKCPNDFWSN 592
 QY 601 ENHTSCIABIEYLSWTEPFGIALTIPAVLIGLITISFVLGVFIKPRNTPIVAKTNRELSY 660
 DB 593 ENHTSCIABIEYLSWTEPFGIALTIPAVLIGLITISFVLGVFIKPRNTPIVAKTNRELSY 652
 QY 661 LLLFSLICCFSSSLIFIGEPDWTCLROPAGISFVLGICILVKTNRVLLVFEAKIPT 720
 DB 653 LLLFSLICCFSSSLIFIGEPDWTCLROPAGISFVLGICILVKTNRVLLVFEAKIPT 712
 QY 721 SLHRKMWGLNLQFLVFLCIVITCIIWLVTAPSSYRNHELEDEVIFITCDEGLMA 780
 DB 713 SPHRKMWGLNLQFLVFLCIVITCIIWLVTAPSSYRNHELEDEVIFITCDEGLMA 772
 QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENENAEKIFITFSLIIFVIWISFIPAVVSTYGF 840
 DB 773 LGFLIGYTCLLAAICFFFAFKSRKLPENENAEKIFITFSLIIFVIWISFIPAVVSTYGF 832
 QY 841 VSAVEVIALASSPGLGCIYNNKCYIILFKPCRNTEIEVRCSTRAHAFKVAARATLRS 900
 DB 833 VSAVEVIALASSPGLGCIYNNKCYIILFKPCRNTEIEVRCSTRAHAFKVAARATLRS 892
 QY 901 AASRKSSSLGSGTSSPASS*CGPG-----LTWEM 931
 DB 893 NVSRKRSSSLGSGTSSPASS*CGPG-----LTWEM 931
 QY 932 Q-----RCSTQKVSFGSGVTLSLSPFETGRYATLSRTARSNSADGRSGDLPSSHH 984
 DB 953 QQRSSQOPRCK-QKVFSGSGVTLSLSPFETGRYATLSRTARSNSADGRSGDLPSSHH 984
 QY 985 DOGPPQKCEPQANDARYKAAPTGTLSPPGSGKEP 1021
 DB 1011 -----QPLFLQCGTDLTLTVQETGLQGVGGDQRP 1042

RESULT 11
 US-10-416-588-3
 ; Sequence 3, Application US/10416588
 ; Publication No. US20040030100A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer AG
 ; TITLE OF INVENTION: REGULATION OF HUMAN EXTRACELLULAR CALCIUM-SENSING G PROTEIN-COUPLE
 ; TITLE OF INVENTION: RECEPTOR
 ; FILE REFERENCE: LIO221 Foreign Countries
 ; CURRENT APPLICATION NUMBER: US/10/416,588
 ; CURRENT FILING DATE: 2003-05-13
 ; PRIOR APPLICATION NUMBER: US 60/246,981
 ; PRIOR FILING DATE: 2000-11-13
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 1078
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-416-588-3

Query Match 74.8%; Score 4044.5; DB 15; Length 1078;
 Best Local Similarity 74.0%; Pred. No. 3e-306;
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;
 QY 1 MAQLHCOLLFLGFTLLQSYNVSGYGNQRAQKGGDIILGGLPPIHFGVAAKQDQLKSRE 60
 DB 1 MAFYSCCWLLALT-----WHTSAYGDPQRAQKGGDIILGGLPPIHFGVAAKQDQLKSRE 56
 QY 61 ATKCIYRNFGRFWLQAMIFATEEINNSMTFLPNTLGVRIFDTCNTVSKALEATLSFVA 120

```

Db 57 SVECIYRFRGRFWLQAMIFAIEEINSSPALLNLTLGYRIPDTCTNTVSKALEATLSFVA 116
Qy 121 QNKIDSLNLDPCNCSDDHISTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180
Db 117 QNKIDSLNLDPCNCSDDHISTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 176
Qy 181 KNEYKAFRLTIPNDEQOATAMAEIIIEHFQWNVWGTAAADDDYGRPGIDKPREEAVKRDIC 240
Db 177 QNKQKSFRLTIPNDEQOATAMAEIIIEHFQWNVWGTAAADDDYGRPGIEKEFEAEERDIC 236
Qy 241 IDFSEMIQYITKQLEFIADVIQNSAKVIVFSGNDPLBPLQIEIVRNRITDRILWAS 300
Db 237 IDFSLISQYSDDEEIQHVVVEIQNSAKVIVFSSGPDLEPLKIEIVRNRITDRILWAS 296
Qy 301 EAWASSSLIAKPEYFHVHVGTTIGFALRAGRIPGFNFKLKEVHPSRSDNGFVKFWBEET 360
Db 297 EAWASSSLIAKPEYFHVHVGTTIGFALRAGRIPGFNFKLKEVHPSRSDNGFVKFWBEET 356
Qy 361 NCYFTEKTLTQLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEBENITSVETPYLDYT 420
Db 357 NCHLOEGAKGPL--PVDTFLRGHEESGDRFNS--STAFRLCTGDNISSEVETPYLDYT 412
Qy 421 HLRISYVNVAVYSIAHALQDIHSCPGTGFANGSCADIKKVEAWQVNLHLLKFTNS 480
Db 413 HLRISYVNVAVYSIAHALQDIYTCLPGRGFTNGSCADIKKVEAWQVNLHLLKFTNS 472
Qy 481 MGEQVDFDDQGLKQNYTIINWQSAEDSVLFHEVGNVYAKPSPDLNINEKKILWSG 540
Db 473 MGEQVDFDECDLVGNYSIINWHLSPEDGSIKVEGYNVYAKKGERLFINEEKILWSG 532
Qy 541 FSKVVPFNSCRDVPYGRKGIIEGPTCCPECMACAEGBESDENDASACTKCPDNFWSN 600
Db 533 FSREVPFNSCRDVLGAGRKGIIEGPTCCPECMACAEGBESDENDASACTKCPDNFWSN 592
Qy 601 ENHTSCIAKEIEFLSWTEPFGIALTFVAVLGILITSVLGFVKPRNTPIVKATNRELSY 660
Db 593 ENHTSCIAKEIEFLSWTEPFGIALTFVAVLGILITSVLGFVKPRNTPIVKATNRELSY 652
Qy 720 LLLFSLICFSSSLIFIGEPDWTCLRQAPAGISFVLICISILVKNRVLVFEAKIPT 720
Db 653 LLLFSLICFSSSLIFIGEPDWTCLRQAPAGISFVLICISILVKNRVLVFEAKIPT 712
Qy 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNKAFITFSMLIFFIIVISFIPAYVSTYKGF 840
Db 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNKAFITFSMLIFFIIVISFIPAYVSTYKGF 832
Qy 841 VSAVEVIALASSFGLLCIYFNKYIILFKPCNTIEEVRCSAAHAFKVAARATLRS 900
Db 833 VSAVEVIALASSFGLLCIYFNKYIILFKPCNTIEEVRCSAAHAFKVAARATLRS 892
Qy 901 AASRRKSSLCGSTISSPASSTCGP-----LTWEM 931
Db 893 NVSRKSSSLGGSTGTFSSSISSKNSGDPFPQPERKQKQPLALTOEQEQQLTLTPQ 952
Qy 932 Q-----RCSTQKVSFGSVTLTSLFEETGRVATLSRTARSNSADGRSGDLLPSRH 984
Db 953 QORSOQQPRCK-QKVFISGVTFSLSFDEPQKNAMAHNRTHQNSLEAQSSDTLTRH- 1010
Qy 985 DQGPQKCEPOPANDARYKAAPTKGTLESPPGSKERP 1021
Db 1011 -----QPLLPLQCGTDDLTLVQETGLQGVGGDQRP 1042

```

RESULT 12

US-10-408-765A-171

; Sequence 171, Application us/10408765A

; Publication No. US200401018741

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Scumitra S.

```

; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408, 765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-171

```

Query Match 74.8%; Score 4044.5; DB 16; Length 1078;
 Best Local Similarity 74.0%; Pred. No. 3e-306;
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

```

Qy 1 MAQLHCOLLFLGFTLLQSNVSGYGNORAKKGDIIILGLPFIHFGVAAKQDCLSRPE 60
Db 1 MAYSCCVLLAUT---WHTSAYQDQRAKKGDIILGLPFIHFGVAAKQDCLSRPE 56
Qy 61 ATKCIYRFRGRFWLQAMIFAIEEINSSMTFLPNTILGYRIPDTCTNTVSKALEATLSFVA 120
Db 57 SVECIYRFRGRFWLQAMIFAIEEINSSPALLNLTLGYRIPDTCTNTVSKALEATLSFVA 116
Qy 121 QNKIDSLNLDPCNCSDDHISTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180
Db 117 QNKIDSLNLDPCNCSDDHISTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 176
Qy 181 KNEYKAFRLTIPNDEQOATAMAEIIIEHFQWNVWGTAAADDDYGRPGIDKPREEAVKRDIC 240
Db 177 QNKQKSFRLTIPNDEQOATAMAEIIIEHFQWNVWGTAAADDDYGRPGIEKEFEAEERDIC 236
Qy 241 IDFSEMIQYITKQLEFIADVIQNSAKVIVFSGNDPLBPLQIEIVRNRITDRILWAS 300
Db 237 IDFSLISQYSDDEEIQHVVVEIQNSAKVIVFSSGPDLEPLKIEIVRNRITDRILWAS 296
Qy 301 EAWASSSLIAKPEYFHVHVGTTIGFALRAGRIPGFNFKLKEVHPSRSDNGFVKFEWEET 360
Db 297 EAWASSSLIAKPEYFHVHVGTTIGFALRAGRIPGFNFKLKEVHPSRSDNGFVKFEWEET 356
Qy 361 NCYFTEKTLTQLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEBENITSVETPYLDYT 420
Db 357 NCHLOEGAKGPL--PVDTFLRGHEESGDRFNS--STAFRLCTGDNISSEVETPYLDYT 412
Qy 421 HLRISYVNVAVYSIAHALQDIHSCPGTGFANGSCADIKKVEAWQVNLHLLKFTNS 480
Db 413 HLRISYVNVAVYSIAHALQDIYTCLPGRGFTNGSCADIKKVEAWQVNLHLLKFTNS 472
Qy 481 MGEQVDFDDQGLKQNYTIINWQSAEDSVLFHEVGNVYAKPSPDLNINEKKILWSG 540
Db 473 MGEQVDFDECDLVGNYSIINWHLSPEDGSIKVEGYNVYAKKGERLFINEEKILWSG 532
Qy 541 FSKVVPFNSCRDVPYGRKGIIEGPTCCPECMACAEGBESDENDASACTKCPDNFWSN 600
Db 533 FSREVPFNSCRDVLGAGRKGIIEGPTCCPECMACAEGBESDENDASACTKCPDNFWSN 592
Qy 601 ENHTSCIAKEIEFLSWTEPFGIALTFVAVLGILITSVLGFVKPRNTPIVKATNRELSY 660
Db 593 ENHTSCIAKEIEFLSWTEPFGIALTFVAVLGILITSVLGFVKPRNTPIVKATNRELSY 652
Qy 720 LLLFSLICFSSSLIFIGEPDWTCLRQAPAGISFVLICISILVKNRVLVFEAKIPT 720
Db 653 LLLFSLICFSSSLIFIGEPDWTCLRQAPAGISFVLICISILVKNRVLVFEAKIPT 712
Qy 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNKAFITFSMLIFFIIVISFIPAYVSTYKGF 840
Db 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNKAFITFSMLIFFIIVISFIPAYVSTYKGF 832
Qy 841 VSAVEVIALASSFGLLCIYFNKYIILFKPCNTIEEVRCSAAHAFKVAARATLRS 900
Db 833 VSAVEVIALASSFGLLCIYFNKYIILFKPCNTIEEVRCSAAHAFKVAARATLRS 892
Qy 901 AASRRKSSLCGSTISSPASSTCGP-----LTWEM 931
Db 893 NVSRKSSSLGGSTGTFSSSISSKNSGDPFPQPERKQKQPLALTOEQEQQLTLTPQ 952
Qy 932 Q-----RCSTQKVSFGSVTLTSLFEETGRVATLSRTARSNSADGRSGDLLPSRH 984
Db 953 QORSOQQPRCK-QKVFISGVTFSLSFDEPQKNAMAHNRTHQNSLEAQSSDTLTRH- 1010
Qy 985 DQGPQKCEPOPANDARYKAAPTKGTLESPPGSKERP 1021
Db 1011 -----QPLLPLQCGTDDLTLVQETGLQGVGGDQRP 1042

```


Db 713 SPHRKRWGLNQLFLVFLCTFMQIVCVIWLVTADPPSYRNQOELEDEIIFITCHEGSLMA 772
 QY 781 LGFLICYTCLLAACIFFPAFKSRKLPENFNEAKFITPSMLIFFIIVWISFIPAYVSTYKGF 840
 Db 773 LGFLICYTCLLAACIFFPAFKSRKLPENFNEAKFITPSMLIFFIIVWISFIPAYVSTYKGF 832
 QY 841 VSAVEVIAILASSPGLGCIYKCYIILFPCRNTEIEEVRCSTAAHAFKVAARATLRRS 900
 Db 833 VSAVEVIAILASSPGLGCIYKCYIILFPCRNTEIEEVRCSTAAHAFKVAARATLRRS 892
 QY 901 AASRRKSSSLGSGTSSPASSCTGPG-----LTWEM 931
 Db 893 NVSRKSSSLGSGTSSPASSCTGPG-----LTWEM 952
 QY 932 Q-----RCSTOKVSFGSGTWTLSLSEFTGRYATLSRTARSNSADGRGDDLPDRHH 984
 Db 953 QORSQQPRCK-QKVFSGSGTWTLSLSEFTGRYATLSRTARSNSADGRGDDLPDRHH 1010
 QY 985 DQGPQKCEPQANDARYKAAPTGTLESPPGSGKEP 1021
 Db 1011 -----QPLLPQCGETDLDLTVOETGLOGVGGDQRP 1042

RESULT 13
 US-10-002-854-2
 ; Sequence 2, Application US/10002854
 ; Publication No. US20020132224A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Scadden, David T.
 ; APPLICANT: Pozhansky, Mark C.
 ; APPLICANT: Olszak, Ivona T.
 ; APPLICANT: Brown, Edward M.
 ; TITLE OF INVENTION: THE CAR RECEPTOR AS A MEDIATOR OF
 ; MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS
 ; FILE REFERENCE: M0765/7038/ERG/KA
 ; CURRENT APPLICATION NUMBER: US/10/002,854
 ; CURRENT FILING DATE: 2001-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/15440
 ; PRIOR FILING DATE: 2000-06-02
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1078
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)...(1078)
 ; OTHER INFORMATION: Ca-sensing Receptor

Query Match 74.7%; Score 4039.5; DB 13; Length 1078;
 Best Local Similarity 73.9%; Pred. No. 7.4e-306;
 Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

QY 1 MAQLHCQLLFLGFTLLQSNVSGYGNQRAQKGGDIIILGGLFPHFGVAADQDLKSRPE 60
 Db 1 MAFYSCWVLLALT-----WHTSAYGPDQRAQKGGDIIILGGLFPHFGVAADQDLKSRPE 56
 QY 61 ATKIRYNFRGRFWLQAMIFATEEINNSMTFLPNTITLGYRFDTCNTVSKALEATLSFVA 120
 Db 57 SVECIYNFRGRFWLQAMIFATEEINNSMTFLPNTITLGYRFDTCNTVSKALEATLSFVA 116
 QY 121 QNKIDSLNDEFNCSDHPTSTIAVVGATGSGISTAVANLGLFVPOVSVASSRLLSN 180
 Db 117 QNKIDSLNDEFNCSEHPTSTIAVVGATGSGISTAVANLGLFVPOVSVASSRLLSN 176
 QY 181 KNEYKAFRTIPNDEQOATAMEIIEHFQWVWVGTAAADDDYGRPGIDKFRFEAAVRDIC 240
 Db 177 KNOFSFLRTIPNDEHQAAMADIIIEYFKNWVWGTAAADDDYGRPGIDKFRFEAAVRDIC 236
 QY 241 IDPSEMISQYTKQLEFIADYQNSAKVIVVFGSGPDLEPLIQEIVERNITPRILWAS 300

Db 237 IDSELIQSDEEBEIQHVVEVIQNSTAKVIVVFGSGPDLEPLIKEIVERNITGKIWLAS 296
 QY 301 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIIPGNKFLKEVHPSSSDNGFVKBWEETF 360
 Db 297 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIIPGNKFLKEVHPSSSDNGFVKBWEETF 356
 QY 361 NCVFTEKTLTQKNKSVPSHGPAQDGGKAGNSRRTALRHPTCTEENITTSVETPVDYT 420
 Db 357 NCHLQAGKPL---PDTFLRGHEESGDRFNS--STAFPLCTGDNISSTVETPIDYT 412
 QY 421 HLRISNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVNLHLHLKFTNS 480
 Db 413 HLRISNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVNLHLHLKFTNS 472
 QY 481 MGEQVDFDQGDILKGNVTIINWLSAEDSVLPHEVGNYNAYAKPSDRNLNINEKILWSG 540
 Db 473 MGEQVDFDQGDILKGNVTIINWLSAEDSVLPHEVGNYNAYAKPSDRNLNINEKILWSG 532
 QY 541 FSKVVPFNSCRDVCPTGRKGIIEGPTCCFCMACAEGEFSDENDASACTCPNDPWSN 600
 Db 533 FSREVPFNSCRDVCPTGRKGIIEGPTCCFCMACAEGEFSDENDASACTCPNDPWSN 592
 QY 601 ENHTSCIAKEIEYLSWTEPFGIATLIFAVLGLILITSLFVLGVFIKPRNTPIVKATRELISY 660
 Db 593 ENHTSCIAKEIEYLSWTEPFGIATLIFAVLGLILITSLFVLGVFIKPRNTPIVKATRELISY 652
 QY 661 LLLFSLICCFSSSLIFIGEPDWTCLROPATFGISFVLCISILVKTNRVLLVFEAKIPT 720
 Db 653 LLLFSLICCFSSSLIFIGEPDWTCLROPATFGISFVLCISILVKTNRVLLVFEAKIPT 712
 QY 721 SLHRKWGNLQFLVFLCIVLQIVTCIILWTAPSSYRNHELEDEVIITCDGSLMA 780
 Db 713 SPHRKRWGLNQLFLVFLCTFMQIVCVIWLVTADPPSYRNQOELEDEIIFITCHEGSLMA 772
 QY 781 LGFLICYTCLLAACIFFPAFKSRKLPENFNEAKFITPSMLIFFIIVWISFIPAYVSTYKGF 840
 Db 773 LGFLICYTCLLAACIFFPAFKSRKLPENFNEAKFITPSMLIFFIIVWISFIPAYVSTYKGF 832
 QY 841 VSAVEVIAILASSPGLGCIYKCYIILFPCRNTEIEEVRCSTAAHAFKVAARATLRRS 900
 Db 833 VSAVEVIAILASSPGLGCIYKCYIILFPCRNTEIEEVRCSTAAHAFKVAARATLRRS 892
 QY 901 AASRRKSSSLGSGTSSPASSCTGPG-----LTWEM 931
 Db 893 NVSRKSSSLGSGTSSPASSCTGPG-----LTWEM 952
 QY 932 Q-----RCSTOKVSFGSGTWTLSLSEFTGRYATLSRTARSNSADGRGDDLPDRHH 984
 Db 953 QORSQQPRCK-QKVFSGSGTWTLSLSEFTGRYATLSRTARSNSADGRGDDLPDRHH 1010
 QY 985 DQGPQKCEPQANDARYKAAPTGTLESPPGSGKEP 1021
 Db 1011 -----QPLLPQCGETDLDLTVOETGLOGVGGDQRP 1042

RESULT 14
 US-10-225-567A-118
 ; Sequence 118, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LifeSpan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Barner, Glenna C.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 118

```

; LENGTH: 1078
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-118

Query Match      74.6%; Score 4037.5; DB 14; Length 1078;
Best Local Similarity 73.9%; Pred. No. 1.1e-305;
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

Qy 1 MAQLHCOLLFLGFTLLQSNVSGVGNQRAOKKGGDIILGGLPPIHFGVAAKDDQLKSPE 60
Db 1 MAFVSCCWLALT---WHTSAYGPDQRAQKGGDIILGGLPPIHFGVAAKDDQLKSPE 56
Qy 61 ATKIRYNFRGRFLWQAMIFAIIEINNSMTFLPNITLGYRIPDTCTVSKALEATLSFVA 120
Db 57 SVECIYNFRGRFLWQAMIFAIIEINNSPALLPNLTGLYRIPDTCTVSKALEATLSFVA 116
Qy 121 QNKIDSLNLDNFCNCSHDHPSTIAVVGATGSGISSTAVANLLGLFYIPOVSYASSRLLSN 180
Db 117 QNKIDSLNLDNFCNCSHDHPSTIAVVGATGSGVSTAVANLLGLFYIPOVSYASSRLLSN 176
Qy 181 KNEYKAFRTIPNDEQOATAMAEIIEHFQNNWVGTLAADDYGRGIDKFREAEVRDIC 240
Db 177 KNQPKSFLRTIPNDEQOATAMADIIEYFRNNWVGTLAADDYGRGIDKFREAEVRDIC 236
Qy 241 IDFSEMIQYTKOLEFIADVIQNSAKVIVVFSNGPDLPLIOBIVRNITDRIWLAS 300
Db 237 IDFSEMIQYSDSEEEQHVVVEIQNSTAKVIVVFSNGPDLPLIOBIVRNITDRIWLAS 296
Qy 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGKFLKEVHPSRSDNGFVKFEWETF 360
Db 297 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGKFLKEVHPSRSDNGFVKFEWETF 356
Qy 361 NCYFTEKTLTQLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420
Db 357 NCHLQEGAGPL--PVDFTLGRHEESGDRPNS--STAFRLCTGDNISSVETPYIDYT 412
Qy 421 HURISYNTVAVYSTAHALODTHSKPGTGIPANGSCADIKKVEAWQVNLHLHLKFTNS 480
Db 413 HLRISYNTVAVYSTAHALQDITCLPGRGLTNGSCADIKKVEAWQVNLHLHLNFTNN 472
Qy 481 MGEQVDFDDQGLKNTYIINWOLSAEDSVLFHEVGNVNAVAKDPSDRININEKKILWSG 540
Db 473 MGEQVTFDECGLDVGNSYIINWHLSPEDGSIIVKGVYNNYAKGERLFINEEKILWSG 532
Qy 541 FSKVYFNCSDCVGTRKGIIEGPTCCFCFMAEAGEFSDENDASACTKCPNDFWSN 600
Db 533 FSRVYFNCSDCLAGTRKGIIEGPTCCFCFCEPCDGEYSDETDASACNKCPCDFWSN 592
Qy 601 ENHTSCIAKEIYLSWTPPGTALTIPAVLGLTITSFVLGVTFIKERNTPYKATNRELSY 660
Db 593 ENHTSCIAKEIBFLSWTPPGTALTIPAVLGLTITSFVLGVTFIKERNTPYKATNRELSY 652
Qy 661 LLLFSLICFSSSLIFIGEPDRWTCRLQPAFGISFVLCSICILVKTNRVLLVFEAKIPT 720
Db 653 LLLFSLICFSSSLIFIGEPDQWTCRLQPAFGISFVLCSICILVKTNRVLLVFEAKIPT 712
Qy 721 SLHRKVGUNLQFLVFLCILVQIVTCIWLITAPSSYRNHELEDEVIPTCEGSLMA 780
Db 713 SPHRKVGUNLQFLVFLCFTQIVCIVWLITAPSSYRNQOELEDEVIPTCEGSLMA 772
Qy 781 LGFLGYTCLLAAICFFFAFKSRKLPENENEAKFTTFSMLPFIWISFIPAYSTYKGF 840
Db 773 LGFLGYTCLLAAICFFFAFKSRKLPENENEAKFTTFSMLPFIWISFIPAYSTYKGF 832
Qy 841 VSAVEVIALASFGLLGCIYKNYKIILFKPCRNITBEVRGSTAAHAFKVAARATLRS 900
Db 833 VSAVEVIALAASFGLLACIFENKIYIILFKPSRNTIBEVRCSTAAHAFKVAARATLRS 892
Qy 901 AASRKSLSLGGSTISSPASSCGPG-----LTWEM 931
Db 893 NVSRKRSLSLGGSTGSPSSISSKNSDEDPFPQPEROKQOQPLALTOEQOQOPLLPQ 952

```

```

Qy 932 Q-----RCSTQKVSFGSGTSLTSLSFEBETGRVATLSRTARSNGADGRSGDDLPSSRH 984
Db 953 QRSQQQPRCK-QKVIKSGTSLTSLSFDBEPQKNAMAHGNSHTONSLEAKSSDILTRH- 1010
Qy 985 DQPPPKCBQBPANDARYKAAPTKGTLESPGGSKERP 1021
Db 1011 -----QPLLPLQCGTDLDTLVOETGLQGVGDQRP 1042

RESULT 15
US-10-673-888-1
; Sequence 1, Application US/10673889
; Publication No. US20040082588A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Ellen
; APPLICANT: Choy, Wai Nang
; APPLICANT: Mirro, Elmer
; TITLE OF INVENTION: METHODS FOR TREATING DISORDERS OF CALCIUM HOMEOSTASIS
; FILE REFERENCE: OC01600-US
; CURRENT APPLICATION NUMBER: US/10/673,888
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: 60/414,948
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (537)..(546)
; OTHER INFORMATION: deleted in human calcium ion sensing receptor variant
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (936)..(936)
; OTHER INFORMATION: Q in human calcium ion sensing receptor variant
; NAME/KEY: VARIANT
; LOCATION: (1000)..(1000)
; OTHER INFORMATION: G in human calcium ion sensing receptor variant
US-10-673-888-1

Query Match      74.5%; Score 4029.5; DB 15; Length 1088;
Best Local Similarity 73.3%; Pred. No. 4.5e-305;
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

Qy 1 MAQLHCOLLFLGFTLLQSNVSGVGNQRAQKGGDIILGGLPPIHFGVAAKDDQLKSPE 60
Db 1 MAFVSCCWLALT---WHTSAYGPDQRAQKGGDIILGGLPPIHFGVAAKDDQLKSPE 56
Qy 61 ATKIRYNFRGRFLWQAMIFAIIEINNSMTFLPNITLGYRIPDTCTVSKALEATLSFVA 120
Db 57 SVECIYNFRGRFLWQAMIFAIIEINNSPALLPNLTGLYRIPDTCTVSKALEATLSFVA 116
Qy 121 QNKIDSLNLDNFCNCSHDHPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
Db 117 QNKIDSLNLDNFCNCSHDHPSTIAVVGATGSGVSTAVANLLGLFYIPOVSYASSRLLSN 176
Qy 181 KNEYKAFRTIPNDEQOATAMAEIIEHFQNNWVGTLAADDYGRGIDKFREAEVRDIC 240
Db 177 KNQPKSFLRTIPNDEQOATAMADIIEYFRNNWVGTLAADDYGRGIDKFREAEVRDIC 236
Qy 241 IDFSEMIQYTKOLEFIADVIQNSAKVIVVFSNGPDLPLIOBIVRNITDRIWLAS 300
Db 237 IDFSEMIQYSDSEEEQHVVVEIQNSTAKVIVVFSNGPDLPLIOBIVRNITDRIWLAS 296
Qy 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGKFLKEVHPSRSDNGFVKFEWETF 360
Db 297 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGKFLKEVHPSRSDNGFVKFEWETF 356
Qy 361 NCYFTEKTLTQLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420

```

Db 357 NCHLOBGAAGPL---PVDTFLECHESGDRFENS-STAFPRCLCTDENISSVETPYIDYT 412
QY 421 HLRISYNYVAVYIAHALQDIHSCKPGTGIFANGSCADIKKVEAQVNLHLHLKFTNS 480
Db 413 HLRISYNYVAVYIAHALQDIYTCPLGRGLFTNGSCADIKKVEAQVNLHLHLFTNN 472
QY 481 MGEQVDFDQDGLKGNYYIINWQLSAEDSVLFHEVGNVYAKPSDRNLNINEKILWSG 540
Db 473 MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFEKVGYNVYAKGERLFINEEKILWSG 532
QY 541 FSK-----VVPFNSCRDVCVGRKGIIEGPTCCPECMACAEGFSDENDASAC 590
Db 533 FSRBPLTFVLVSVLQVFFNSCRDCLAGTRKGIIEGPTCCPECVCPDGEYSDETDASAC 592
QY 591 TKCPNDFWSENHTSCIAKEIYLSWTEPPFGIALTIFAVLGILITSFVLGVFIKFRNTPI 650
Db 593 NKCPDDFWSENHTSCIAKEIEFLSWTEPPFGIALTFAVLGIFLFAVLGVFIKFRNTPI 652
QY 651 VKATNRELSYLLLSLICCFSLSLIFIGEPRDWTCLRQPAFGISFVLCISCLLVKTRV 710
Db 653 VKATNRELSYLLLSLCCFSLSLIFEPEQDWTCLRQPAFGISFVLCISCLLVKTRV 712
QY 711 LLVFEAKIPTSLHRKWVGNLQFLVFLCIVQIVTCIWLVTAPPSSYRNHELEDEVIP 770
Db 713 LLVFEAKIPTSPHRKWVGNLQFLVFLCTFMQIVICVWLVTAPPSSYRNQELEDEIIF 772
QY 771 ITCDEGSLMALGLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWIISFI 830
Db 773 ITCHEGSLMALGLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWIISFI 832
QY 831 PAYVSTYKGFVSAVEVIAIASSFGLGCIYFNKCYIILFKPCNTIIEVRCSTAAHAFK 890
Db 833 PAYASTYKGFVSAVEVIAIASSFGLACIFFNKIYIILFKPSRNTIEVRCSTAAHAFK 892
QY 891 VAARATLRSASAKRSSSLCGSTISSPASSTCGPG----- 926
Db 893 VAARATLRSNSVRKSSSLGSGTGSTPSSISSKSNSBEDPFRPERKQOQPLALTOQE 952
QY 927 -----LTMEMQ-----RCSTQKVSFGSGTVTLISLPEETGRVATLSRTARSNSADGR 974
Db 953 QOQOPLTLPOQORSQOQPRCK-QKVFISGTVTFSLSPDEPKAMAHNRNTHQNSLEAQ 1011
QY 975 SGDDLPSRHHQGPQKCEPQANDARYKAAPTCKTLESPPGSKERP 1021
Db 1012 KSSDTLTRH-----QPLLPLQCGETDLDTVOETGLQGPVGGDQRP 1052

Search completed: November 17, 2004, 12:37:31
Job time : 520 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 11:02:39 ; Search time 73 Seconds
(without alignments)

1353.625 Million cell updates/sec

Title: US-10-016-496-2

Perfect score: 5410

Sequence: 1 MAQHCCQLFLGFTLLQSYN.....KGTLESFGSKSRPTTMEET 1027

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4037.5	74.6	1078	2 A56715	calcium receptor (
2	4029.5	74.5	1088	2 B56715	calcium receptor (
3	3998.5	73.9	1085	2 S40476	Ca(2+)-sensing rec
4	3996	73.9	1079	2 I59362	calcium/polyvalent
5	1145	21.2	879	2 JH0562	metabotropic gluta
6	1137	21.0	879	2 JCT160	metabotropic gluta
7	1115.5	20.6	912	2 JH0563	metabotropic gluta
8	1114.5	20.6	872	2 JH0561	metabotropic gluta
9	1108.5	20.5	871	2 A46742	metabotropic gluta
10	1092.5	20.2	915	2 A49874	metabotropic gluta
11	1077	19.9	908	2 I49142	metabotropic gluta
12	1056.5	19.5	1212	2 JCT131	metabotropic gluta
13	1052	19.4	1199	2 A41939	G protein-coupled
14	1044	19.3	1171	2 A42916	metabotropic gluta
15	1040	19.2	1180	2 JCT132	metabotropic gluta
16	1017.5	18.8	858	2 JCT683	taste receptor T1R
17	1015.5	18.8	1218	2 S71376	glutamate receptor
18	1005.5	18.6	999	2 T27628	hypothetical prote
19	888	16.4	1267	2 T21340	hypothetical prote
20	682	12.6	551	2 T30806	metabotropic gluta
21	365	6.7	1099	2 T16283	hypothetical prote
22	216	4.0	921	2 T51136	ionotropic glutama
23	215	4.0	923	2 P84732	probable ligand-ga
24	210.5	3.9	953	2 E84732	probable ligand-ga
25	206	3.8	997	2 S33754	glutamate receptor
26	205	3.8	951	2 T51132	probable glutamate
27	203	3.8	950	2 T51134	ionotropic glutama
28	201	3.7	925	2 T51133	ligand gated chann
29	199	3.7	965	2 I51244	N-methyl-D-asparta

RESULT 1

A56715

calcium receptor (clone pncAR-4.0) - human

C:Species: Homo sapiens (man)

C:Date: 19-Oct-1995 #sequence revision 19-Oct-1995 #text_change 01-Dec-2000

C:Accession: A56715; S49341; A49419; B49419; C49419

R:Garrett J.E.; Capuano I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.

J. Biol. Chem. 270, 12919-12925, 1995

A:Title: Molecular cloning and functional expression of human parathyroid calcium receptor

A:Reference number: A56715; MUID:95279439; PMID:7759551

A:Accession: A56715

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1078 <GAR>

A:Cross-references: GB:020759; NID:9683744; PIDN:AAA86503.1; PID:9683745

R:Pearce, S.H.S.; Thakker, R.V.

submitted to the EMBL Data Library, August 1994

A:Reference number: S49341

A:Accession: S49341

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-180, 'Q', 182-989, 'R', 991-1078 <PEA>

A:Cross-references: EMBL:X81086

R:Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, J.

Cell 75, 1297-1303, 1993

A:Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemic

A:Reference number: A49419; MUID:94094324; PMID:7516660

A:Accession: A49419

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 178-192 <POL>

A:Experimental source: family N

A:Note: sequence inconsistent with nucleotide translation

A:Note: sequence modified after extraction from NCBI backbone

A:Note: 186-Arg mutation is associated with familial hypocalcemic hypercalcemia and neor

A:Note: sequence extracted from NCBI backbone (NCBIN:142453)

A:Accession: B49419

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 289-303 <PO2>

A:Experimental source: family E

A:Note: sequence modified after extraction from NCBI backbone

A:Note: 298-Lys mutation is associated with familial hypocalcemic hypercalcemia and neor

A:Note: sequence extracted from NCBI backbone (NCBIN:142455)

A:Accession: C49419

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 788-802 <PO3>

A:Experimental source: family J

A:Note: sequence modified after extraction from NCBI backbone

A:Note: 796-Trp mutation is associated with familial hypocalcemic hypercalcemia and neor

A:Note: sequence extracted from NCBI backbone (NCBIN:142457)

C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 74.6%; Score 4037.5; DB 2; Length 1078;
Best Local Similarity 73.3%; Pred. No. 2.8e-287;
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

```
QY 1 MAQLHCQLLFLGFTLLQSYNVSGYGNQRAQKGGDIILGGLPFIHFGVAAKQDQLKSPE 60
DB 1 MAFYSCWVLLALT----WHTSAYGPDQRAQKGGDIILGGLPFIHFGVAAKQDQLKSPE 56

QY 61 ATKCYRNFRGRFWLQAMIFAEIINNMTFIPNITLGYRIEDTCTNTVSKALEATLSFVA 120
DB 57 SVECIYRNFRGRFWLQAMIFAEIINNMTFIPNITLGYRIEDTCTNTVSKALEATLSFVA 116

QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 180
DB 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSN 176

QY 181 KNEYKAFLATIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRGIDKFRFEAVKRDIC 240
DB 177 KNQFKSFLATIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRGIDKFRFEABERDIC 236

QY 241 IDPSEMIQSYVTKOLEFTADVIQNSAKVIVVFSNGPDLEPLIOEIVRRNITDRIWLAS 300
DB 237 IDPSELISQYSDDEEIQHVVEIQNSTAKVIVVFSNGPDLEPLIOEIVRRNITDRIWLAS 296

QY 301 EAWASSLIAKPEYFHVVGTTGFALRAGRIPOGKFKLKEVHPSSSDNGFVKEFWEEFP 360
DB 297 EAWASSLIAMPQYFHVVGTTGFALRAGRIPOGKFKLKEVHPSSSDNGFVKEFWEEFP 356

QY 361 NCYFTEKTLTQKNKVPKSHGPAAGDGSKAGNSRRTALRHPCTGENTTSVETPYLDYT 420
DB 357 NCHLQGAAGPL---PVDTFLRGHESGDRFNS--STAFPLCTGDNISVETPYIDYT 412

QY 421 HLRISYNYVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAQVNLHLHLKFTNS 480
DB 413 HLRISYNYVAVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAQVNLHLHLFTNN 472

QY 481 MGEQVDFDQGDILKGYNTIINQLSAEDSVLPHEVGNVYAKPSDRNLNNEKILLWSG 540
DB 473 MGEQVTFDCGLVGNYSIINWHLSPEDGSIYFKEVGNVYAKGERLFINNEKILLWSG 532

QY 541 FSKVVPFNSCRDVPGRKGIIIEGPTCCFECMACAEFGSDENDASACTKCPDNFWSN 600
DB 533 FSRVFPFNSCRDCLAGTRKGIIEGPTCCFECVCECPDGEYSDETDASACNKPDDFWSN 592

QY 601 ENHTSCIAKEIYLSWTEPFGIATLIFAVLGLITTSFVLGVFKPRNTPIVKATNRELSY 660
DB 593 ENHTSCIAKEIYLSWTEPFGIATLIFAVLGLITTSFVLGVFKPRNTPIVKATNRELSY 652

QY 661 LLLFSLICCFSSLPFIQBPDRWTCLRPAPGISFVLICISILVKNRLLVPEAKIPT 720
DB 653 LLLFSLICCFSSLPFIQBPQWTCLRPAPGISFVLICISILVKNRLLVPEAKIPT 712

QY 721 SLHRKVGUNLOFLVFLICILVOITCIIWLTAPPSYRNHELEDEVIPTCDGSLMA 780
DB 713 SFHRKVGUNLOFLVFLICILVOITCIIWLTAPPSYRNHELEDEVIPTCDGSLMA 772

QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITPSMLIFFIWIISFIPAYVSTYKGF 840
DB 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITPSMLIFFIWIISFIPAYVSTYKGF 832

QY 841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNITIEEVRCSSTAHAFAKVAARATLRS 900
DB 833 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNITIEEVRCSSTAHAFAKVAARATLRS 892

QY 901 AASRRSSSLCGSTISSPASSTCGPG-----LTWEM 931
DB 893 NVSRKRSSSLGGSTGTPSSSSISSKSNBEDPPQEPQKQOQALATQOEOQOQPLTLFQ 952

QY 932 Q-----RCSTQKVSFGSGVTLLSLSPTEETGRVATLRSRTARSNSADGRSGDILLPRHH 984
DB 953 QOESQOQPRCK-QKVIKFGSGTVPFSLSPDEPKNAWAGNSHTQNSLEAKSSDTLTFH- 1010
```

QY 985 DOGPPQKCEPQANDARYKAAPTGTLESPPGSKERP 1021

DB 1011 -----QPLLFLQCGETDLDTVQETGLQGVGVGDQRP 1042

RESULT 2

B56715

calcium receptor (clone phpCar-5.2) - human

C;Species: Homo sapiens (man)

C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000

C;Accession: B56715

R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.

J. Biol. Chem. 270, 12919-12925, 1995

A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor

A;Reference number: A56715; MUID:95279439; PMID:7759551

A;Accession: B56715

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1088 <GAR>

A;Cross-references: GB:U02760; NID:9683746; PIDN:AAA86504.1; PID:9683747

C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 74.5%; Score 4029.5; DB 2; Length 1088;

Best Local Similarity 73.3%; Pred. No. 1.1e-286;

Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

QY 1 MAQLHCQLLFLGFTLLQSYNVSGYGNQRAQKGGDIILGGLPFIHFGVAAKQDQLKSPE 60

DB 1 MAFYSCWVLLALT----WHTSAYGPDQRAQKGGDIILGGLPFIHFGVAAKQDQLKSPE 56

QY 61 ATKCYRNFRGRFWLQAMIFAEIINNMTFIPNITLGYRIEDTCTNTVSKALEATLSFVA 120

DB 57 SVECIYRNFRGRFWLQAMIFAEIINNMTFIPNITLGYRIEDTCTNTVSKALEATLSFVA 116

QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 180

DB 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSN 176

QY 181 KNEYKAFLATIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRGIDKFRFEAVKRDIC 240

DB 177 KNQFKSFLATIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRGIDKFRFEABERDIC 236

QY 241 IDPSEMIQSYVTKOLEFTADVIQNSAKVIVVFSNGPDLEPLIOEIVRRNITDRIWLAS 300

DB 237 IDPSELISQYSDDEEIQHVVEIQNSTAKVIVVFSNGPDLEPLIOEIVRRNITDRIWLAS 296

QY 301 EAWASSLIAKPEYFHVVGTTGFALRAGRIPOGKFKLKEVHPSSSDNGFVKEFWEEFP 360

DB 297 EAWASSLIAMPQYFHVVGTTGFALRAGRIPOGKFKLKEVHPSSSDNGFVKEFWEEFP 356

QY 361 NCYFTEKTLTQKNKVPKSHGPAAGDGSKAGNSRRTALRHPCTGENTTSVETPYLDYT 420

DB 357 NCHLQGAAGPL---PVDTFLRGHESGDRFNS--STAFPLCTGDNISVETPYIDYT 412

QY 421 HLRISYNYVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAQVNLHLHLKFTNS 480

DB 413 HLRISYNYVAVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAQVNLHLHLFTNN 472

QY 481 MGEQVDFDQGDILKGYNTIINQLSAEDSVLPHEVGNVYAKPSDRNLNNEKILLWSG 540

DB 473 MGEQVTFDCGLVGNYSIINWHLSPEDGSIYFKEVGNVYAKGERLFINNEKILLWSG 532

QY 541 FSKVVPFNSCRDVPGRKGIIIEGPTCCFECMACAEFGSDENDASACTKCPDNFWSN 590

DB 533 FSRVFPFNSCRDCLAGTRKGIIEGPTCCFECVCECPDGEYSDETDASAC 592

QY 591 TKCPNDFWSENHTSCIAKEIYLSWTEPFGIATLIFAVLGLITTSFVLGVFKPRNTP 650

DB 593 NKCPDDFWSENHTSCIAKEIYLSWTEPFGIATLIFAVLGLITTSFVLGVFKPRNTP 652

QY 651 VKATNELSYLLFSLICCFSSLPFIQBPDRWTCLRPAPGISFVLICISILVKNRNV 710

Db 653 VKATNRELVSLLFSLCCPSSSFFIGEPQDWTCLRPQAFGISFVLCISILVKNRV 712
 Qy 711 LLVFEAKIPTSLHRKRWGLNLQFLVFLCILVQIVTCIIMLYTAPPSSYNHLEDEVIP 770
 Db 713 LLVFEAKIPTSFHRKRWGLNLQFLVFLCITPMQVICVIMLYTAPPSSYNHLEDEIIF 772
 Qy 771 ITCEGSLMAGFLIGYTCLLAAICFFAFKSRKLPENFNEAKITTSMLIFFVWISFI 830
 Db 773 ITCEGSLMAGFLIGYTCLLAAICFFAFKSRKLPENFNEAKITTSMLIFFVWISFI 832
 Qy 831 PAYVSTYKGFYSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 890
 Db 833 PAYASTYKGFYSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 892
 Qy 891 VAARATLRRSASKRSSSLCGSTISSPASSTCGPG----- 926
 Db 893 VAARATLRRSNVSRKSSSLCGSTGTPSSISKSNSDEDPFPERKQOQPLALTCQE 952
 Qy 927 -----LTMEMO-----RCSTQKVSFGSGVTLSLSPETGRVATLSRTARSNSADGR 974
 Db 953 QOQOPLTLPOQRSOQPRCK-QKVFSGGIVTFSLSFDEPKVMAMAHENSTHONSLEAQ 1011
 Qy 975 SGDDLPFRRHQDQPPKQCEPQANDARYKAAPTGTLESPOGSKERP 1021
 Db 1012 KSSDLTRH-----QPLLPQCGETDLTLVQETGLOGPVGGDQRP 1052

RESULT 3
 S40476
 Ca(2+)-sensing receptor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S40476
 R:Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; H
 Nature 366, 575-580, 1993
 A:Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from b
 A:Reference number: S40476; MUID:94077182; PMID:8255296
 A:Accession: S40476
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1085

 A:Cross-references: UNIPROT:P35384; GB:S67307; NID:9453108; PIDN:AAB29171.1; PID:9453109

Query Match 73.9%; Score 3999.5; DB 2; Length 1085;
 Best Local Similarity 72.8%; Pred. No. 1.7e-284;
 Matches 778; Conservative 92; Mismatches 141; Indels 57; Gaps 8;

Qy 1 MAQLHCQLLFLGFTLLQSNVSGYGNPQAKKGGDIIILGGLFPIHFGVAAKDQDLKSRPE 60
 Db 1 MALYSCCWTLTAPS---TWCTSAYGPDQRAQKGGDIIILGGLFPIHFGVAAXDQDLKSRPE 57
 Qy 61 ATKCYRNPGRFRWLQAMIFAEIEINNSMTFLPNITLGVRIEDTNTVSKALEATLSFVA 120
 Db 58 SVECTRYNPRGRFWLQAMIFAEIEINNSPALLPNMTLGVRIEDTNTVSKALEATLSFVA 117
 Qy 121 QNKIDSLNDEFNCNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180
 Db 118 QNKIDSLNDEFNCNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 177
 Qy 181 KNEYKAFATIPNDEQATAMAEIIEHFQWNVMTLAADDYGRPGIDKFRFEAVKRDIC 240
 Db 178 KNQFKSFLTIPNDEQATAMADIEYFQWNVMTLAADDYGRPGIEKFEFEAEERDIEC 237
 Qy 241 IDFSEMISQYTKQLEFIADVIQNSAKVIVFVNGPDLPLQIEIVRNITDRINWLAS 300
 Db 238 IDFSELISQYSDBEKIQVVEIQNSAKVIVFVSSGPDLEPLQIEIVRNITGRIMLAS 297
 Qy 301 EAWASSLLAKPEYFHVVGTTGFPALRAGRIGENKFLKEVHPSSSDNGFVKETWEETF 360
 Db 298 EAWASSLLIAMPEYFHVVGTTGFGKAGQIPGREFLOKVPKRSVNGFAKEWEETF 357
 Qy 361 NCVFTEKTLTLQKNKSVPGHGAQGDGSKAGNSRRATLRHPCTEENITSVETPYDYT 420

Db 358 NCHLQBGAKGPL---PVDTFLRGHEGGARLNS-PTAFRPLCTGEEISSVETPYMDYT 413
 Qy 421 HLRISNVYVAVYSTAHALQDHSCKPGGIFANGSCADIKKVEAQVNLHLHLKFTNS 480
 Db 414 HURISNVYVAVYSTAHALQDIYTCIPGRGLFTNSCADIKKVEAQVNLHLHLFTSN 473
 Qy 481 MGEQVDFDQDGLKGNYYIINMQLSAEDSVLFEHVGNYNAYAKPSDRNLINEXKILMSG 540
 Db 474 MGEQVTFDCGDLGAGNYSIINWHLSPEDGSIIVKEVGYNYVYAKKGERLFINDEKILMSG 533
 Qy 541 FSKVPFNSCRDVPGRKGLIEGEPTCCPCMACAEGEFSDENDASACTKCPDNFWSN 600
 Db 534 FSREVPFNSCRDCLAGTRKGLIEGEPTCCFCVCEGPDGEYSDETDASACDPCPDFWSN 593
 Qy 601 ENHTSCIAKEIEYLSWTEPFGLIATIFAVLGIITTSFVLGVFIKFRNTPIVKATNRELS 660
 Db 594 ENHTSCIAKEIEYLSWTEPFGLIATIFAVLGIATLFAVLGIFLTAFLGVFIKFRNTPIVKATNRELS 653
 Qy 661 LLLFSLICFSSSLIFIGBPRDWTCLRPQAFGISFVLCISILVKNRVLLVFEAKIPT 720
 Db 654 LLLFSLICFSSSLIFIGBPDWTCRLQPAFGISFVLCISILVKNRVLLVFEAKIPT 713
 Qy 721 SLHRKRWGLNLQFLVFLCITPMQVICVIMLYTAPPSSYNHLEDEVIFITCEGSLMA 780
 Db 714 SFHRKRWGLNLQFLVFLCITPMQVICVIMLYTAPPSSYNHLEDEVIFITCEGSLMA 773
 Qy 781 LGFLIGYTCLLAAICFFAFKSRKLPENFNEAKITTSMLIFFVWISFIPAVSTYKGF 840
 Db 774 LGFLIGYTCLLAAICFFAFKSRKLPENFNEAKITTSMLIFFVWISFIPAVSTYKGF 833
 Qy 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 900
 Db 834 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 893
 Qy 901 AASRKSSSLICGSTISSPASSTCG-----P 925
 Db 894 NVSRQSSSLICGSTGTPSSISKSNSDEDPFQKQKQKQKQPLALSPHNAQOQPRP 953
 Qy 926 GLTNEMQ-----RCSTQKVSFGSGVTLSLSPETGRVATLSRTARSNSADGSGDD 978
 Db 954 PSTPQPOQSQOQPRCK-QKVFSGGIVTFSLSFDEPKQTAFAHRNSTHQTLSLEAQKND 1012
 Qy 979 LPSEHHDQGPQKQCEPQANDARYKAAPTGTLESPOGSKERTTME 1026
 Db 1013 ALTKH-----QALLPQCGETSELTSQETGLOGPVG-EDHOLEMED 1053

RESULT 4
 159362
 calcium/polyvalent cation-sensing receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 159362; A55594
 R:Ruut, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995
 A:Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve ter
 A:Reference number: 159362; MUID:95241465; PMID:7724534
 A:Accession: 159362
 A:Status: translated from GB/ENBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1079 <RES>
 A:Cross-references: UNIPROT:P48442; EMBL:U20289; NID:970578; PIDN:AAC52195.1; PID:g79057
 A:Experimental source: striatal
 R:Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.
 Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995
 A:Title: Cloning and functional expression of a rat kidney extracellular calcium/polyval
 A:Reference number: A55594; MUID:95116508; PMID:7816802
 A:Accession: A55594
 A:Molecule type: mRNA
 A:Residues: 1-133, 'X', 135-1079 <RIC>
 A:Cross-references: GB:U10354
 A:Experimental source: kidney
 C:Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;197-212/Region: hydrophobic
F;613-635/Domain: transmembrane #status predicted <TM1>
F;650-670/Domain: transmembrane #status predicted <TM2>
F;683-700/Domain: transmembrane #status predicted <TM3>
F;725-744/Domain: transmembrane #status predicted <TM4>
F;770-790/Domain: transmembrane #status predicted <TM5>
F;806-828/Domain: transmembrane #status predicted <TM6>
F;841-860/Domain: transmembrane #status predicted <TM7>
F;90-261-287-386-468-488-594-893-1005/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;994/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;899-901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 73.9%; Score 3996; DB 2; Length 1079;
Best Local Similarity 73.7%; Pred. No. 3.1e-284;
Matches 780; Conservative 85; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAQLHQLLFLGFTLLQSNVSGYGNQRAQKGGIILGLPIIHFGVAAKQDLSRPE 60
DB 1 MASYSCLALLAL- ---AWHSSAYGPDQRAQKGGIILGLPIIHFGVAAKQDLSRPE 56
QY 61 ATKIRYFRGFWLQAMIFAEIENNSMTPLNITLGYRIFDTCTNTYSKALEATLSFVA 120
DB 57 SVCEIRYFRGFWLQAMIFAEIENNSMTPLNITLGYRIFDTCTNTYSKALEATLSFVA 116
QY 121 QNKIDSLNDFNCSDHPISTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 180
DB 117 QNKIDSLNDFNCSEHPISTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 176
QY 181 KNEYKAFRTIPNDEQATAMAEIIEHFQWNVGTAAADDDYGRGIDKFEREEAVKRDIC 240
DB 177 KNOYKSLRTIPNDEQATAMAEIIEHFQWNVGTAAADDDYGRGIDKFEREEAVKRDIC 236
QY 241 IPSEMSIYYTQKLEFIADVIQNSAKVIVVFSNGPDLEPLIOEIVRNITRIWLAS 300
DB 237 IDPSLISQYSDEEIIQVVEIQNSAKVIVVFSNGPDLEPLIOEIVRNITRIWLAS 296
QY 301 EAWASSLLIAPEYFHVVGTTGTFALRAGRIIPGNKFLKEVHPSRSSNGVFKFWETFP 360
DB 297 EAWASSLLIAPEYFHVVGTTGTFALRAGRIIPGNKFLKEVHPSRSSNGVFKFWETFP 356
QY 361 NCYFEKTLTQLK-NSKVPDSHPAAQGDGSKAGNSRRRTALRHPCITGEENITSVETPYLDY 419
DB 357 NCHLOEAGKGLPVDTFVRSH- ---EEGNRLNLS- STAFRLCTGDENINSVETPYWDY 411
QY 420 THLRISYNYVAVYIAHALQDIHCKPGTGFANGSCADIKKVEAWOVNHLHLKFTN 479
DB 412 EHLRISYNYVAVYIAHALQDIHCKPGTGFANGSCADIKKVEAWOVNHLHLKFTN 471
QY 480 SMGEQVDFDDQDGLKGNVYIINWQLSADESVLPHEVGNVYAYAKPSRLNINEKILLWS 539
DB 472 NNGEQVTFDECDLGVNYSIINWHLSPEDGSIVFKEVGYNYAKKGERLFINKEILLWS 531
QY 540 GRSKVVPNSCRDCVPTGRKGIIEGPTCCPECMACAEGFSDENDASATKCPNDFWS 599
DB 532 GFSREVVPNSCRDCVPTGRKGIIEGPTCCPECMACAEGFSDENDASATKCPNDFWS 591
QY 600 NENHTSCIAKETYLISWTEPFGIATIPAVLIGLITTSFVLGVFKFRNTPVVKATNRELS 659
DB 592 NENHTSCIAKETYLISWTEPFGIATIPAVLIGLITTSFVLGVFKFRNTPVVKATNRELS 651
QY 660 YLLFSLICCFSSSLIFIGEPDWTCLRLQPAFGISFVLCISCLVKTNRVLLVFEAKIP 719
DB 652 YLLFSLICCFSSSLIFIGEPDWTCLRLQPAFGISFVLCISCLVKTNRVLLVFEAKIP 711
QY 720 TSLHKKWGLNQLFLLVFLCILVQITCIIMLYTAPSSSYNHELEDEVIITCEGLSM 779
DB 712 TSFHRKWWGLNQLFLLVFLCITFMQLICIIMLYTAPSSSYNHELEDEVIITCEGLSM 771
QY 780 ALGFLIGYTCLLAAICFFFAFKSKRLPENFNEAKPIFMSLIFIVWISFIPAVSYTYGK 839
DB 772 ALGSLIGYTCLLAAICFFFAFKSKRLPENFNEAKPIFMSLIFIVWISFIPAVSYTYGK 831

QY 840 FVSAVEVIAIASSFGLLGCIFYFNKCYIILFKPCRNTEIEVRCSSTAHAFAKVAARATLRR 899
DB 832 FVSAVEVIAIASSFGLLGCIFYFNKCYIILFKPCRNTEIEVRCSSTAHAFAKVAARATLRR 891
QY 900 SAASRKSSSLCGSTISSPASSTCGPG- -----LTWE 930
DB 892 PNISRKSSSLGSGTSGIPSSSISSKNSNDRFPQPERKQKQPLSLTQOEQQQPLTLH 951
QY 931 MQ-----RCSTQKVSFGSGVTVLSLPEETGRVATLSRTARSNSADGRSGDDLPSR 982
DB 952 PQQQQQPQPRCK-QKVFISGVTLSLSPDEPKNAHNRNQRNQLSLEAQRNNTLGR 1010
QY 983 HHDQGPQKCEPQFANDARYKAAFTKGTLESPPGSKERP 1021
DB 1011 H-----QALLPQCADADSEMTIQETGLQGPWVGDPH 1043

RESULT 5

JH0562
metabotropic glutamate receptor 3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0562
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002; PMID:1309649
A:Accession: JH0562
A:Molecule type: mRNA
A:Residues: 1-879 <TM>
A:Cross-references: UNIPROT:P31422
A:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of functions by me
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
F;577-599/Domain: transmembrane #status predicted <TM1>
F;614-634/Domain: transmembrane #status predicted <TM2>
F;646-664/Domain: transmembrane #status predicted <TM3>
F;689-709/Domain: transmembrane #status predicted <TM4>
F;735-756/Domain: transmembrane #status predicted <TM5>
F;770-791/Domain: transmembrane #status predicted <TM6>
F;804-828/Domain: transmembrane #status predicted <TM7>
F;208,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 21.2%; Score 1145; DB 2; Length 879;
Best Local Similarity 32.0%; Pred. No. 1.8e-75;
Matches 306; Conservative 159; Mismatches 362; Indels 128; Gaps 33;

QY 7 QLFLF-----GFTL-LOSNVSGYGNQRAQKGGIILGLPIIHFGVAAKQDLSRPE 60
DB 8 QILMLALFKSGFTLSLGDHNF- ---RREIKTEGLVLGLGLFPIN- -----EKGTG 53
QY 61 ATKIRYN- FRGFRWQAMIFAEIENNSMTPLNITLGYRIFDTCTNTYSKALEATLSFV 119
DB 54 TEBCGRINEDRGRIQRLLEMLPAIDINKDNYLLPGVGLVHLDTCRSRTYALEQSLEFV 113
QY 120 --AQNKIDSLN---DEFNCSDHIPSTIA-VVGATGSGISTAVANLLGLFYIPQVSYAS 173
DB 114 RASLTQVDEAEYMCPPDGSAIQENIPLIAGVIGSSVSIVQVANLLRLFLQIPQISYAS 173
QY 174 SSRLLSNKNEYKAFRTIPNDEQATAMAEIIEHFQWNVGTAAADDDYGRGIDKFEREE 233
DB 174 TSAKSDSKRYDYFARTVPPDFYQAKMAEIRFFNWTYVTVSAGEGYGETGIBAFQE 233
QY 234 AVKRDICIDSEMSIQQYTTQKLE-FIADVIONSSAKVIVVFSNGPDLEPLIOEIVRNITRI 292
DB 234 ARLNRNICIAETAKVGRSNIRKSYDVSIVRELLQKPNARVVVLFMRDSDRELIAAANRVN- 292
QY 293 TDRWLASAWASSSLIAKPEYFHVVGTTGTFALRAGRIIPGNKFLKEVHPSRSSNGV 352

293 ASFTWASDGGWGAQESIVKGE-HVAYGAILTELASHPVQDFRYFQSLNPNHRRPWF 351
 353 KEFWEETNCFVTEKTLTQLKNSKVPKSHGPAQDGGKAGNSRRTALRHPCTSEENTSV 412
 352 RDFWEQKFC-----SLQNK-----NHRQVCDKHLAIDSSN--- 383
 413 ETPVLDYTHLRISYNYVAVSYIAHALQDI-HSCKPGTGIFANGSCADIKKVAQWVLN- 470
 384 ---YEQSKIMFVN---AVYMAHALHMKORTLCNPT-----TKLCDAMKILDG 427
 471 -----HLLHLKFTNSMGEQ-----VDFDQDGLKNGYTIINQLSAEDESULFHEVGN 518
 428 KKLYKEYLLKINFTAPFNPNKAGDSIVKFDFTFGDMGRYVNFNLQQTGGKYSYL--KVGH 485
 519 YNAVAKSDRLNINEKILMWSGFKVVPFNSCRDQVPGTRKGIIEGBCPCCECMACAE 578
 486 W-----AETLSLDVDSIHWRSN--VPTSCSDPCAPNEMKNMQPGD-VCCWICICEP 536
 579 GEFSDENDASACTKCPNDFWSENHSTCIAKEIEBYLSWTEPFGIALTIFAVLGLITSV 638
 537 YEYL--VDEFTCMDCGPGQWPTADLSGCYNLPEDYIKWEDAWAIGPVTTIACLGFLCTCIV 594
 639 LGVFIKFTNTIVKATNRELKSYLLFSLICFSSSLFIPGEPDWTCELQPAFGISFVL 698
 595 ITVFIKHNTPLVKASGRELCTYLLFGVSLSYCMVTFPIAKPSVICALRLGLGTGFAI 654
 699 CISCILVKNRVLLVFEAKIPTSLHRKWVGNLQFLVFLC---ILVQIVTCTIILWLTAP 755
 655 CYSALLTKTNCIARIEDGVKNGAQPXKPISSQ---VFICGLGLILVQIVMVSVMILET 711
 756 PSSYRNHELED--EVIFITC---DEGSLMALGFLIGYTCLLAAICFFPFAPKSRKLPENFN 810
 712 PGT-RRYTLPEKRETVILKCNVDSMLISL---TYDWLVILCTVYAFKTRKCPENFN 766
 811 EAKFTFSLMFFIWNISFIYAYSTYKGF--VSAVEVAILLAGSLGLGCIYFNKCVII 868
 767 EAKFTGFTYTTCTIILWLAFLPIFYVTSDDYRVQITMTCISVLSGVFVGLCLFAPKXIV 826
 869 LFKPCRNTEIEVRCSAAHAFKVAARATLRRSAASRKSLSLQ-----STISS 917
 827 LFQPKQNVVTH---RLHLNRFVSCTATYSQSSASTVPTVCNGREVLDSTSS 878

RESULT 6
 JC7160
 metabotropic glutamate receptor subtype 3 precursor - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
 C.Accession: JC7160
 R.Minoshima, T.; Nakanishi, S.
 J. Biochem. 126, 889-896, 1999
 A.Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3
 A.Reference number: JC7160, MUID:20012997, PMID:10544282
 A.Accession: JC7160
 A.Molecule type: DNA
 A.Residues: 1-879 <MIN>
 A.Cross-references: GB:AF170696
 C.Genetics:
 A.Gene: mGluR3
 C.Superfamily: metabotropic glutamate receptor 4
 C.Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>
 F:577-599/Domain: transmembrane #status predicted <TM1>
 F:614-634/Domain: transmembrane #status predicted <TM2>
 F:646-664/Domain: transmembrane #status predicted <TM3>
 F:689-709/Domain: transmembrane #status predicted <TM4>
 F:735-756/Domain: transmembrane #status predicted <TM5>
 F:770-791/Domain: transmembrane #status predicted <TM6>
 F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match 21.0%; Score 1137; DB 2; Length 879;
 Best Local Similarity 32.1%; Pred. No. 7.1e-75;

Matches 295; Conservative 152; Mismatches 361; Indels 112; Gaps 29;
 33 KGDILGLGFFPHFGVAAQDQLKSRPEATKCIRYN-PRGFRWLQAMIFAIEEINNSMTF 91
 36 EGDVLGGLGFFPN-----EKGTEECRCGNEDEGIGORLEAMLAFAIDEINKDNYL 85
 92 LPNITLGYRIFPTONTVSKALEATISFV--ANQKIDSLNL-----DEFCNSDHPSTIA-V 145
 86 LPGVKLGVLHDTCSRDTYALEQSLFEFVRASLTQVDEAYMCPDGSYAIQENIPILLIAGV 145
 146 VGNATSGSISTAVANLLGLEFVPOVSVASSRLLSNKNKYEKAFRLTIPNDEQOQATMAEII 205
 146 IGGSSVSVSIQVANLLRULFQISYSTASAKLSKSRDYFARTVFPDPFYQAKAMAEIL 205
 206 EHFQMNWVGTAAADDDYGRPGIDKFREEAVKRDICIDFSEMISQYTKQLE-FIADVIQ 264
 206 RYENMYTVSTVASEGDTGETIEAPEQEARLNICIATAEKVGRNIRKSYDSVIRELIQ 265
 265 NSAKVIVVPSNGPDLPLIQIIVRNITDRWLASEAWASSSLIAKPIFYFHVVGTTGCF 324
 266 KPNARVVVLFMRSDSDRELIAAASRYN-ASFRTWASDGMGAQESIVKGE-HVAYGAILT 323
 325 ALRAGRIPGFNKFLKRVHPSRSDNGFVKEFEETFCYFTEKTLTQLKNSKVPKSHGPA 384
 324 ELASHPVRFQDFYFQSLNPNHNNHNPFRDFWEQKFC-----SLQNK----- 367
 385 QDGSKAGNSRRTALRHPCTGEBNITSVTPYLDYTHLRISYNYVAVSYIAHALQDIHS 444
 368 -----NHRQICDKHLAIDSSN-----YEQSKIMFVN---AVYMAHALHMKOR 409
 445 --CKPGTGIFANGSCADIKKVEAWQLNHLHLKFTNSMGEQ-----VDFDQDGLKGN 496
 410 TLCPTNTKLCDAWKILDGKKL-----YKDYLLKINFTAPFNKNGADSIKVFDTYDGMGR 465
 497 YTIINQLSAEDBSVLFEHVGNTNAYAKP---SDRLNINEKILMWSGFKVVPFNSCRD 553
 466 YNVFN-----FQHIGGKYSYLKVGHMAETLYLDVDSIHWRSN--VPTSCSDP 512
 554 CVPGRKRIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWSENHSTCIAKEIEY 613
 513 CAPNEMKNMQPGD-VCCWICICEPEYEL--VDEFTCMDCGPGQWPTADLSGCYNLPEDY 569
 614 LSWTEPFGIALTIFAVLGLITISFVLGVFIKFTNTIVKATNRELKSYLLFSLICCFSS 673
 570 IRWEDAWAIGPVTTIACLGFMCTCIVTFIKHNTPLVKASGRELCTYLLFGVSLSYCM 629
 674 LFIPEPRDWTCLRQPAFGISVLCISLIVKTNRVLLVFEAKIPTSLHRKWVGNLQF 733
 630 FFFIAKSPVICALRLRLGLGTSPACVSAITKNCIARIFDGVKNGAQRPKFISPSQ- 688
 734 LLYFLC---ILVQIVTCTIILWLTAPSSYRNHELED--EVIFITC---DEGSLMALGFLI 785
 689 --VFICGLGLILVQIVMVSVMILETPTGT-RRYTLPEKRETVILKCNVDSMLISL---- 741
 786 GYTCLLAAICFFPFAPKSRKLPENFNEAKFTFSGMLIFFIWNISFIYAYSTYKGF--VSA 843
 742 TYDVVLVILCTVYAFKTRKCPENFNEAKFTGFTMYTTCTIILWLAFLPIFYVTSDDYRV 801
 844 VEVITAILASSFGILLGCIYFNKCVIIILFKPCRNTEIEVRCSAAHAFKVAARATLRRSA 903
 802 TMCISVLSGSLGVGLCLFAPKXIVILFQPKQNVVTH---RLHLNRFVSCTATYSQSSA 858
 904 RKRSSSLCG-----STISS 917
 859 STYVPTVCNGREVLDSTSS 878

RESULT 7
 JH0563
 metabotropic glutamate receptor 4 precursor - rat
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C.Accession: JH0563; I58149

R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A;Title: A family of metabotropic glutamate receptors.
A;Reference number: JH0561; MUID:92110002; PMID:1309649
A;Accession: JH0561
A;Molecule type: mRNA
A;Residues: 1-912 <TAN>
A;Cross-references: UNIPROT:P31421
A;Experimental source: brain
R;O'Hara, P.J.; Sheppard, P.O.; Thogersen, H.; Venezia, D.; Haldeman, B.A.; McGrane, V.;
Neuron 11, 41-52, 1993
A;Title: The ligand-binding domain in metabotropic glutamate receptors is related to bac
A;Reference number: 158149; MUID:9332699; PMID:8338667
A;Accession: I58149
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-123, 'R', 125-912 <RES>
A;Cross-references: GB:M90518; NID:G205400; PIDN:AAA931190.1; PID:G205401
C;Comment: This protein is coupled to a G protein and evokes a variety of functions by m
C;Genetics:
A;Gene: GLUR4
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-912/Product: metabotropic glutamate receptor 4 #status predicted <MET>
F;588-610/Domain: transmembrane #status predicted <TRI>
F;625-645/Domain: transmembrane #status predicted <TII>
F;657-675/Domain: transmembrane #status predicted <III>
F;700-720/Domain: transmembrane #status predicted <TIV>
F;751-772/Domain: transmembrane #status predicted <TEV>
F;786-807/Domain: transmembrane #status predicted <TVI>
F;822-847/Domain: transmembrane #status predicted <VII>
F;96,301,454,484,569/Binding site: carboxylate (Asn) (covalent) #status predicted
F;621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 20.6%; Score 1115.5; DB 2; Length 912;
Best Local Similarity 31.4%; Pred. No. 2.8e-73;
Matches 293; Conservative 167; Mismatches 350; Indels 133; Gaps 31;

QY 34 GDIILGGLPPIHFGVAADQDLKSPKPCIRYNFRGRLQAMFAIBENINSMFLP 93
DB 47 GDIILGGLPPIHFGVAADQDLKSPKPCIRYNFRGRLQAMFAIBENINSMFLP 97
QY 94 NITLGRILDTCTNTVSKALEATLSFAONKIDSLNLDPCNSDHP-----STIAVVG 147
DB 98 NITLGRILDTCTNTVSKALEATLSFAONKIDSLNLDPCNSDHP-----STIAVVG 155
QY 148 ATGSGISTAVANLLGLFVYIPQVSASSRLLSNKNEYKAFLETPNDQQATAMAEIIEH 207
DB 156 ASGSSVSIWVANILRLFKIPQISYASTAPDLSDNSKRYDFSRVPSDYQAQAVDIVRA 215
QY 208 FQWNVGTLAADDVCRPIDKPEREAVR-DICIDFSEMISQYTKQLRP-----IADVI 263
DB 216 LKWNVYTLASSGSGESGVEAFIQKRENGVCVIAQVKIPR--EPKTKGFDFKIIKRL 273
QY 264 QNSSAKVIVFNGPDLEPLIQEIYRNRITDR-IWLASEAWASSL-LAKEPEYHVVGVT 321
DB 274 ETSNARGIIIFANEDDIRVLEAARRAQTGHFWGSDSGSKSAPVRLLE--EVAEGA 331
QY 322 IGFAIRAGRIPOGFKLKEVHPSRSDNG----FVKREWETFCNYFFTEKTLTKLNKSKV 377
DB 332 VTILPKRMSVRFGRDYFS-----SRTLNNRRNRNIMFAEFWEDNPFCKLSRHALKKGSHIK- 386
QY 378 PSHPGAAQGDGSKAGNSRRRTALRHPCTEGEMITSVETPYLDYTHLRISYNNVVAVSIH 437
DB 387 -----KCTNREI-GQDSAYEKGKQP---VIDAVYANGH 418
QY 438 ALQDTHS--CKPGTGIFANGCADIKKVEAWQVLNHLHFKTNSMGQVDQDQGLKG 495
DB 419 ALHAMHRLIC-PG-----RVGLCPRPDPVDTGQLLKYIRNVNFSGIAGNPFVTFNENGDPAG 473
QY 496 NYTLINWQI---SABDESIVLHEVGNYNAYAKPSDRNLNINEKKILWSGFSKVPFNSCR 552

DB 474 RYDIYQYQLRNGSAE-----YKVGSMWTDHLHLRIERMQWPGSQQLPRISCSL 522
QY 553 DCVPGTRKGIIEGPTCCFECMACBEGFSDENDASACTCPNDFWNENHTSCIAKEIE 612
DB 523 PCQFGERKTKVG-MACCHCEPCTGYQ--QVDRYTKCTCPYDMRPTENRTSCQPIPIV 579
QY 613 YLSWTEPFGIALTIFAVLGLITLITSVGLGVKIKRNTPIVKATNRELSYLLLSLCOFSS 672
DB 580 KLEWDSFWAVLPFLAVGVGAATLVVVTVFVRNDPIVKAASGRELSYVLAGIFLCYAT 639
QY 673 SLIFIGEPDWTCLRPAPFGIFVLVCISILVKNRVLVFEAKIPTSLHRKXWGLNLQ 732
DB 640 TFLMIAEPDLGTCSLRIFLGLGMSISYAALLTKNRIYRIFEQGRSVSAPRIFSPASQ 699
QY 733 FLAVFLCILVQIVTCITLWLTAPSSVYNHLEDEVF-----ITCDEGSMALGFL 784
DB 700 LAITFIIISQLGICVWFVDP--SHSVVDFOQRTLDPRFARGVLKDISL-SLICL 756
QY 785 IGYTCLLAAICFFFAFKSRKLPENFEAKETFSMLIFFIWNISFIPAYVSTYKGFVSAY 844
DB 757 LGYSMLLWVTCTVVAIKTRGVPTENAEKPIGFTWVTCIVLWLAIFIP--FGTSQAD 813
QY 845 EV-----IAILASSFGLIGCIYFNKCVIILFKPCRNTEIEVRCSTAHAFKVAARAT 896
DB 814 KLIQTTLTVSVLSASVSLGMLYMPKVYIILFHPEQNVNPKRSLKA-----VVTAAT 868
QY 897 LRRSAASR-----KRSSSLGSGTSSPASST 922
DB 869 MSNKFTQKGNFRNGEAKSELCL-ENLETPALAT 900

RESULT 8
JH0561
metabotropic glutamate receptor 2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JH0561
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A;Title: A family of metabotropic glutamate receptors.
A;Reference number: JH0561; MUID:92110002; PMID:1309649
A;Accession: JH0561
A;Molecule type: mRNA
A;Residues: 1-872 <TAN>
A;Cross-references: UNIPROT:P31421
A;Experimental source: brain
C;Comment: This protein is coupled to a G protein and evokes a variety of functions by m
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
F;588-590/Domain: transmembrane #status predicted <TRI>
F;605-625/Domain: transmembrane #status predicted <TII>
F;637-655/Domain: transmembrane #status predicted <III>
F;680-700/Domain: transmembrane #status predicted <TIV>
F;726-747/Domain: transmembrane #status predicted <TEV>
F;761-782/Domain: transmembrane #status predicted <TVI>
F;795-819/Domain: transmembrane #status predicted <VII>
F;203,286,338,402,547/Binding site: carboxylate (Asn) (covalent) #status predicted
F;601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted
F;832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 20.6%; Score 1114.5; DB 2; Length 872;
Best Local Similarity 31.7%; Pred. No. 3.1e-73;
Matches 295; Conservative 150; Mismatches 366; Indels 119; Gaps 28;

QY 11 LGF-TLLOSINSGVGNQRA-QKKGDIILGLFPIHFGVAADQDLKSRPEATKIRYN 68
DB 5 LGFALLLLWGAVAEGPAKKVLTLEGLVGLGFLPVH-----QKGGP-AEECGPN 54
QY 69 -FRGFNLQAMFAIBENINSMFLPNTLGVRIEDTCNTVSKALEATLSFAONKIDSL 127
DB 55 EHRGQRLAMFLALDRINRDPHLLPGVRLGAIHLDSCSKDTHALEQALDFV-----RA 108

[illegible]

Db 306 IGSWSGSK---IAPVYQOEIEAGAVTILPKRASIDGDFRYSRRTLANNRRNVWPAEF 362
 QY 356 WEETENCYFTEKLTQLKNSKVPSHGPAAGDGGKAGNSRRRTALRHPCTGENTISVETP 415
 Db 363 SEGNGFC-----KSGSHG-----KNSHKKTGGLERAR-DSS 395
 QY 416 YLDYTHLRISYVAVYSIAHALQDIHS--CKPGTGFANGSCADIKKVEAWOVNLHL 473
 Db 396 YEQEKVQF---VIDAVYSMAVALHNMKELC-FG----YIGLPRVVTIDGKELGYIR 447
 QY 474 HLKFTNSMGEOVDFDQDGLKGNYYTINWQLSADESVLFHVGNYNAYAKSPDLNINE 533
 Db 448 AVNFNGSAGTPVTENENGDAFGYDIFQYQIN--NKSTEYKIIIGH-----TNQLHLKV 499
 QY 534 KKLWSGSKVPFNSCSDCVPGTRKGIIEGEPTCCPEOVACAEGBFSDENDASATKC 593
 Db 500 EDMQWANEHTHPASVCSLPCPKGBRKTIVKGPV-CWHGRC-EG-YNYQVDSLSCLC 556
 QY 594 PNDFWNSNHTSCIAKETEYLSWTPEFGIALTIFAVLGILITFSVLGVFIKFRNTPIVKA 653
 Db 557 PLDQRPINRTGCQRIPIIKLEWSPWAVPVLLAILGIIATTFFIVTFVRYNDPIVRA 616
 QY 654 TNRELSYLLSLCCFPSSLIIFGEPRDWTCLRQPAFGISFVLCISCLVKNRVLLV 713
 Db 617 SGRELSYLLGFIPLCYISITFLMAAPDTIICSPRRIFLGLMCFSYAALTKNRHRI 676
 QY 714 FEAKIPTSLHRKRWGLNQLVFLCILVQIVTCIIWLYTAPP-----SSYRHELEDE 767
 Db 677 FEQKKSVTAPKFISPAQLVITFSLISVQLLVFVWFVDPPTIIDYGEQRTLDPENA 736
 QY 768 VIFITCDGSLMALGFLGYTCLLAAICFFPAFKSRKLPENFNBAKFTFSLMLFFIWI 827
 Db 737 RGVLCXDISDL-SLICSLGYSTLLMVTCTVVAIKTRGVPEFNEAKPIGFTMYTTCIWL 795
 QY 828 SFIPAVVSTYKGFSAVEV-----TAILASFGLLGCVYENKCVIILPKPCRNTEE 879
 Db 796 AFIPF---FGTAQAEKMYIQTTLTVMSLSASVSLGMLYMPKVYIIIFHPQNVQR 852
 QY 880 VRCSTAHAFAKVAARATLRRSAERKS-----SSLGSTISSPASST 922
 Db 853 KR-----SFKAVVTAATMQSKLIQKGNDRPNGEVKSELCELS-LEITNTST 896

RESULT 12
 JC2131
 metabotropic glutamate receptor 5 B - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
 C:Accession: JC2131
 R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
 Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
 A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
 A:Reference number: JC2131; PMID:94197696; PMID:7908515
 A:Accession: JC2131
 A:Molecule type: mRNA
 A:Residues: 1-1212 <MIN>
 C:Comment: this protein is coupled to guanine nucleotide binding proteins.
 C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
 F:580-604/Domain: transmembrane #status predicted <TM1>
 F:617-637/Domain: transmembrane #status predicted <TM2>
 F:644-664/Domain: transmembrane #status predicted <TM3>
 F:694-714/Domain: transmembrane #status predicted <TM4>
 F:738-759/Domain: transmembrane #status predicted <TM5>
 F:773-794/Domain: transmembrane #status predicted <TM6>
 F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 19.5%; Score 1056.5; DB 2; Length 1212;
 Best Local Similarity 28.5%; Pred. No. 9e-69;
 Matches 302; Conservative 196; Mismatches 422; Indels 139; Gaps 35;

QY 8 LLFLQFTLLQSNVSGYGNQR----AOKGDIILGGLFPIHFGVAAQDLKSRPATK 63
 Db 4 LLILSVLLKE-DVRGSAQSSERRVVAHPMGDIIGALFSVH-----HQPTVDKVERK 56

RESULT 13

A41939

G protein-coupled glutamate receptor - rat

QY 64 C--IRYNFRGRFRLQAMIFAIEBINNSMTFLNITLGYRIFDTCNTVSKALEATLSFVAQ 121
 Db 57 CGAVRQY-GIQRVAMWHTLERINSDPTLLNITLGEIRDSCHWHAVALDEQISFIRD 115
 QY 122 NKIDSNLNDFCNCSDFPST-----IAVVGATSGISTAVANLLGLFYIQQVSYASS 174
 Db 116 SLISSEEEGLVRCVDSGSSSPESKKPIGVIGPGSSVAIQVONLLQLFNIPQIAYSAT 175
 QY 175 SRLLSKNNEYKALRTIPNDEQOATAMABIIIEHFQNWVGTLLAADDDYGRPGIDKREBA 234
 Db 176 SMDLSKTLFKYPMRVPSDAQARAWDIVKRYNWTYVSAVHTEGNYESGHEAFKQMS 235
 QY 235 VKRDICIDISEMISQVYTKOLEFIADVION--SSAKVWFSNGSDLPLETOEIVRRI 292
 Db 236 AKEGICIAISYKISYNAGEQSPDKLKLKLTSLPKARVVACCEGVTVGLLMAWRRLGL 295
 QY 293 T-DRIMLASAWASSLIAKPEYFHVVGTFGIFALRAGRIPGFNKFLKEVHPSRSDNGF 351
 Db 296 AGEFLLLGSDGMDRYDVTGQREAVGG-ITIKLQSPDKWPFDDYLLKLRPETNHRNP 354
 QY 352 VKEFWEETENCY---FTEKTLTOLKNSKVPSHGPAAGDGGKAGNSRRRTALRHPCTGEEN 408
 Db 355 FQBFWQHRFQCRLEGPPQ-----ENSKY-----NKTCSNLSLTKTH----- 390
 QY 409 ITSVEPYLDYTHLRISYVYV--AVYSIAHALQDIH-SCKPGTGIFANGSCADIKKVEA 465
 Db 391 -----HVQDSKMGFVINAISYMAVGLHNMQMSLCPGYA---GLCDAMKPIDG 434
 QY 466 WQVNLHLHLKFTNSMGEOVDQDGLKGNYYTINWQLSADESVLFHVGNYNAYAKP 525
 Db 435 RKLLSLMKTNFTGVSQDITLEDNGDSPGRVEIMFMKMGKD---XYDINVGVSDNG 490
 QY 526 SDRLTNNEKKILWSGSKVPFNSCSDCVPGTRKGIIEGEPTCCPEOVACAEGBFSDEN 585
 Db 491 ELKMDDE---VMSKSNIR-SVCSEPCCKGQIVIRKGEVSCCWTCTPCKENY--VF 544
 QY 586 DASACTKPNDFWNSNHTSCIAKETEYLSWTPEFGIALTIFAVLGILITFSVLGVFIK 645
 Db 545 DEYTKACQLGSWPTDGLTCDLIPQVYLRWGDPEPIAAVFACLGLLATLFTVVVFIIY 604
 QY 646 RNTPIVKATNRELSYLLSLCCFPSSLIIFGEPRDWTCLRQPAFGISFVLCISCLV 705
 Db 605 RDTPVVKSRELCYIILAGICLGYLCTCLIAKQIYCYLQRIQIGISPMASYALVT 664
 QY 706 KTNRVLLVF---BAKIPTSLHRKRWGLNQLVFLCILVQIVTCIIWLYTAPPSSYRNH 762
 Db 665 KTNRIARILAGSKKIKCTKKPR-FMSACAQLVIAFLICIQLGIIIVAFIMEPPDIMHDY 723
 QY 763 ELEDEVIFITCDGSLMALGFL--IGYTCLLAAICFFPAFKSRKLPENFNBAKFTFMSL 820
 Db 724 PSIREV-YLICNTTN--LGVVTPLGYNGLLISCTFFYAFKTRNVNPANFEAKYTAFTWY 779
 QY 821 IFFIVMISPIPAYVSTYKGFSAVEVIAILASFGLLGCVYENKCVIILPKPCRNTEE 880
 Db 780 TTCIILWAFVPIYFGSNYKIIIMCFVSLSATV--ALGCMFVPKVYIILAKERNVRSAP 837
 QY 881 RCTAAHAFKVAARATLRRSAERKSLSIC-----GSTISSPASSTCGPGITMEMQR- 933
 Db 838 TTSTV-----VRMHVGDGKSSAASSSSLVNLKRGSS-----GETLRYKDRRL 883
 QY 934 -----CSTQKVSPGS-GTVTLSLSFEETGRYATLSRTASRSNADGRSGDDLPSR-- 982
 Db 884 AQHSIEIEFTPKSGMNGRATMSSS---NGKSVTWAQNEKSSR-----CGHLWQLRS 934
 QY 983 ---HHDQGPQKC--EPQPANDARYKAAPTKGTLESPPG 1016
 Db 935 IHINKENPNQTAIVKPPFKSTESRGLGPGRGAGGSAGG 973


```
Db 296 GEFLLGSGWADRVDTGQYREAVGG-ITIKLQSPDVKWFDDYYLKLRETNLRNPF 354
Qy 353 KEFWEETENCY---FTEKTLTQLKNSKVPFSGHPAAQGGQKAGNRRRTALRHPCTGEENI 409
Db 355 QEFWQHRFCRLGFAQ-----ENSKY-----NKTCSNLSLRLTH----- 389
Qy 410 TSVETPYLDYTHLRISYNYVY--AVYSTAHALQDIH-SCKPGTGIFANGSCADIKKVEAW 466
Db 390 -----HVQDSKMGFVFNATYSMAYLHNMQSLCPGYA-----GLCDAMKPIDGR 434
Qy 467 QVLNHLHLKFTNSGEOVDQDGLKGNNTIINWLSAEDSVLFHEVGNVYAYAKPS 526
Db 435 KLLDSLMKTNFTGVSGDMLFDENGSDPGRYEIMNFKEMGKD----YFYINVGSDNGE 490
Qy 527 DLNINNEKKILNFGSKVVPFNSCRSDCVPTGRKGIIEGPTCCPECMACAEGFSDND 586
Db 491 LKWDDE---VMSKKNIIIR-SVCSEPCCKGQIKVIRKGEVSCCWTCTPCKENY--VF 544
Qy 587 ASACTKCPNDFNSNHNHTSCIAKETYSWTEPPFGIALTIIPAVLGILITSFVLGVFIKFR 646
Db 545 EYTCACQLGSWPTDGLTGCGLIPVQYLRWGDPEPIAAVVFACUGLLATLFTVVFIIYR 604
Qy 647 NTPVIAKTNRELKSLFLLSCFSSSLIFIGEPDWTCLRPQAFGIFSLCISILV 706
Db 605 DTPVVKSSRELCTIILAGICLGLCTCLIAKPKQIYCYLQRIIGIGLSPAWSYALVTK 664
Qy 707 TNRVLLVF---EAKPTSLHRKWGLNQFLVFLCILVQIVTCIILWLYTAPPSSYRNHE 763
Db 665 TNRIARILAGSKKIKCTKKPR-FMSACAQLVIAFILIQIQLGIIIVAFIMEPPDIMHDP 723
Qy 764 LEDEVIFITCDGSLMALGFL--IGYTCLLAAICFFFAFKRKLPEPNEAKFITFSLI 821
Db 724 SIREV-YLICNTN---LGVVTPLYNGLLILSCITFYAFKTRNVPANENAKYIAFTMYT 779
Qy 822 PFIWISIPAVSYTYGFVSAVEVAILASSGLLGCITYFNKCVIILFKPCRNITIEVR 881
Db 780 TCIIWLAFVPIYFGSNYKIITMCFVSLSATV--ALGCMFVPKVIILAKPERNVRSAFT 837
Qy 882 CSTAAHAFKVAARATLRSAASRKSSSI-----CGSTISSPASSTCGPGLTMBQ 932
Db 838 TSTV-----VRMHVGDGKSSAASRSSLVNLWKRGSSETLSN-----GKSVTWAQN 887
Qy 933 RCST-----QKVSPF-----GSG----- 944
Db 888 EKSTRGQHLWQLSVEINKENPNQTAIVKPPKSTENRGPAAGGGSGPGVAGAGNAG 947
Qy 945 -TVT-----LSLSPEETGR-----YATLSRTARSNSADGESGDDL 979
Db 948 CTAATGPPPDAGPKALYDVAEABESFPAAKPRSPISITLSHLGSA-----GRTDGDA 1003
Qy 980 PSRHH 985
Db 1004 PSLHSE 1009

RESULT 15
JC2132
metabotropic glutamate receptor 5 A - human
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2132
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: JC2131, MUID:94197696; PMID:7908515
A:Accession: JC2132
A:Molecule type: mRNA
A:Residues: 1-1180 <MN>
C:Comment: This protein is coupled to guanine nucleotide binding proteins.
C:Keywords: G-protein; neurotransmitter; receptor; transmembrane protein
F:580-604/Domain: transmembrane #status predicted <TM1>
F:617-637/Domain: transmembrane #status predicted <TM2>
```

```
F:644-664/Domain: transmembrane #status predicted <TM3>
F:694-714/Domain: transmembrane #status predicted <TM4>
F:738-759/Domain: transmembrane #status predicted <TM5>
F:773-794/Domain: transmembrane #status predicted <TM6>
F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 19.2%; Score 1040; DB 2; Length 1180;
Best Local Similarity 27.7%; Pred. No. 1.4e-67;
Matches 299; Conservative 197; Mismatches 435; Indels 150; Gaps 33;

Qy 8 LLFLGFTLLSYNVGYPNQNR---AQRKGDILGLFPIHFGVAAKQDQLKSRPEATK 63
Db 4 LLILSVLLKE-DVRGSAQSSERRVAHMFQDIIIGALFSVH-----HQPTVDKVERK 56
Qy 64 C--IRYNFRGFRWLQAMIFAEIENNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVAQ 121
Db 57 CGAVREQY-QIQRVEAMLHTLERINSDPTLPLNITLGEIRDSCHMSVALEISIFIRD 115
Qy 122 NKIDSLNLDNCFNCSDHIPST-----IAVVGATGSGISTAVANLLGFIYIPQVSYASS 174
Db 116 SLISSEEEGLVRCVDGSSSSFRSKPIYGVIGVSGSSVAIQVONLLQLENIPQIAYSAT 175
Qy 175 SRLLSNKNYKAFRLTIPNDEQOATAMAEIIHFQNNWVGTLAADDYDGRPGIDKREEA 234
Db 176 SMDLSKDTLFKYFMRVVPVSDAQARAMVDIVKRYNWTYVSAVTEGNYGESGMEAFKDS 235
Qy 235 VKSDICIDRESEMISQYYTOKOLEFIADVIQN--SSAKVIVFVNSGPDLEPLIQEIVERNI 292
Db 236 AKGICIAHSYKIYSNAGEOSFDKLKLTSHLPKRVVACFCEGTVTRGLIMAMERLGL 295
Qy 293 T-DRIMLASAWASSLIAPKEFYHVVGTTIGFALRAGRIPGFNKLKEVHPSSSDNGF 351
Db 296 AGEFLLGSGWADRVDTGQYREAVGG-ITIKLQSPDVKWFDDYYLKLRETNLRNPF 354
Qy 352 VKSEWETENCY---FTEKTLTQLKNSKVPFSGHPAAQGGQKAGNRRRTALRHPCTGEEN 408
Db 355 QEFWQHRFCRLGFAQ-----ENSKY-----NKTCSNLSLTKH----- 390
Qy 409 ITSVPYLDYTHLRISYNYVY--AVYSTAHALQDIH-SCKPGTGIFANGSCADIKKVEA 465
Db 391 -----HVQDSKMGFVFNATYSMAYLHNMQSLCPGYA-----GLCDAMKPIDG 434
Qy 466 WQVINHLHLKFTNSGEOVDQDGLKGNNTIINWLSAEDSVLFHEVGNVYAYAKP 525
Db 435 RKLESIMKTNFTGVSGDITLFDENGSDPGRYEIMNFKEMGKD----YFYINVGSDNG 490
Qy 526 SDRINNEKKILNFGSKVVPFNSCRSDCVPTGRKGIIEGPTCCPECMACAEGFSDEN 585
Db 491 ELKMDDE---VMSKKNIIIR-SVCSEPCCKGQIKVIRKGEVSCCWTCTPCKENY--VF 544
Qy 586 DASACTKCPNDFNSNHNHTSCIAKETYSWTEPPFGIALTIIPAVLGILITSFVLGVFIK 645
Db 545 DEVTCACQLGSWPTDGLTGCGLIPVQYLRWGDPEPIAAVVFACUGLLATLFTVVFIIY 604
Qy 646 RNTPIVIAKTNRELKSLFLLSCFSSSLIFIGEPDWTCLRPQAFGIFSLCISILV 705
Db 605 RDPVVKSSRELCTIILAGICLGLCTCLIAKPKQIYCYLQRIIGIGLSPAWSYALV 664
Qy 706 KTNRVLLVF---EAKPTSLHRKWGLNQFLVFLCILVQIVTCIILWLYTAPPSSYRNH 762
Db 665 KTNRIARILAGSKKIKCTKKPR-FMSACAQLVIAFILIQIQLGIIIVAFIMEPPDIMH 723
Qy 763 ELDEVIFITCDGSLMALGFL--IGYTCLLAAICFFFAFKRKLPEPNEAKFITFSL 820
Db 724 PSIREV-YLICNTN---LGVVTPLYNGLLILSCITFYAFKTRNVPANENAKYIAFTMY 779
Qy 821 IFIWMISIPAVSYTYGFVSAVEVAILASSGLLGCITYFNKCVIILFKPCRNITIEV 880
Db 780 TTCIWLAFVPIYFGSNYKIITMCFVSLSATV--ALGCMFVPKVIILAKPERNVRSAF 837
Qy 881 RCSTAAHAFKVAARATLRSAASRKSSSI-----CGSTISSPASSTCGPGLTMBQ 931
Db 838 TSTV-----VRMHVGDGKSSAASRSSLVNLWKRGSSETLSN-----GKSVTWAQ 887
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 07:02:14 ; Search time 425 Seconds

(without alignments)

1390.376 Million cell updates/sec

Title: US-10-016-496-2

Perfect score: 5410

Sequence: 1 MAQLHCQLLFLGFTLLQSYN.....XGTLESPPGSKERTTWEET 1027

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	5410	100.0	1027	Q8J104	Q8J104 squalus aca
2	4044.5	74.8	1078	1 CASR HUMAN	P41180 homo sapien
3	3999.5	73.9	1085	1 CASR BOVIN	P35384 bos taurus
4	3996	73.9	1079	1 CASR RAT	P43442 rattus norv
5	3986	73.7	1079	2 Q80ZAB	Q80ZAB rattus norv
6	3976.5	73.5	1079	1 CASR MOUSE	Q9QY96 mus musculu
7	3728	68.9	941	2 Q6XAF1	Q6XAF1 salmo salar
8	3728	68.9	941	2 AAP79925	AAP79925 salmo sal
9	3721	68.8	941	2 Q6XAF3	Q6XAF3 salmo salar
10	3721	68.8	941	2 AAP79923	AAP79923 salmo sal
11	3705.5	68.5	940	2 Q90WL6	Q90WL6 sparus aca
12	3644.5	67.4	940	2 Q73635	Q73635 figu rubrip
13	3456	63.9	850	2 Q6XAF2	Q6XAF2 salmo salar
14	3456	63.9	850	2 AAP79924	AAP79924 salmo sal
15	2707.5	50.0	783	2 Q8CDP3	Q8CDP3 mus musculu
16	1879	34.7	880	2 Q73639	Q73639 figu rubrip
17	1804	33.3	856	2 Q73638	Q73638 figu rubrip
18	1790.5	33.1	864	2 Q73637	Q73637 figu rubrip
19	1776.5	32.8	848	2 Q93553	Q93553 carassius a
20	1772	32.8	912	2 Q70410	Q70410 mus musculu
21	1683.5	31.1	501	2 Q86UN7	Q86UN7 homo sapien
22	1611.5	29.8	854	2 Q6UNX3	Q6UNX3 ictalurus p
23	1611.5	29.8	854	2 AAP64679	AAP64679 ictalurus
24	1593	29.3	875	2 Q73640	Q73640 figu rubrip
25	1577.5	29.2	868	2 Q73636	Q73636 figu rubrip
26	1558	28.8	844	2 Q93552	Q93552 carassius a
27	1362	25.2	877	2 Q9FW88	Q9FW88 carassius a
28	1344.5	24.9	928	2 Q8K4Z6	Q8K4Z6 mus musculu
29	1335	24.7	928	2 Q70VB1	Q70VB1 rattus norv
30	1335	24.7	928	2 CAD59483	CAD59483 rattus no
31	1329.5	24.6	926	2 Q8NHZ9	Q8NHZ9 homo sapien

ALIGNMENTS

RESULT 1

ID	Q8J104	PRELIMINARY;	PRT; 1027 AA.
AC	Q8J104;		
DT	01-OCT-2002 (Tremblrel. 22, Created)		
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)		
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)		
DE	Calcium polyvalent cation receptor/salinity sensing protein.		
OS	Squalus acanthias (Spiny dogfish).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;		
OC	Elasmobranchii; Squala; Hypnosqualea; Squaliformes; Squaloidei;		
OC	Squalidae; Squalus.		
OX	NCBI_TaxID=7797;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RX	MEDLINE=22103704; PubMed=12093923;		
RA	Nearing J., Betka M., Quinn S., Hentschel H., Elger M., Baum M.,		
RA	Bai M., Chattopadhyay N., Brown E.M., Hebert S.C., Harris H.W.;		
RT	"Polyvalent cation receptor proteins (Cars) are salinity sensors in fish."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:9231-9236 (2002).		
DR	EMBL; AF406649; AAM77700.1; -		
DR	HGSP; P23385; IEWK.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . . ; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR001828; ANF_receptor.		
DR	InterPro; IPR000337; GPCR_Mgr.		
DR	InterPro; IPR011500; NCD3G_GPCR.		
DR	Pfam; PF00003; 7tm_3; 1.		
DR	Pfam; PF01094; ANF_receptor; 1.		
DR	Pfam; PF07582; NCD3G; 1.		
DR	PRINTS; PR00592; CASENSINGR.		
DR	PRINTS; PR00248; GPCRNGR.		
DR	PROSITE; PS00979; G_PROTEIN_REC_P3_1; 1.		
DR	PROSITE; PS00980; G_PROTEIN_REC_P3_2; UNKNOWN_1.		
DR	PROSITE; PS00981; G_PROTEIN_REC_P3_3; 1.		
DR	PROSITE; PS00259; G_PROTEIN_REC_P3_4; 1.		
DR	Receptor.		
SK	SEQUENCE 1027 AA; 114412 MW; 189FF1E323B5B7C7 CRC64;		

Query Match	100.0%; Score 5410; DB 2; Length 1027;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1027; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MAQLHCQLLFLGFTLLQSYNVSQYGNQAKKGDIIILGGLPIHFVGAAKODLSRPE 60
Db	1 MAQLHCQLLFLGFTLLQSYNVSQYGNQAKKGDIIILGGLPIHFVGAAKODLSRPE 60
Qy	61 ATTCIRNFRGFRWLQAMIPAEIENNSMTFLPNITLGYRIPTCNTVSKALEATLSFVA 120
Db	61 ATTCIRNFRGFRWLQAMIPAEIENNSMTFLPNITLGYRIPTCNTVSKALEATLSFVA 120

QY 121 QNKIDSLNDEFNCSDHPISTIAVVGATGSGISTAVANLLGLFIPQVSVASSRLLSN 180
 Db 121 QNKIDSLNDEFNCSDHPISTIAVVGATGSGISTAVANLLGLFIPQVSVASSRLLSN 180
 QY 181 KNEYKAFILTIINDEQOQATAMAEIIEHPQWNVVGTAAADDDYGRGIDKPFEEAVKRDIC 240
 Db 181 KNEYKAFILTIINDEQOQATAMAEIIEHPQWNVVGTAAADDDYGRGIDKPFEEAVKRDIC 240
 QY 241 IDPSEMISSYYTQKOLEFIADVIQNSSAKVIVVFSNGPDLEPLIOEIVRRNITDRILWAS 300
 Db 241 IDPSEMISSYYTQKOLEFIADVIQNSSAKVIVVFSNGPDLEPLIOEIVRRNITDRILWAS 300
 QY 301 EAWASSLIAKEIYFHVVGTTGFPALRAGRIPGFNKFKEVHPSSSDNGFVKPFWETP 360
 Db 301 EAWASSLIAKEIYFHVVGTTGFPALRAGRIPGFNKFKEVHPSSSDNGFVKPFWETP 360
 QY 361 NCYFTEKTLTOLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420
 Db 361 NCYFTEKTLTOLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420
 QY 421 HLRISYNTVAVYSIAHALQDIHSCPKPTGTFPANGSCADIKKVEAWQVNLHLHLKFTNS 480
 Db 421 HLRISYNTVAVYSIAHALQDIHSCPKPTGTFPANGSCADIKKVEAWQVNLHLHLKFTNS 480
 QY 481 MGEQVDFDQDGLKGYNTIINQLSAEDSVLFHEVGNVNAVAKPSDRNLNNEKKILWSG 540
 Db 481 MGEQVDFDQDGLKGYNTIINQLSAEDSVLFHEVGNVNAVAKPSDRNLNNEKKILWSG 540
 QY 541 FSKVVPFNSCSDVCPGTRKGIIEGPTCCFCMACAEFSDENDASACTKCPNDFWSN 600
 Db 541 FSKVVPFNSCSDVCPGTRKGIIEGPTCCFCMACAEFSDENDASACTKCPNDFWSN 600
 QY 601 ENHTSCIAKEIYLSWTEPFGIATIFAVLGLITISFVLGVFIFKPNTPIVKATNRELSY 660
 Db 601 ENHTSCIAKEIYLSWTEPFGIATIFAVLGLITISFVLGVFIFKPNTPIVKATNRELSY 660
 QY 661 LLLFSLICCFSSLIFFIGPRDWTCLRQAPAGISFVLCISCLVKTNRVLLVPEAKIPT 720
 Db 661 LLLFSLICCFSSLIFFIGPRDWTCLRQAPAGISFVLCISCLVKTNRVLLVPEAKIPT 720
 QY 721 SLHRKVGWNLQFLVFLICILVQIVTCIILWYVTPAPPSSYRNHELEDEVIPTCDGSLMA 780
 Db 721 SLHRKVGWNLQFLVFLICILVQIVTCIILWYVTPAPPSSYRNHELEDEVIPTCDGSLMA 780
 QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWIWISFIPAYVSTYKGF 840
 Db 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWIWISFIPAYVSTYKGF 840
 QY 841 VSAVEVIALASSFGLGCIYFNKCYIILFKPCRNITIEVRCSTAAHAFKVAARATLRS 900
 Db 841 VSAVEVIALASSFGLGCIYFNKCYIILFKPCRNITIEVRCSTAAHAFKVAARATLRS 900
 QY 901 ASARXSSSLCSTISSPASSCTGGLTWMORCSTOKVSGSGVTVLSLFEETGRVAT 960
 Db 901 ASARXSSSLCSTISSPASSCTGGLTWMORCSTOKVSGSGVTVLSLFEETGRVAT 960
 QY 961 LSRTARSNSADGRSGDDLPSRHHDQGPQKCEPOPANDARYKAAPTGTLESPPGSKER 1020
 Db 961 LSRTARSNSADGRSGDDLPSRHHDQGPQKCEPOPANDARYKAAPTGTLESPPGSKER 1020
 QY 1021 PTTMEET 1027
 Db 1021 PTTMEET 1027

RESULT 2

CASR_HUMAN STANDARD; PRT: 1078 AA.
 ID P41180; Q13912; Q16108; Q16109; Q16110; Q16379;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid
 DE Cell calcium-sensing receptor).
 GN Name=CASR; Synonyms=GPRC2A, PCAR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP Pearce S.H.S., Thakker R.V.;
 RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 RL [2] SEQUENCE FROM N.A.
 RP TISSUE=Parathyroid;
 RX MEDLINE=95279439; PubMed=7759551;
 RA Garrett J.E., Capuano I.V., Hammerland L.G., Hung B.C., Brown E.M.,
 RA Hebert S.C., Nemeth E.F., Fuller F.;
 RT "Molecular cloning and functional expression of human parathyroid
 RT calcium receptor cDNAs.";
 RL J. Biol. Chem. 270:12919-12925(1995).
 RN [3] SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RX MEDLINE=95408281; PubMed=7677761;
 RA Aida K., Koishi S., Tawata M., Onaya T.;
 RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
 RT human kidney.";
 RL Biochem. Biophys. Res. Commun. 214:524-529(1995).
 RN [4] SEQUENCE FROM N.A.
 RP MEDLINE=96343808; PubMed=8756555;
 RA Freichel M., Zink-Lorenz A., Holloschi A., Hafner M., Flockerzi V.,
 RA Raue P.;
 RT "Expression of a calcium-sensing receptor in a human medullary thyroid
 RT carcinoma cell line and its contribution to calcitonin secretion.";
 RL Endocrinology 137:3842-3848(1996).
 RN [5] SEQUENCE OF 643-908 FROM N.A.
 RP MEDLINE=96193893; PubMed=861352;
 RA Bikle D.D., Ratnam A., Mauro T., Harris J., Pillai S.;
 RT "Changes in calcium responsiveness and handling during keratinocyte
 RT differentiation. Potential role of the calcium receptor.";
 RL J. Clin. Invest. 97:1085-1093(1996).
 RN [6] VARIANTS FHH GLN-185; LYS-297 AND TRP-795.
 RP MEDLINE=94094324; PubMed=7916660;
 RA Pollak M.R., Brown E.M., Chou Y.-H.W., Hebert S.C., Marx S.J.,
 RA Seidman B., Levi T., Seidman C.E., Seidman J.G.;
 RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial
 RT hypocalcemic hypercalciuria and neonatal severe hyperparathyroidism.";
 RL Cell 75:1297-1303(1993).
 RN [7] VARIANT ADH ALA-127.
 RP MEDLINE=95179179; PubMed=7874174;
 RA Pollak M.R., Brown E.M., Estep H.L., McLaine P.N., Kifor O., Park J.,
 RA Hebert S.C., Seidman C.E., Seidman J.G.;
 RT "Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor
 RT gene mutation.";
 RL Nat. Genet. 8:303-307(1994).
 RN [8] VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.
 RP MEDLINE=95243222; PubMed=7726161;
 RA Chou Y.-H.W., Pollak M.R., Brandi M.L., Toss G., Aronqvist H.,
 RA Atkinson A.B., Papapoulos S.E., Marx S., Brown E.M., Seidman J.G.,
 RA Seidman C.E.;
 RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause
 RT familial hypocalciuric hypercalcaemia.";
 RL Am. J. Hum. Genet. 56:1075-1079(1995).
 RN [9] SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
 RP MEDLINE=95403641; PubMed=7673400;
 RA Aida K., Koishi S., Inoue M., Nakazato M., Tawata M., Onaya T.;
 RT "Familial hypocalciuric hypercalcaemia associated with mutation in the

RT human Ca(2+)-sensing receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
 RN [10]
 RP VARIANTS NSHPT LEU-227 AND TYR-582.
 RX MEDLINE=96292293; PubMed=8675635;
 RA Pearce S.H.S., Trump D., Wooding C., Besser G.M., Chew S.L.,
 RA Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,
 RA Thakker R.V.;
 RT "Calcium-sensing receptor mutations in familial benign hypercalcaemia
 RT and neonatal hyperparathyroidism.";
 RL J. Clin. Invest. 96:2683-2692(1995).
 RN [11]
 RP VARIANTS F1H THR-116; HIS-681 AND SER-806, AND VARIANT SER-851.
 RX MEDLINE=96311554; PubMed=8733126;
 RA Baron J., Winer K.K., Yanovski J.A., Cunningham A.W., Laue L.,
 RA Zimmerman D., Cutler G.B. Jr.;
 RT "Mutations in the Ca(2+)-sensing receptor gene cause autosomal
 RT dominant and sporadic hypoparathyroidism.";
 RL Hum. Mol. Genet. 5:601-606(1996).
 RN [12]
 RP VARIANT F1H ARG-174.
 RX MEDLINE=97442275; PubMed=9298824;
 RA Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T.,
 RA Ratajczak T.;
 RT "A novel mutation (L174P) in the Ca2+-sensing receptor gene associated
 RT with familial hypocalcaemic hypercalcaemia.";
 RL Hum. Mutat. 10:233-235(1997).
 RN [13]
 RP VARIANT F1H VAL-616.
 RX MEDLINE=99415602; PubMed=10487661;
 RA Stock J.L., Brown R.S., Baron J., Coderre J.A., Mancilla E.,
 RA De Luca F., Ray K., Mericq M.V.;
 RT "Autosomal dominant hypoparathyroidism associated with short stature
 RT and premature osteoarthritis.";
 RL J. Clin. Endocrinol. Metab. 84:3036-3040(1999).
 RN [14]
 RP VARIANT F1H GLU-557.
 RX MEDLINE=21603957; PubMed=11762699;
 RA Nakayama T., Minato M., Nakagawa M., Soma M., Tobe H., Aoi N.,
 RA Kosegi K., Sato M., Ozawa Y., Kamatsuse K., Kokubun S.;
 RT "A novel mutation in Ca2+-sensing receptor gene in familial
 RT hypocalcaemic hypercalcaemia.";
 RL Endocrine 15:277-282(2001).
 CC -!- FUNCTION: Senses changes in the extracellular concentration of
 CC calcium ions. The activity of this receptor is mediated by a G-
 CC protein that activates a phosphatidylinositol-calcium second
 CC messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P41180-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P41180-2; Sequence=VSP_002035;
 CC -!- TISSUE SPECIFICITY: Found in kidney, but not in brain, lung,
 CC liver, heart, skeletal muscle, or placenta.
 CC -!- DISEASE: Defects in CASR are the cause of familial hypocalcaemic
 CC hypercalcaemia, type 1 (FHH) [MIM:145980]; in which the receptor
 CC has reduced activity. FHH is characterized by altered calcium
 CC homeostasis. Affected individuals exhibit mild or modest
 CC hypercalcaemia, relative hypocalciuria, and inappropriately normal
 CC PTH levels.
 CC -!- DISEASE: Defects in CASR are the cause of neonatal severe primary
 CC hyperparathyroidism (NSHPT) [MIM:239200]; in which the receptor
 CC has reduced activity. NSHPT is a rare autosomal recessive life-
 CC threatening disorder characterized by very high serum calcium
 CC concentrations, skeletal demineralization, and parathyroid
 CC hyperplasia. In some instances NSHPT has been demonstrated to be
 CC the homozygous form of FHH.
 CC -!- DISEASE: Defects in CASR are the cause of autosomal dominant
 CC hypocalcaemia (ADH) [MIM:601198]; in which the receptor is
 CC activated at subnormal Ca(2+) levels.
 CC -!- DISEASE: Defects in CASR are the cause of autosomal dominant

hypoparathyroidism (FHH) [MIM:146200]. FHH is characterized by
 hypocalcaemia and hypophosphatemia due to inadequate secretion of
 parathyroid hormone. Symptoms are seizures, tetany and cramps.
 -!- SIMILARITY: Belongs to the G-protein coupled receptor family 3.

 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 or send an email to license@isb-sib.ch).

 CC
 DR EMBL; X81086; CAAS6990.1; -;
 DR EMBL; U20755; AAA86503.1; -;
 DR EMBL; U20760; AAA86504.1; -;
 DR EMBL; D50855; BAA09453.1; -;
 DR EMBL; S83176; AAB46873.1; -;
 DR EMBL; S79217; AAB35262.2; -;
 DR EMBL; S68032; AAB29413.2; ALT_SEQ.
 DR EMBL; S68033; AAB29414.1; -;
 DR EMBL; S68036; AAB29415.1; -;
 DR EMBL; S81755; AAD14370.1; -;
 DR HSSP; P23385; LEWK.
 DR Genew; HGNC:1514; CASR.
 DR MIM; 601199; -;
 DR MIM; 145980; -;
 DR MIM; 239200; -;
 DR MIM; 601198; -;
 DR MIM; 146200; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; TAS.
 DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
 DR GO; GO:0005513; P:calcium ion sensing; TAS.
 DR GO; GO:0007635; P:chemosensory behavior; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; TAS.
 DR GO; GO:0009653; P:osmogenesis; TAS.
 DR GO; GO:0001503; P:osmification; TAS.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000068; Ca_sens_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PRINTS; PR00248; GPCR_MGR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
 DR PROSITE; PS00983; G_PROTEIN_RECEP_F3_5; 1.
 Query Match 74.8%; Score 4044.5; DB 1; Length 1078;
 Best Local Similarity 74.0%; Pred. No. 2.5e-275;
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;
 Qy 1 MAQLHCOLLFLGFTLLQSNVSGVGNQRAQKGGDIILGLFFPHFGVAAKQDLSRPE 60
 Db 1 MAFVSCCVLLALT- ---WHTSAYGPDQRAQKGGDIILGLFFPHFGVAAKQDLSRPE 56
 Qy 61 ATKIRYNFRGFRWLQAMIFAEIENNNMTFLENITLGYRIFPTCNTVSKALEATLSFVA 120
 Db 57 SVECIYNFRGFRWLQAMIFAEIENNNMTFLENITLGYRIFPTCNTVSKALEATLSFVA 116
 Qy 121 QNKIDSNLNDFPCNSDHIPTTAVGATSGISTAVANLLGLFYIPQVSAYSSRLSN 180
 Db 117 QNKIDSNLNDFPCNSDHIPTTAVGATSGISTAVANLLGLFYIPQVSAYSSRLSN 176
 Qy 181 KNEYKAFRLTIPNDEQOATAMAEIIHFQNNWVGTLAADDYGRPGIDKFRFEAVKRDIC 240
 Db 177 KNQKFSRLTIPNDEHQATAMADIIIEFRNNWVGTLAADDYGRPGIEKFEAEERDIC 236
 Qy 241 IDFSMTSQYTKQLFEFIADVIQNSSAKIVVFNFGPDLEPLIQEIVRNITDRIWLAS 300
 Db 237 IDFSSELISQYSDEEBEIQHVVVEIQNSTAKIVVFNFGPDLEPLIKIVRNITKIVLAS 296

Db	58	SVEICIRNFRGRFLQAMIFAIBINSPPALLPNMTILGYRIFDTCNTVSKALEATLSFVA	117	DT	05-JUL-2004 (Rel. 44, Last annotation update)
Qy	121	QNKIDSLNLDKFCNCSHPISTIAVGTATGSGISTAVANLLGLFYIPQVSYASSRLLSN	180	DE	Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid Cell calcium-sensing receptor).
Db	118	QNKIDSLNLDKFCNCSHPISTIAVGTATGSGISTAVANLLGLFYIPQVSYASSRLLSN	177	GN	Name=CaSR; Synonyms=Gprc2a, Pcar1;
Qy	181	KNEYKAFLETPINDEQQATAMAEIIEHFQWNVGTAAADDYGRPGIDKFREEAVKEDIC	240	OS	Rattus norvegicus (Rat).
Db	178	KNQFKSLRTIPNDEHQATAMADIEFPRNVWGTIAADDYGRPGIEKFREEAEERDIC	237	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Qy	241	IDFSEMISQYTOQLEFIADIVONSSAKVAVFNSGPDLEPLICEIVRRNITDRILWAS	300	CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Db	238	IDFSELISQYDBEIKQVVEIONSTAKVIVFSSGPDLEPLICEIVRRNITDRILWAS	297	CX	NCBI_TaxID=101116;
Qy	301	EAWASSSLIAKPEYFHVHVGTTIGFALRAGRIPGFNKFKEVHPSRSSDNGFVKFEWETP	360	RN	SEQUENCE FROM N.A.
Db	298	EAWASSSLIAKPEYFHVHVGTTIGFALRAGRIPGFNKFKEVHPSRSSDNGFVKFEWETP	357	RP	STRAIN=Grawley; TISSUE=Kidney outer medulla;
Qy	361	NCYFTEKTLTOLKNSKVPSSHGPAAGDQSGSKAGNSRRTALRHPCTGEENITVETPYLDYT	420	RC	MEDLINE=95116508; PubMed=7816802;
Db	358	NCHLQEGAKGPL---PVDFTLRGHEGGARLSNS--PTAFRPLCTGGEENISVETPYMDYT	413	RA	Riccardi D., Park J., Lee W., Gamba G., Brown E.M., Hebert S.C.;
Qy	421	HLRISYVNVAVYSTAHALQDIHSCPKGTGFANGSCADIKKVEAMQVNLHLLHLKPTNS	480	RT	"Cloning and functional expression of a rat kidney extracellular calcium/polyvalent cation-sensing receptor".
Db	414	HLRISYVNVAVYSTAHALQDIHSCPKGTGFANGSCADIKKVEAMQVNLHLLHLKPTNS	473	RL	Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).
Qy	481	MGEQVDFDDQGLKGNYYTIINWLSAEDSVLFHEVGNYNAYAKPSDLNINEKKILWSG	540	CC	-1- FUNCTION: Senses changes in the extracellular concentration of calcium ions. The activity of this receptor is mediated by a G-protein that activates a phosphatidylinositol-calcium second messenger system.
Db	474	MGEQVDFDECGDLAGNYSIINWLSPEDEGSIVFKEVGNYNAYAKGERLINDEXILWSG	533	CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
Qy	541	FSKVYFNSCSDCVPGTKGIIEGPTCCPEMACAGESSDENDASACTKCPNDPWSN	600	CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor family 3.
Db	534	FSREYFNSCSDCLAGTKGIIEGPTCCPEMACAGESSDENDASACTKCPNDPWSN	593	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Qy	601	ENHTSCIAKEIBLWTEPFGIALTIFAVLGLITLSFVLGVFIKPRNTPIVKATNRELSY	660	CC	EMBL; U10354; AAC52149.1; -
Db	594	ENHTSCIAKEIBLWTEPFGIALTIFAVLGLITLSFVLGVFIKPRNTPIVKATNRELSY	653	DR	EMBL; U20289; AAC52195.1; -
Qy	661	LLLSLICFSSSLPIGEPRDWTCLRQAPAGISFVLCISCLVKNRVLVFEAKIPT	720	DR	PIR; I59362; I59362.
Db	654	LLLSLICFSSSLPIGEPRDWTCLRQAPAGISFVLCISCLVKNRVLVFEAKIPT	713	DR	HSSP; P23385; LEWK.
Qy	721	SHRKWGNLQFLAVFLCIVITCIILWLTAPPSSYRNHELEDEIVITCDGSLMA	780	DR	RGD; 2277; Casr.
Db	714	SHRKWGNLQFLAVFLCIVITCIILWLTAPPSSYRNHELEDEIVITCDGSLMA	773	DR	InterPro; IPR001828; ANF receptor.
Qy	781	LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWMISFIPAYASTYKGF	840	DR	InterPro; IPR000337; GPCR_MgR.
Db	774	LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIWMISFIPAYASTYKGF	833	DR	Pfam; PF00003; 7tm_3; 1.
Qy	841	VSAREVIALASFGILGCIYFNKCVIILFKCRNTIEVRCTAAHAFKVAARATLRS	900	DR	Pfam; PF01094; ANF receptor; 1.
Db	834	VSAREVIALASFGILGCIYFNKCVIILFKCRNTIEVRCTAAHAFKVAARATLRS	893	DR	PRINTS; PR00248; GPCR_MgR.
Qy	901	AASRKRSSSLGSGTSSPASSTCG-----P	925	KW	PROSITE; PS00979; G-PROTEIN_RECEP_F3_1; 1.
Db	894	NVSQRSSSLGSGTSSPASSTCKNSDPPDQQQPKQKQPQLALSPHNAQQPQPR	953	FT	PROSITE; PS00980; G-PROTEIN_RECEP_F3_2; 1.
Qy	926	GLTMEWQ-----RGTQKVSFGSTVLSLFSFTGYATLSRTARSNADGSGDD	978	FT	PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.
Db	954	PSTPQPOSQPPRCK-QKVFSGSTVLSLFSFDEPQKTAHARNSTHQTSLAQKND	1012	FT	PROSITE; PS0259; G-PROTEIN_RECEP_F3_4; 1.
Qy	979	LPGRHDDQPPKCEPQANDARYKAAPTGTLESPPGSGKERPTTME	1026	FT	G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
Db	1013	ALTRH-----QALLPQCGTDSLTQSQETGLQGPVG-EDHOLEMED	1053	FT	Potential.
Qy	1079	AA.	90	FT	Extracellular calcium-sensing receptor.
Db	1079	AA.	90	FT	Extracellular (Potential).
Qy	1079	AA.	90	FT	1 (Potential).
Db	1079	AA.	90	FT	Cytoplasmic (Potential).
Qy	1079	AA.	90	FT	2 (Potential).
Db	1079	AA.	90	FT	Extracellular (Potential).
Qy	1079	AA.	90	FT	3 (Potential).
Db	1079	AA.	90	FT	Cytoplasmic (Potential).
Qy	1079	AA.	90	FT	4 (Potential).
Db	1079	AA.	90	FT	Extracellular (Potential).
Qy	1079	AA.	90	FT	5 (Potential).
Db	1079	AA.	90	FT	Cytoplasmic (Potential).
Qy	1079	AA.	90	FT	6 (Potential).
Db	1079	AA.	90	FT	Extracellular (Potential).
Qy	1079	AA.	90	FT	7 (Potential).
Db	1079	AA.	90	FT	Cytoplasmic (Potential).
Qy	1079	AA.	90	FT	N-linked (GlcNAc...) (Potential).

RESULT 4
CASR_RAT
ID_CASR_RAT
AC P48442; 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

```

FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 287 287 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 386 386 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 446 446 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 468 468 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 541 541 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential)
SQ SEQUENCE 1079 AA; 120867 MW; D7664550361F9736 CRC64;

Query Match
Best Local Similarity 73.9%; Score 3996; DB 1; Length 1079;
Matches 780; Conservative 85; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAQLHCQLLFLGFTLLQSYNVSGYGNQRAQKGGDIILGGLPFIHFGVAAKQDQLKS RPE 60
D 1 MASYSCLALLAL---AWHSSAYGPDQRAQKGGDIILGGLPFIHFGVAAKQDQLKS RPE 56
61 ATKCIYRNGRFRWLQAMIFALFEINNSMTLPNTITLGYRIEDTCTNTVSKALEATLSFVA 120
D 57 SVCEIYRNGRFRWLQAMIFALFEINNSMTLPNTITLGYRIEDTCTNTVSKALEATLSFVA 116
121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 180
D 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 176
181 KNEYKAFRTINDEQCATAMAEIIEHFQWNVGTLAADDYGRGIDKFEAEAVKRDI 240
D 177 KNEYKAFRTINDEQCATAMAEIIEHFQWNVGTLAADDYGRGIDKFEAEAEABERDI 236
241 IDFSEMISQYTKQLEFIADYQNSAKVIVFSGNGDPLELQIEIVRRNITDRIMLAS 300
D 237 IDFSELIQSDEEIQQVEVQNSAKVIVFSSGGDPLELQIEIVRRNITGRILWAS 296
301 EAWASSLIATBEYFHVUGGTFGLRAGRIKPGFNKFLKEVHPSRSSNGVFGFWBETP 360
D 297 EAWASSLIATBEYFHVUGGTFGLRAGRIKPGFNKFLKEVHPSRSSNGVFGFWBETP 356
361 NCYFTEKTLTQK-NKSPVSHGPAAGDGSAGNSRTALRHPCTGGEINITSVETPYLDY 419
D 357 NCHLQEGAKPLPVDTFVRSH---EEGNRLNS-STAFPLCTGGEINITSVETPYNDY 411
420 TRLRSYNYVAVYIAHALQDIHCKPGTGFANGSCADIKKVEAWQVNLHLLKFTN 479
D 412 EHLRSYNYVAVYIAHALQDIYCLPGRGIFTNGSCADIKKVEAWQVNLHLLKFTN 471
480 SMGEQVDFDDQGLKGYNTIINQWLSAEDSVLFEVGNVYAKPSDLNINEKKILWS 539
D 472 NMGEQVDFDECDLVNYSIINWHLSPDGSIVFKEVGYNYVYAKKGRLEFINSEKILWS 531
540 GFSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAEGFSDENDASACTKPNDFWS 599
D 532 GFSREVVPFNSCRDCQAGTRKGIIEGPTCCFECVCEPDGYSGETDASACDKCPDFWS 591
600 NENHTSCATKEIYLSWTEPGIATITFVGLIITSVLGVFKFNTPIVKATNELS 659
D 592 NENHTSCATKEIYLSWTEPGIATITFVGLIITSVLGVFKFNTPIVKATNELS 651
660 YLLFSLCCFSSSLIFICEPRDWTCLRQPAFGISFVLICISILVKNRVLVFEAKIP 719
D 652 YLLFSLCCFSSSLIFICEPRDWTCLRQPAFGISFVLICISILVKNRVLVFEAKIP 711
720 TSLHRKWGLMLQFLVFLCILVQIVTCIWIYTAPESSYRNHELEDEVIPTCDEGLM 779
D 712 TSFRKMWGLMLQFLVFLCILVQIVTCIWIYTAPESSYRNHELEDEVIPTCDEGLM 771
780 ALGFLIGYTCLLAATCFEFAFKSKLPENFNEAKFITFSLMIFIVMISFIPAVVSTYK 839
D 772 ALGSLIGYTCLLAATCFEFAFKSKLPENFNEAKFITFSLMIFIVMISFIPAVVSTYK 831
840 FVSAVEVIAIALASSGFLGCIYFNKCYIILFKPCNTIEEVRCSAAHAFKVAARATLRR 899

```

```

832 FVSAVEVIAIALASSGFLGCIYFNKCYIILFKPCNTIEEVRCSAAHAFKVAARATLRR 891
900 SAARSKRSSSLCGSTISSPASSITCGPG-----LTME 930
892 PNISRKSSSLGGSTGSIPISSSSSKNSNSDRPQPERQKQQQLSLTQEQQQQLTLH 951
931 MQ-----RCSTQKVSFGSGVTLSLSEFTGRVATLSRTARSNSADGRSGDDLPSR 982
952 PQQQQQPQPRCK-QKVFISGVTLSLSEFTGRVATLSRTARSNSADGRSGDDLPSR 1010
983 HHDGQPPQKCEPOPANDARYKAAPTKGTLESPPGSKERP 1021
1011 H-----QALLPLQCADSEMIIQETGLQGPVWDHQP 1043

PRT; 1079 AA.

AC Q80ZA8 PRELIMINARY;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Calcium sensing receptor.
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [.]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Dorsal root ganglion;
RA Bukoski R., Bian K., Wang Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214122; AB059490.1;
DR HSP; P23385; IWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto...; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASSENSINGR.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 1079 AA; 120830 MW; 50A2D026AE65CE81 CRC64;

Query Match 73.7%; Score 3986; DB 2; Length 1079;
Best Local Similarity 73.5%; Pred. No. 3.3e-271;
Matches 778; Conservative 87; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAQLHCQLLFLGFTLLQSYNVSGYGNQRAQKGGDIILGGLPFIHFGVAAKQDQLKS RPE 60
D 1 MASYSCLALLAL---AWHSSAYGPDQRAQKGGDIILGGLPFIHFGVAAKQDQLKS RPE 56
61 ATKCIYRNGRFRWLQAMIFALFEINNSMTLPNTITLGYRIEDTCTNTVSKALEATLSFVA 120
D 57 SVCEIYRNGRFRWLQAMIFALFEINNSMTLPNTITLGYRIEDTCTNTVSKALEATLSFVA 116
121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 180
D 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN 176
181 KNEYKAFRTINDEQCATAMAEIIEHFQWNVGTLAADDYGRGIDKFEAEAVKRDI 240
D 177 KNEYKAFRTINDEQCATAMAEIIEHFQWNVGTLAADDYGRGIDKFEAEAEABERDI 236
241 IDFSEMISQYTKQLEFIADYQNSAKVIVFSGNGDPLELQIEIVRRNITDRIMLAS 300
D 237 IDFSELIQSDEEIQQVEVQNSAKVIVFSSGGDPLELQIEIVRRNITGRILWAS 296
301 EAWASSLIATBEYFHVUGGTFGLRAGRIKPGFNKFLKEVHPSRSSNGVFGFWBETP 360
D 297 EAWASSLIATBEYFHVUGGTFGLRAGRIKPGFNKFLKEVHPSRSSNGVFGFWBETP 356
361 NCYFTEKTLTQK-NKSPVSHGPAAGDGSAGNSRTALRHPCTGGEINITSVETPYLDY 419
D 357 NCHLQEGAKPLPVDTFVRSH---EEGNRLNS-STAFPLCTGGEINITSVETPYNDY 411
420 TRLRSYNYVAVYIAHALQDIHCKPGTGFANGSCADIKKVEAWQVNLHLLKFTN 479
D 412 EHLRSYNYVAVYIAHALQDIYCLPGRGIFTNGSCADIKKVEAWQVNLHLLKFTN 471
480 SMGEQVDFDDQGLKGYNTIINQWLSAEDSVLFEVGNVYAKPSDLNINEKKILWS 539
D 472 NMGEQVDFDECDLVNYSIINWHLSPDGSIVFKEVGYNYVYAKKGRLEFINSEKILWS 531
540 GFSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAEGFSDENDASACTKPNDFWS 599
D 532 GFSREVVPFNSCRDCQAGTRKGIIEGPTCCFECVCEPDGYSGETDASACDKCPDFWS 591
600 NENHTSCATKEIYLSWTEPGIATITFVGLIITSVLGVFKFNTPIVKATNELS 659
D 592 NENHTSCATKEIYLSWTEPGIATITFVGLIITSVLGVFKFNTPIVKATNELS 651
660 YLLFSLCCFSSSLIFICEPRDWTCLRQPAFGISFVLICISILVKNRVLVFEAKIP 719
D 652 YLLFSLCCFSSSLIFICEPRDWTCLRQPAFGISFVLICISILVKNRVLVFEAKIP 711
720 TSLHRKWGLMLQFLVFLCILVQIVTCIWIYTAPESSYRNHELEDEVIPTCDEGLM 779
D 712 TSFRKMWGLMLQFLVFLCILVQIVTCIWIYTAPESSYRNHELEDEVIPTCDEGLM 771
780 ALGFLIGYTCLLAATCFEFAFKSKLPENFNEAKFITFSLMIFIVMISFIPAVVSTYK 839
D 772 ALGSLIGYTCLLAATCFEFAFKSKLPENFNEAKFITFSLMIFIVMISFIPAVVSTYK 831
840 FVSAVEVIAIALASSGFLGCIYFNKCYIILFKPCNTIEEVRCSAAHAFKVAARATLRR 899

```

241 IDSEMIQYTKQLEFIADVIQSSAKVIVVFSNGPDLEPLIQEIVRNRITDRWLAS 300
237 IDPESLIQSDSEBEEIQQWEVIQNSAKVIVVFSNGPDLEPLIKETVRNRITGRWLAS 296
301 EAWASSLIAPYFHVVGTTIGFALBAGRIKPGNKELKVEHPSRSSDNGFVKFEWETF 360
297 EAWASSLIAPYFHVVGTTIGFALBAGRIKPGNKELKVEHPSRSSDNGFVKFEWETF 356
361 NCYFTEKTLTKLQK-NSKVPSPGAAQDGGKAGNSRRTALRHPCTGENTISVETPYLDY 419
357 NCHLQEGAKGFLPVDTFVRSH- ---EEGNNLLNS- STAFRPLCTGDNINSVETPYMDY 411
420 THLRISYNYVAVYSIAHALQDIHSCPGTGFANGSCADIKKVEAWQVNLHLLHAFKN 479
412 EHLRISYNYVAVYSIAHALQDIHSCPGTGFANGSCADIKKVEAWQVNLHLLHAFKN 471
480 SMGQVDDDDGDLKGNVTIINWLSADESVLFHEVGNVNAVAKPSDRNLNINEKKILWS 539
472 NMGQVTFDECGDLVGNYSIINWLSADESVLFHEVGNVNAVAKPSDRNLNINEKKILWS 531
540 GFSKVPSPNSRDCVPTKRIIEGPTCCFCMACABGFSFSDENASACTKPNDFWS 599
532 GFSRVPSPNSRDCVPTKRIIEGPTCCFCMACABGFSFSDENASACTKPNDFWS 591
600 NENHTSCIAKEIYLSWEPFGIALTIYAVLIGLITSFVLGFTKFRNTPIVKATNRELS 659
592 NENHTSCIAKEIYLSWEPFGIALTIYAVLIGLITSFVLGFTKFRNTPIVKATNRELS 651
660 YLLFLSLACCFSSSLIFIGEPDWTCLRQPAFGISFVLCISCLVKNRVLVLEAKIP 719
652 YLLFLSLACCFSSSLIFIGEPDWTCLRQPAFGISFVLCISCLVKNRVLVLEAKIP 711
720 TSLRHKVGLNLOFLVFLCLVQVITCIILYTPAPSSYHNHELEDEVIITCDEGLM 779
712 TSFHSKMWGLNLOFLVFLCLVQVITCIILYTPAPSSYHNHELEDEVIITCDEGLM 771
780 ALGFLIGYTCLLAAACFFPAKSKRLPENFNEAKETISMLIFFTWISFIPAVSYVYK 839
772 ALGSLIGYTCLLAAACFFPAKSKRLPENFNEAKETISMLIFFTWISFIPAVSYVYK 831
840 FVSAVEVIAILASSGGLGCIYFNKCYIILFKPCNTTIEVRCSTAAHAFKVAARATLR 899
832 FVSAVEVIAILASSGGLGCIYFNKCYIILFKPCNTTIEVRCSTAAHAFKVAARATLR 891
900 SAASKRSSLGSISSPASSTCGP- ---LTM- 930
892 PNISKRSSLGSISSPASSTCGP- ---LTM- 931
931 MQ- ---RCSTQKVSFGTIVTSLISFEETGRIATLSRTARSNSADGRSGDLPGR 982
952 PQQQQPQPPCK- QKVIFSGTIVTSLISFEETGRIATLSRTARSNSADGRSGDLPGR 1010
983 HHQDQPPQCKPQANDARYKAAPTKGILESFGGSKERP 1021
1011 H- ---QALLPLQCADADSEMTIQTGLQGPWVGDHQP 1043

RESULT 6
CASR_MOUSE
ID CASR_MOUSE STANDARD; PAT: 1079 AA
AC Q9QY96; Q88519; Q9QY95; Q9QZ08; Q9RID6; Q9R1Y2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid
DE Cell calcium-sensing receptor).
GN Name=Casr; Synonyms=Gprc2a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.

RC STRAIN=C57BL/6; TISSUE=Kidney;
RX MEDLINE=20092890; PubMed=10625662;
RA Oda Y., Tu C.-L., Chang W., Crumrine D., Koemueves L., Mauro T.,
RA Elias P.M., Bixle D.D.;
RT "The calcium sensing receptor and its alternatively spliced form in
RT murine epidermal differentiation.";
RL J. Biol. Chem. 275:1183-1190(2000).
RN [2] SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.
RP STRAIN=Black Swiss X 129/SV0; TISSUE=Kidney;
RX MEDLINE=20119279; PubMed=10652312;
RA Pi M., Garner S.C., Flannery P., Spurney R.F., Quarles L.D.;
RT "Genes of extracellular cations in Casr-deficient osteoblasts.
RT murine epidermal differentiation.";
RL J. Biol. Chem. 275:3256-3263(2000).
RN [3] SEQUENCE OF 256-600 FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.
RP TISSUE=Epiphyseal cartilage;
RX MEDLINE=20043955; PubMed=10579354;
RA Chang W., Tu C., Chen T.-H., Komueves L., Oda Y., Pratt S.A.,
RA Miller S., Shoback D.;
RT "Expression and signal transduction of calcium-sensing receptors in
RT cartilage and bone.";
RL Endocrinology 140:5883-5893 (1999).
RN [4] SEQUENCE OF 507-582 FROM N.A. (ISOFORM A).
RP STRAIN=NMRI; TISSUE=Brain;
RA Hildenbrand J., Ammon H.P.T., Wahl M.A.;
RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [5] SEQUENCE OF 562-814 FROM N.A.
RP TISSUE=Kidney;
RA Moawad T.I., Riccardi D.;
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [6] SEQUENCE OF 646-799 FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=97231187; PubMed=9076582;
RA Charles L.D., Hartle J.E. II, Siddhanti S.R., Guo R., Hinson T.K.;
RT "A distinct cation-sensing mechanism in MC3T3-E1 osteoblasts
RT functionally related to the calcium receptor.";
RL J. Bone Miner. Res. 12:393-402(1997).
CC -!- FUNCTION: Senses changes in the extracellular concentration of
CC calcium ions. The activity of this receptor is mediated by a G-
CC protein that activates a phosphatidylinositol-calcium second
CC messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=A;
CC IsoId=Q9QY96-1; Sequence=Displayed;
CC Name=B;
CC IsoId=Q9QY96-2; Sequence=VSP_002036;
CC -!- TISSUE SPECIFICITY: Epidermis, kidney and cartilage.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor family 3.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; AF110178; AAD28371.1; -
CC EMBL; AF110179; AAD28372.1; -
CC EMBL; AF128842; AAD40638.1; -
CC EMBL; AF068900; AAC19388.1; -
CC EMBL; AF027140; BAA77688.1; -
CC EMBL; AF020215; AAC53252.1; -
CC EMBL; AF195965; AAF00193.1; -
CC HSPF; P23385; LEWK.
CC MGD; MGI:1351351; Gprc2a.
CC InterPro; IPR001828; ANF_receptor.

DR InterPro; IPR000069; Ca_sens_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR Pfam; PF00003; 7tm_3; 1. _Mg.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
 DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
 DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
 DR PROSITE; PS00259; G_PROTEIN_RECP_F3_4; 1.
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
 KW Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 1079 Extracellular calcium-sensing receptor.
 FT DOMAIN 20 612 Extracellular (Potential).
 FT TRANSMEM 613 635 1 (Potential).
 FT DOMAIN 636 649 Cytoplasmic (Potential).
 FT TRANSMEM 650 670 2 (Potential).
 FT DOMAIN 671 681 Extracellular (Potential).
 FT TRANSMEM 682 700 3 (Potential).
 FT DOMAIN 701 724 Cytoplasmic (Potential).
 FT TRANSMEM 725 745 4 (Potential).
 FT DOMAIN 746 769 Extracellular (Potential).
 FT TRANSMEM 770 792 5 (Potential).
 FT DOMAIN 793 805 Cytoplasmic (Potential).
 FT TRANSMEM 806 828 6 (Potential).
 FT DOMAIN 829 836 Extracellular (Potential).
 FT TRANSMEM 837 862 7 (Potential).
 FT DOMAIN 863 1079 Cytoplasmic (Potential).
 FT CARBOHYD 90 90 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 130 130 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 261 261 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 287 287 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 386 386 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 446 446 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 468 468 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 488 488 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 541 541 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc. .) (Potential).
 FT VARSPIC 461 537 Missing (in isoform B).
 FT /Fric-VSP_002036.
 FT A -> S (in Ref. 2).
 FT L -> P (in Ref. 3).
 FT G -> D (in Ref. 2 and 3).
 FT V -> A (in Ref. 2).
 FT Y -> H (in Ref. 2).
 FT E -> V (in Ref. 2, 3 and 5).
 FT F -> L (in Ref. 5).
 FT L -> I (in Ref. 2).
 FT TGSN -> SGWI (in Ref. 2).
 FT V -> M (in Ref. 2).
 FT V -> A (in Ref. 2).
 FT I -> V (in Ref. 2).
 Query Match 1079 AA; 120839 MW; AAF8D8D472736D6E CRC64;
 Best Local Similarity 73.5%; Score 3976.5; DB 1; Length 1079;
 Matches 772; Conservative 88; Mismatches 124; Indels 55; Gaps 7;
 QY 15 LLOQSVNSYGNORAKKQKDIILGLPFIHFGVAKKDOLKSRPEATKIRYNFRGRW 74
 DB 11 LALTWHSAYGPDQQAQKKKDIILGLPFIHFGVAKKDOLKSRPEATKIRYNFRGRW 70
 QY 75 LOAMIFAEIENNSMTFLPNITLGYRIEDTNTVSKALEATLSVAQNKIDSLNDEFN 134
 DB 71 LOAMIFAEIENNSMTFLPNITLGYRIEDTNTVSKALEATLSVAQNKIDSLNDEFN 130
 QY 135 CSDHIPSTIANVGATSGISAVANLLGLFPIPOVSASSRLLSNKNEYAKFLRTIPND 194
 DB 131 CSEHIPSTIANVGATSGISAVANLLGLFPIPOVSASSRLLSNKNEYAKFLRTIPND 190
 QY 195 EQQATAMAEIIEHFQWNVGTLAADDYGRPGIDKFREEAVKRDICIDFGEMISQYQTK 254
 DB 191 EQQATAMAEIIEHFQWNVGTLAADDYGRPGIDKFREEAVKRDICIDFGEMISQYQTK 250

QY 255 QLEFIADIVIONSSAKVIVFSGPDLEPLTOEIVRNITDRIWLASEAWASSSLIAKPEY 314
 DB 251 EIQQVVEIVONSTAKVIVFSGPDLEPLTOEIVRNITDRIWLASEAWASSSLIAKPEY 310
 QY 315 FHVGGTIGFALRAGRIIPGFKELKEVHPSRSDNGFVKFWEETFCYFETKTLQLK- 373
 DB 311 FHVGGTIGFALRAGRIIPGFKELKEVHPSRSDNGFVKFWEETFCYFETKTLQLK- 370
 QY 374 NSKVPISGHPAAQGDGSAKNSRRATLRHPCTGENTISVETPYLDYTHLRISNNVAVY 433
 DB 371 DTFVRSH---EKGNNLLNS-STAFRPLCTGDNINSVETPYNGYEHLRISNNVAVY 425
 QY 434 SIAHALQDIHSCKPGTGFIFANGSCADIKKVEAQVNLHLHLKFTNSMGQVDFDQGD 493
 DB 426 SIAHALQDIYTCPLPGRGLFNGSCADIKKVEAQVNLHLHLKFTNSMGQVDFDQGD 485
 QY 494 KGNITIIWQLSAEDSVLPHEVGNVNAKPSDRNLNINEKKILWSGPKVVPFNSCRD 553
 DB 486 VGNYSIINWHLSPEDGSIKVEGYNYVAKKGERLFINEGKILWSGPKVVPFNSCRD 545
 QY 554 CVPGRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDPFWNENHTSCIAKEIEY 613
 DB 546 CQAGTRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDPFWNENHTSCIAKEIEY 605
 QY 614 LSWTEPPGIALTIPAVLGILITSFVLGVFKFRNTPIVKATNRELSYLLFSLICFSS 673
 DB 606 LSWTEPPGIALTIPAVLGILITSFVLGVFKFRNTPIVKATNRELSYLLFSLICFSS 665
 QY 674 LIIFIGPRDWTCLROPAGISFVLCISCLVKNRVLVFEAKIPTSLHRKWGNLQF 733
 DB 666 LIIFIGPRDWTCLROPAGISFVLCISCLVKNRVLVFEAKIPTSLHRKWGNLQF 725
 QY 734 LLVFLCILVQIVTCIIWLYTAPSSYRNHELEDEVIFITCDEGSLMALGFLGYTCLAA 793
 DB 726 LLVFLCILVQIVTCIIWLYTAPSSYRNHELEDEVIFITCDEGSLMALGFLGYTCLAA 785
 QY 794 ICFFAFKSKLPENENKAFITFSMLIPIFVWISPIPAYSTYKGFVSAAVEIALAS 853
 DB 786 ICFFAFKSKLPENENKAFITFSMLIPIFVWISPIPAYSTYKGFVSAAVEIALAS 845
 QY 854 FGLLGCIYFNKCVIILFKPCRNTEIEVRCSAAHAKVAARATLRSAASRKSLSLGS 913
 DB 846 FGLLGCIYFNKCVIILFKPCRNTEIEVRCSAAHAKVAARATLRSAASRKSLSLGS 905
 QY 914 TTSSPASSTCGPG-----LTWEMQ-----RCST 936
 DB 906 TGSNPPSSISKSNSNEDRFPQKQQLALTOEQEQQLTLQPOQQQPPQPRCK- 964
 QY 937 QKVFSFGVTVTLSPTEEGRYATLSRTARSNSADGRSGDDLPSRHHDQGPQKCEQP 996
 DB 965 QKVFSFGVTVTLSPTEEGRYATLSRTARSNSADGRSGDDLPSRHHDQGPQKCEQP 996
 QY 997 ANDARYKAAPTGTUESPG 1015
 DB 1022 -----ADSEWTIGETG 1032
 RESULT 7
 Q6XAF1
 ID Q6XAF1 PRELIMINARY; PRT; 941 AA.
 AC Q6XAF1;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Calcium polyvalent cation receptor 1.
 OC Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 RN [1]_TaxID=8030;
 RP SEQUENCE FROM N.A.

RC	TtSUB=Kidney;
RA	Nearing J.A., Harris W.;
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY245445; AAF79925.1; -.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	InterPro; IPR001828; ANF receptor.
DR	InterPro; IPR00068; Ca_sens_receptor.
DR	InterPro; IPR000337; GPCR_Mgr.
DR	InterPro; IPR011500; NCD3G_GPCR.
DR	Pfam; PF00003; 7tm_3; 1.
DR	Pfam; PF01094; ANF_receptor; 1.
DR	Pfam; PF07562; NCD3G; 1.
DR	PRINTS; PR00592; CASENSINGR.
DR	PRINTS; PR00248; GPCRMGR.
DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR	PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.
KW	Receptor.
SQ	SEQUENCE 941 AA; 106130 MW; 06119219CDF62D1F CRC64;

Query Match	68.9%; Score 3728; DB 2; Length 941;
Best Local Similarity	74.7%; Pred No. 3.9e-253;
Matches 711; Conservative	97; Mismatches 116; Indels 28; Gaps 6;

Qy	8	LLEFLGLTLOSYNVGYGPNQRAKKGDII LGGI LPPIHFGVAAKDQLKSPEATKCIRY	67
Dd	8	LVL LGGFSV---ISTYGHQRAKTKGDILLGGLPMWHGVTSKDQDLAARPESTECVRY	63
		: :	
Qy	68	NFRGFRWLQAMI PAIEBINNSMTLPNITLG YRIFDTCNTVSKALEATLSFAVNKDIDL	127
Dd	64	NFRGFRWLQAMI PAIEBINNSSTLLPNITLGYRI FDTCNTVSKALEATLSFAVNKDIDL	123
		: :	
Qy	128	NLDSEFCNSDHIPSTIAVVGATGSGISTAVANLLGLFIPOVSYASSRLLSNKNKYKAF	187
Dd	124	NLDSEFCNCTHH PSTIAVVGASGSASTAVANLLGLFIPOISYASSRLLSNKNQPKSF	183
		: :	
Qy	188	LRTIPNDQQATAMAEIHHPQWNWGTLAADDYGRPGIDKFREBAVKRDCIDDFSEMI	247
Dd	184	MRTIPTDEHQATAMADIIDFPQWNVI AVASDDYGRPGIEKFKEMEERDICHLSEL	243
		: :	
Qy	248	SOYVTOKLEPIADVIONSSAKVTVPSNGPDLEPLIQEIVVRNITDIRILASAWASS	307
Dd	244	SOVEEWQIQCLVDRIENSSAKVIVPASGPDIEPLIKEMVRNITDIRILASAWATT	303
		: :	
Qy	308	LIAPPEYHVVGTTIGTFALRAGRIPGNKFLUKEVHPRSSDNGFVKFEWEETFCNYFEK	367
Dd	304	LIAPPEYLDDVVGTIGTFALRAGEIPGFKDFLOEVTPKSSNEFVREFWEETFCYLEDS	363
		: :	
Qy	368	TLTOLKNSKVPSHGPAAGDSKAGNSRRPTALRHCPGTEENITSVETPELYDYTHLRISY	427
Dd	364	--QELRDE-----NGS-----TSFRPLCTGEEDIMGAETPYLDYTHLRISY	404
		: :	
Qy	428	VYVAVYSIAHALQDIHSCKPDTGITFANGSCADIKKVEAWQLNLHLKFTNSMGEOYDF	487
Dd	405	VYVAVHSIAQAQLDILTICIPRGGLFSNNSCADIKKIEAWQLKQLRHNFNSMGEKVHF	464
		: :	
Qy	488	DDQDGLKQNYTIINWOLSADESULFHVBGVNNAYAKPSDRLINEKKILLWSGSKVVPF	547
Dd	465	DENADPPSGNYTIINWHRSPDGSVVFEEVGFYNNRKARGVOLFDINTKILWNGYINTEVPF	524
		: :	
Qy	548	SNCSRDCVPGHKGTIGEPTCCPECMACAGEPSDENDAAGCTKCPNDFWSNHNHTSCI	607
Dd	525	SNCSDEDCEPGTRKGIIIESNPCTCCPECTCSGEGYSDHKDASVCYKCPNDSWSNHNHTSCF	584
		: :	
Qy	608	AKELEYLSWTFFPGIALTIFAVLGLIITISFVLGVPIKFRNTPIVKATNRILSYLLLFSL	667
Dd	585	LKEIEFLSWTEFFGIALCALCSVLGVLFAFMVGVFIFKRNPPIVKATNRILSYLLLFSL	644
		: :	
Qy	668	CCFSSSLIFCEPDWTCRLQPAGISFVLICISILVKTNRVLVFAEKAIPTSLHRKWV	727
Dd	645	CCFSSSLIFCEPDWTCRLQPAGISFVLICISILVKTNRVLVFAEKAIPTSLHRKWV	704
		: :	
Qy	728	GLNIQLQFLVFLCILIQIVTCAIHWLTAPSSRYRNHELEDEFITFCDGSLMALGFLICY	787
		: :	

Db	705	GLNLQFLLVFLFTFVQVWICVWLYNAPPASYRNHDI-DEIIFITCNEGSMWALGFLIGY	763
Qy	788	TCLLAICFPFAKSRKLPENFNEAKFITPSMLIFITWISFIPAYYSTYCKFVSAYEVI	847
Db	764	TCLLAICFPFAKSRKLPENFNEAKFITPSMLIFITWISFIPAYESTYCKFVSAYEVI	823
Qy	848	AIIASGFLGLGCIYFNKCYIILFKPCRNTEEVRCSTAAAHAFKVAARATLRRSAASRKR	907
Db	824	AIIASGFLGLACIFFNKVYIILFKPSNTIEEVRCSTAAHSFKVAAKATLURHSSASRKR	883
Qy	908	SSICGGSTISSPSS-----TCGPGILTWEMQRCSTQKVSFGSGTIVLSLSPET	955
Db	884	SSYGGSCASTPSSSISLKTNDNDSPSQQRIHKPRVFSFGSGTIVLSLSPES	935
RESULT 8			
ID	AAP79925	PRELIMINARY;	PRT; 941 AA.
AC	AAP79925;		
DT	03-MAR-2004 (T-EMBLrel. 27, Created)		
DT	03-MAR-2004 (T-EMBLrel. 27, Last sequence update)		
DT	03-MAR-2004 (T-EMBLrel. 27, Last annotation update)		
DE	Calcium polyvalent cation receptor 1.		
OS	Salmo salar (Atlantic salmon).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;		
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.		
OC	NCBI_TaxID=8030;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	Nearing J.A., Harris W.;		
RT	"Tissues of Atlantic Salmon (Salmo salar) Express Multiple Polyvalent		
RT	Cation Sensing Receptor (Car) cDNAs that Appear to Mediate Salinity		
RT	Sensing.";		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY245445; AAP79925.1; -.		
KW	Receptor.		
SQ	SEQUENCE 941 AA; 106130 MW; 06119219CDF62D1F CRC64;		
Query Match			
Best Local Similarity 68.9%; Score 3728; DB 2; Length 941;			
Matches 711; Conservative			
Indels 28; Gaps 6			
Qy	8	LLFLGFTLQSYNNVGVGNQRAKGDIIILGGLFPIHFVGAQDKQLKSRPEATKCI	67
Db	8	LVLGLFSSV---ISTYGPQRAKTDGIIILGGLFPMHFGVTSKDQDLAARPESTECV	63
Qy	68	NFRGFRWLQAMIPAIBEINNSMTPLNITILGYRIFDTCNTVSKALEATLSFVAQNKD	127
Db	64	NFRGFRWLQAMIPAIBEINNSMTLLPNITILGYRIFDTCNVSKALEATLSFVAQNKD	123
Qy	128	NLDEFCNCDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF	187
Db	124	NLDEFCNCTDHPSTIAVVGASGSAVAVANLLGLFYIPQISYASSRLLSNKNQPKSF	183
Qy	188	LRITPDEQQTAMAEIIEHFQWNVWGLAADDDYGRPGIDKFPREAVKRDICIDFSEMI	247
Db	184	MRTIPTDEQATAMADIIDYFQWNVAVASDDSYGRPGIEKFKEMEERDICIHLSELI	243
Qy	248	SOYTKQLQSFADIVQNSAKVIVVFSNGPDLPLQIEIVRRNITDRIMLASEAWASS	307
Db	244	SOYFEEHQIQLVDRIENSSAKVIVVFSNGPDLPLQIEIVRRNITDRIMLASEAWATTS	303
Qy	308	LIAPKEVHVVGITGIPALRAGRIIPGNKFLKEVHPSRSSDNGFVKFEWEEFNCYFTEK	367
Db	304	LIAPKEVLDVVVGITGIPALRAGEITPGFKDLQEVTPKSSSNEFVRFEWEEFNCYLD	363
Qy	368	TLTQKSKVPSHGPAQGDGSKAGNSRRRTALRHPCTGEEINITSVETPYLDYTHLRISYN	427
Db	364	--QRLRSE-----NGS-----TSFRPLCTGEEDINGAETPYLDYTHLRISYN	404
Qy	428	VYVAVYGAHALQDHSCKPOTGIFANGSCADIKKVRQWVLNHLHLKFTNSMGQVD	487

Query Match 68.9%; Score 3728; DB 2; Length 941;

Best Local Similarity	74.7%;	Pred. No. 3.9e-253;
Matches 711: Conservative	97;	Mismatches 116;
Indels	28;	Gaps

8 LLEFLGFTLLOSYNVSGYGP NORACKGDIILGGLFPIHFGVAAKDQDLKSRPEATKCIRY 67

[illegible]

Db 8 LVLLGFSSV - - - - I S T Y G P H Q R A Q K T G D I L L G G L F P M H F G V T S K D Q D L A A R P E S T E C V R Y 63

68 NFRGFRWLOAMIFAIEEINNMTFLPNITLGYRIFDTCNTVSKALEATLSFVAQNKIDSL 127

Db 64 NFRGFRWLQAMIFAIEEINNSSLPLPNITLGYRIFDTCNTVSKALEATLSFVAQNKIDSL 123

128 NLDEFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSSRLLSKNKNEYKAF 187

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

Db 124 NLDFCNCCTDHIPSTIAVVGASGSAVSTAVANLLGLFYIPQISYASSRLLSNKNQFKSF 183

188 LRTIPNDEOOATAMAEIIEHFOWNVGTLAADDYGRPGIDKFREEAVKRDICIDFSEMI 247

Db 184 MRTIPTDEHQATAMADIIDYFQWNWVIAVASDDEYGRPGIEKFEKEMEERDICIHLSELI 243

CV 248 SOYTKOLEFIADVIONSSAKVIVFSNGPDLEPLIOEIVRRNITDRWLSEAWASS 307

[illegible]

Db 244 SQYFEENQIQGLVDRIENSSAKVIVVFASGPDIEPLIKEMVRRNITDRIWLASEAWATTS 303

308 LIAKPEYFHVGGTIGFALRAGRI PGFNKFLKEVHPSRSSDNGFVKEFWEEETFNCYFTEK 367

D**b** 304 LIAP EYLDVVGTIGTGFALRAGEIPGFKDFLQEVTPKRSSHNEFVREFWEETFN CYLED S 363

OV 368 TLTOLKNSKVP SHGPA AOGDGSKAGNSRRRTALRHPC TGEENITSVETPYLDYTHLRISYN 427

[illegible]

Db 364 --QRLDSE-----NGS-----TSFRPLCTIGEEDINGAEIPYLDYTHLRISYN 404

428 VYVAVYSIAHALODIHSCCKPGTGFANGSCADIKKVEAWQVLNHLHLKFTNSMGEQVDF 487

Db 405 VYVAVHSIAQALQDILTCIPGRGLFNNSCADIKKTEAMQVLKQLRHLNFSNMGKRVH 464
 Qy 488 DOGDLKGNVTIINWOLSAEDSVLPHEVGNVNAKPSDRININEKKTILWSGFSKVVPF 547
 Db 465 DENADPSGNTIINWRSDEDSVVEEYVFTNMAKRGVQIFDNTKILMNGYITEVPF 524
 Qy 548 SNCRDVCPTGRKGIIEGPTCCFECMACAEFSDENDASACTKCPNDPMSNENHTSCI 607
 Db 525 SNCSDECPGTRKGIIESMPTCCFECTECSEGEYSDHDXASVCTKCPNDSNENHTSCF 584
 Qy 608 AXEIVLWTEPFGIALTIFAVLGLITISFVGVFKRNTPIVKATNRELSYLLFSLI 667
 Db 585 LKEIFLWTEPFGIALCULSVGLVPLTAFVNGVFIKFRNTPIVKATNRELSYLLFSLI 644
 Qy 668 CCFSSSLIFIGPRDWTCLROPAPGIFSVLCISILVKTNRVLLVFEAKIPTSLHRKWV 727
 Db 645 CCFSSSLIFIGPQDWTCLROPAPGIFSVLCISILVKTNRVLLVFEAKIPTSLHRKWV 704
 Qy 728 GLNLQFLVLCILVQIVTCIWLTPAPPSYRNHELEDEVIITCDEGSLMALGFLICY 787
 Db 705 GLNLQFLVLCILVQIVTCIWLTPAPPSYRNHELEDEVIITCDEGSLMALGFLICY 763
 Qy 788 TCLLAACIFFPAPKSKLPENNEAKFITFSMLIFFIWMISFIPAYSTYKGFSAVEVI 847
 Db 764 TCLLAACIFFPAPKSKLPENNEAKFITFSMLIFFIWMISFIPAYSTYKGFSAVEVI 823
 Qy 848 AILASSFGLLGCIFYFNKCVIILFKPCRNTEIEVRGSTAAHAFKVAARATLRSASRKRS 907
 Db 824 AILASSFGLLGCIFYFNKCVIILFKPCRNTEIEVRGSTAAHAFKVAARATLRSASRKRS 883
 Qy 908 SSVGGSCASTPSSISLKTNDNDSFGQRIHKPRVSGFGVTLSLSPES 955
 Db 884 SSVGGSCASTPSSISLKTNDNDSFGQRIHKPRVSGFGVTLSLSPES 935

RESULT 9
 Q6XAF3
 ID Q6XAF3 PRELIMINARY; PRT; 941 AA.
 AC Q6XAF3
 DT 05-JUL-2004 (T=EMBLrel. 27, Created)
 DT 05-JUL-2004 (T=EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T=EMBLrel. 27, Last annotation update)
 DE Calcium polyvalent cation receptor 2.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Procranchiophytarygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Nearing J.A., Harris W.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY254443; AAP79923.1; -.
 DR GO; GO:0004872; Fireceptor activity; IEA.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000068; Ca_sens receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.
 DR PRINTS; PR00592; CASENSINGR.
 DR PRINTS; PR00248; GPCR_MGR.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE; PS02529; G_PROTEIN_RECEP_F3_4; 1.
 KW Receptor.
 SQ SEQUENCE 941 AA; 106072 MW; C72B91C00290FF27 CRC64;

Query Match 68.8%; Score 3721; DB 2; Length 941;
 Best Local Similarity 74.6%; Pred. No. 1.2e-252;
 Matches 710; Conservative 97; Mismatches 117; Indels 28; Gaps 6;

Qy 8 LLFLGFTLLQSYNVSGYGNQRAQKKGDIILGGLFPIHFGVAAKQDQDLKSRPEATKIRY 67
 Db 8 LVLLGFSV---ISTVGPQRAQKTDGILLGGLFMHFGVTSKDQDLAARPESTCVRY 63
 Qy 68 NFRGFRWLQAMIFAIBEINNSMTFLNITLGYRIFPTCNTVSKALBATISFVAQNKIDSL 127
 Db 64 NFRGFRWLQAMIFAIBEINNSMTFLNITLGYRIFPTCNTVSKALBATISFVAQNKIDSL 123
 Qy 128 NLDEFNCSDHIPTSTAVGATCGISTAVANLLGLFYIPOVSYASSSLLSNKNEYKAF 187
 Db 124 NLDEFNCSDHIPTSTAVGATCGISTAVANLLGLFYIPOVSYASSSLLSNKNEYKAF 183
 Qy 188 LRTPNDEQOATAMASIIIEHFQNNWVGTAAADDYGRPGIDKPREBAVRKIDICIDSEMI 247
 Db 184 MRTIPTDEHOATAMADIIDYFQNNWVIAVASDEYGRPGIEKEPEKEMEERDICIHLSELI 243
 Qy 248 SOYTKOLEFIADVTIONSSAKVIVVFSNGPDLLEPIQEIIVRENITDRILWASEANASS 307
 Db 244 SOYFEWQIOGLVRLIENSASAKVIVVFSAGPDLEPIKEKVRNITDRILWASEANASS 303
 Qy 308 LIAKPEYFHVVGTTIGFALRAGRIPGFNKFLKEVHPRSRSDNGFVKEPWEETPCYFTEK 367
 Db 304 LIAKPEYLDVVGTIGFALRAGEIPGKDFLQEVTPKSSHNEFVREFWEETPCYLED 363
 Qy 368 TLTLKNSKVPSPGPAAGDGSKAGNSRRRTALRHPCTGEENITSVETPYLDYTHLISYN 427
 Db 364 --QRLRDS-----NGS-----TSRPLCTGEEDINGAETPYLDYTHLISYN 404
 Qy 428 VYVAVTSIAHALQDIHSCCKPGTGFANGSCADIKKVEAMQVLNHLHLKFTNSMGQVDF 487
 Db 405 VYVAVHSIAQALQDILTCIPGRGLFNNSCADIKKTEAMQVLKQLRHLNFSNMGKRVH 464
 Qy 488 DOGDLKGNVTIINWOLSAEDSVLPHEVGNVNAKPSDRININEKKTILWSGFSKVVPF 547
 Db 465 DENADPSGNTIINWRSDEDSVVEEYVFTNMAKRGVQIFDNTKILMNGYITEVPF 524
 Qy 548 SNCRDVCPTGRKGIIEGPTCCFECMACAEFSDENDASACTKCPNDPMSNENHTSCI 607
 Db 525 SNCSDECPGTRKGIIESMPTCCFECTECSEGEYSDHDXASVCTKCPNDSNENHTSCF 584
 Qy 608 AXEIVLWTEPFGIALTIFAVLGLITISFVGVFKRNTPIVKATNRELSYLLFSLI 667
 Db 585 LKEIFLWTEPFGIALCULSVGLVPLTAFVNGVFIKFRNTPIVKATNRELSYLLFSLI 644
 Qy 668 CCFSSSLIFIGPRDWTCLROPAPGIFSVLCISILVKTNRVLLVFEAKIPTSLHRKWV 727
 Db 645 CCFSSSLIFIGPQDWTCLROPAPGIFSVLCISILVKTNRVLLVFEAKIPTSLHRKWV 704
 Qy 728 GLNLQFLVLCILVQIVTCIWLTPAPPSYRNHELEDEVIITCDEGSLMALGFLICY 787
 Db 705 GLNLQFLVLCILVQIVTCIWLTPAPPSYRNHELEDEVIITCDEGSLMALGFLICY 763
 Qy 788 TCLLAACIFFPAPKSKLPENNEAKFITFSMLIFFIWMISFIPAYSTYKGFSAVEVI 847
 Db 764 TCLLAACIFFPAPKSKLPENNEAKFITFSMLIFFIWMISFIPAYSTYKGFSAVEVI 823
 Qy 848 AILASSFGLLGCIFYFNKCVIILFKPCRNTEIEVRGSTAAHAFKVAARATLRSASRKRS 907
 Db 824 AILASSFGLLGCIFYFNKCVIILFKPCRNTEIEVRGSTAAHAFKVAARATLRSASRKRS 883
 Qy 908 SSVGGSCASTPSSISLKTNDNDSFGQRIHKPRVSGFGVTLSLSPES 955
 Db 884 SSVGGSCASTPSSISLKTNDNDSFGQRIHKPRVSGFGVTLSLSPES 935

RESULT 10
 AAP79923
 ID AAP79923 PRELIMINARY; PRT; 941 AA.
 AC AAP79923;
 DT 03-MAR-2004 (T=EMBLrel. 27, Created)
 DT 03-MAR-2004 (T=EMBLrel. 27, Last sequence update)
 DT 03-MAR-2004 (T=EMBLrel. 27, Last annotation update)

DE	Calcium polyvalent cation receptor 2.
OS	Salmo salar (Atlantic salmon).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Ocyariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX	NCBI_TaxID=8030;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RA	Nearing J.A., Harris W.;
RT	"Tissues of Atlantic Salmon (Salmo salar) Express Multiple Polyvalent
RT	Cation Sensing Receptor (Car) cDNAs that Appear to Mediate Salinity
RT	Sensing.";
RL	Submitted (FEB-2003) to the EMBL/GenBank/DDAJ databases.
DR	EMBL; AY245443; AAP79923.1; --
KW	Receptor.
SQ	SEQUENCE 941 AA; 106072 MW; C72B91C0029DFF27 CRC64;
Query Match 68.8%; Score 3721; DB 2; Length 941;	
Best Local Similarity 74.6%; Pred. No. 1.2e-252;	
Matches 710; Conservative 97; Mismatches 117; Indels 28; Gaps 6	
QY	8 LLFGFTLLSYNVSGVGNORAKKGDIILGGIIPPIHFGVAADKQDLKSPEATKCIRY 67
DG	: :
DB	8 LVLLGFSSV---ISTYGPHORAKTGILLGGIFPMHFGVTSDQDLAARPESTECVRY 63
QY	68 NFRGRMLQAMFALEIEINNSMTFLPNITLTGVRFDTCTNTYSKALEATLSVAONKIDSL 127
DG	: :
DB	64 NFRGRMLQAMFALEIEINNSMTLLPNITLTGVRFDTCTNTYSKALEATLSVAONKIDSL 123
QY	128 NLDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFIPOVSASSRLLSNKNYEYKAF 187
DG	: :
DB	124 NLDEFNCSDHIPSTIAVVGASGSAVSTAVANLLGLFIPOISVASSRLLSNKNQPKSF 183
QY	188 LRTTPNDEQQATAEIIIEHFQNNWGTLAADDDYGRGIDKFEEAAVKRDICIDFSEMI 247
DG	: :
DB	184 MRTPTDEHQATAWADIIFYQNNWVIADVSDGYRGFKPEKEMBERDICHLSEL 243
QY	248 SOYTKQLERFIADVIQNSSAKVIVFNGSPDLEPLIQEIVRNRNITDIRWLASEAWSSS 307
DG	: :
DB	244 SQYEEEWIQGLVGRINSSAKVIVVFASGDIEPLIKEMVRNRNITDIRWLASEAWATS 303
QY	308 LIAKEPYHVHVGTTIGFPALRAGRIDPFNKFLKEVHPSPSSDNGFVKFEWEETFCYFTEK 367
DG	: :
DB	304 LIAKPEYLDVVVGTIGFPALRAGEIPGFDFLQEVPFKSSSHNEFVREEWEETFCYLEDS 363
QY	368 TLTKSKSVPSHGPAAGDGCSKAGNSRRRTALRHPTCGEENITSVETPVLYDTHLRISYN 427
DG	: :
DB	364 --QRURDE-----NQS-----TSFRPLCTGEEDIMGNETPYLDYTHLRISYN 404
QY	428 VYVAVYSTAHALQDIHSCKPGTGTFANGSCADIKKVEAQVNLHLHLKFTNSMGEQYDF 487
DG	: :
DB	405 VYVAVHSIAQAQLDILTICIPGRGLPFSNNSCADIKKIEAWQLKQLRHNFNSMGKCVHF 464
QY	488 DDQGLDKNYTIIINQLSAEDSVLFHEVGNVNAYAKPSDRLININEKILLSGSKVVPF 547
DG	: :
DB	465 DENADPPSGNYTIIINHRSPEGSVVFEVGVFNMAKRGVQLFDINTKILMNGYNTVEYFP 524
QY	548 SNCSRDCVPGTRKGIIEGECTCCFPCMACGEFSDENDASACTCPNDFWASNENHTSCI 607
DG	: :
DB	525 SNGSEDCEPGTRKGIIESMPCTCFCECSGEYESDHKDAVSCTKCPNDSMNENHTSCF 584
QY	608 AKETIELSWTPFGTALTIFAVLGILITISFVLGVFIKFRNPPIVKATNRELSYLLFSL 667
DG	: :
DB	585 LKEIEFLSWTPFGTALCALCSVLGFLTAFYNGVFIKFRNPPIVKATNRELSYLLFSL 644
QY	668 CCFSSSLFICEPRDWTCRLQPARGISFVLCISCIILVKNRVLLVFEAKPTSLSHRXWV 727
DG	: :
DB	645 CCFSSSLFICEPDWTCLRPARGISFVLCISCIILVKNRVLLVFEAKPTSLSHRXWV 704
QY	728 GLNQFLLVFFCILVQIVTCIIMWLTAPPSSYRNHELEDEVIFTCDGSLMALGFLIGY 787
DG	: :
DB	705 GLNQFLLVFFFTFOVMICVWLNYPAPSYRNHDI--DEIFIICNMGSMALGFLIGY 763

Qy	788	TCLLAAICFFFAFKSRKLPENFNCAKFTITSMGLFFIIFWISFIPAYVSTYKGFVSAVEVI	84
Db	764	TCLLAAICFFFAFKSRKLPENFNCAKFTITSMGLFFIIFWISFIPAYVSTYKGFVSAVEVI	823
Qy	848	ATLASGFLGCIYENKCVIILFKPCRNITIEBVCRTAAAHAFKVAARATLRRSAAGRKRS	907
Db	824	ATLASGFLGCIYENKCVIILFKPCRNITIEBVCRTAAAHAFKVAARATLRRSAAGRKRS	883
Qy	908	SSLCGSTISSPASS-----TCGPGLTMEQRCSTOKVSFGSGTVTLSLSPRET 955	
Db	884	SSVGGSCASTPSSISLXTNDNDSPSGQORIKHPRVSGTGTLSLSPFEES 935	
RESULT 11			
ID	Q90WL6	PRELIMINARY; PRT: 940 AA.	
AC	Q90WL6;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Extracellular calcium sensing receptor.		
GN	Nanescsz;		
OS	Spurax aurata (Gilthead sea bream).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neoceratygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;		
OC	Sparidae; Sparus.		
OC	NCBI_TaxID=8175;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MDLINES=21930045; PubMed=11932208;		
RA	Clark M.S., Bendell L., Power D.M., Warner S., Elgar G.,		
RA	Ingilston P.M.;		
RT	"Calcitonin: Characterisation and expression in a Teleost fish: Fugu		
RT	rubripes.";		
RL	J. Mol. Endocrinol. 28:111-123 (2002).		
DR	EWEL; AJ2889717; CAC41352.1; --		
DR	HSP; P23385; IEWK.		
DR	GO: GO:0016020; C:membrane; IEA.		
DR	GO: GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.		
DR	GO: GO:0004872; F:receptor activity; IEA.		
DR	InterPro: IPRO01828; ANF receptor.		
DR	InterPro: IPRO00068; Ca_sens receptor.		
DR	InterPro: IPRO00337; GPCR_MgF.		
DR	InterPro: IPRO11500; NCD3G_GPCR.		
DR	Pfam: PF00003; 7tm_3; 1.		
DR	Pfam: PF01094; ANF_receptor; 1.		
DR	Pfam: PF07562; NCD3G; 1.		
DR	PRINTS; PR00592; CASSENSNGR.		
DR	PRINTS; PR00248; GPCRMRG.		
DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.		
DR	PROSITE; PS00259; G_PROTEIN_RECEP_F3_1; 1.		
KW	RECEPTOR.		
SQ	SEQUENCE 940 AA; 105455 MW; 19C3CEDC75A03E3F9 CRC64;		
Query Match 68.5%; Score 3705.5; DB 2; Length 940;			
Best Local Similarity 73.2%; Pred. No. 1.5e-251;			
Matches 700; Conservative 105; Mismatches 118; Indels 33; Gaps 7			
Qy	8	LLFLGFTLLQSNVSGYGNBPAAKGGDILGLGLFFPIHFVGAAKQDLKSRPEATKCIRY 67	
Db	8	LLILUG----SSVISTYGHQAQWTDGILGLGLFFPIHFVGAAKQDLAARPESSQCVRF 63	
Qy	68	NFRGFRWLQAMIFA:BEINNSMTFLPNITLGYRIFDTCNTVSKALEATLGFVAQNKIDSL 127	
Db	64	NFRGFRWLQAMIFA:DEINNSSTLLPNITLGYRIFDTCNTVSKALEATLGFVAQNKIDSL 123	
Qy	128	NLDEFNCSDHPIPSITAVVGATGSGISTAVANLLGLFVIPPVSVASSRLLSNKNKYKAF 189	
Db	124	NLDEFNCNDIHPIATIAVVGAGSVAVANLLGLFVIPPVSVASSRLLSNKNKYKSF 183	
Qy	188	LRITPNDQQAAMAF:IEHFQNWVWGTLAADDYDREGIDKFFEEAVKRDICIDFSEMI 247	

```

184 MRTIPTDEYQATAMADIIIEFFQWNVYASVADDDYGRPGVEXFEKEMEERDICIHLNELI 243
248 SOYVYTKQLEFADVTNONSAAKVIIVFNGPDLPLQIIVERNITDRIWLASEAWASS 307
244 SQFEDHEIQALADRIENSTAKVIIVFASGPDIEFLIKEMVRNITDRIWLASEAWSSS 303
308 LIAKPYFHVVGTTIGFALRAGRIIPGNKFLKEVHPSSSDNGFVKEFEWETFCYFEK 367
304 LIAKPYLDVAGTTIGFALRAGRIIPGNKFLKEVHPSSSDNGFVKEFEWETFCYFEK 363
368 TITOLKNSKVPBGPAQOGSGKAGNSRRTALRHCTGEENITSVETPYLDYTHLRISYN 427
364 --PRQES-----NGS-----TSRPLCTGEEDITSVETPYLDYTHLRISYN 404
428 VYVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLHLKFTNSMGEOYDF 487
405 VYVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLHLKFTNSMGEOYDF 464
488 DQGLDKGNYTINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILMSGFSKVYVP 547
465 DENADLAANYTINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILMSGFSKVYVP 524
548 SNCSDCVPGTRKGIIEGPTCCFECMACAEFSDENDASACTCPNDFWSNENHTSCI 607
525 SNCSEDCGTRKGIIEGPTCCFECMACAEFSDENDASACTCPNDFWSNENHTCF 584
608 AKIEYLSWTEPFGIALTIFAVLGILITSVFVGVFKFRNTPIVKATNRELSYLLSLI 667
585 LKEIEFLSWTEPFGIALTIFAVLGILITSVFVGVFKFRNTPIVKATNRELSYLLSLI 644
668 CFSSSLIFIGPRWTCRLRPAFGISFVLGICILVKTNRVLVFAKIPTSILHRKW 727
645 CFPSSLLIFIGPRWTCRLRPAFGISFVLGICILVKTNRVLVFAKIPTSILHRKW 704
728 GLNLOFLVFLCILVQIVTCIIWLTAPPSSYRNHELEDEVIFITCDGSLMALGFLIGY 787
705 GLNLOFLVFLCILVQIVTCIIWLTAPPSSYRNHELEDEVIFITCDGSLMALGFLIGY 763
788 TCLLAACFFFAKSKRLBENNEAKPIFTSMILIFVIWISFIPAYVSTYCKFSAVEVI 847
764 TCLLAACFFFAKSKRLBENNEAKPIFTSMILIFVIWISFIPAYVSTYCKFSAVEAI 823
848 AILASFGLLGCTYFNKCVIILFKPCRNTEBVRCTAAHAFKVAARATLRSASAKRS 907
824 AILASFGMLACIFNKVVIILFKPSRNTIEBVRCTAAHAFKVAARATLRSASAKRS 883
908 SSLCGSTISSPASTCGPGLTWEMORCST-----QKVSFGSGTTLTSLSPFEETR 957
884 SSIGGSSSTPSSSI---SLKTNNGDCATSGKRPVRSFGSGTTLTSLSPFEESRR 936

RESULT 12
073635 PRELIMINARY; PRT; 940 AA.
AC 073635;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Calcium2+ sensing receptor
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]_TaxID=31033;
RP SEQUENCE FROM N.A.
RX MEDLINE=98226788; PubMed=9560249;
RA Naito T., Saito Y., Yamamoto J., Nozaki Y., Tomura K., Hazama M.,
RA Nakanishi S., Brenner S.;
RT "Putative pheromone receptors related to the Ca2+-sensing receptor in
RT Fugu.";
```

```

Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
DR EMBL; AB008957; BAA26122.1; -.
DR HSP; P23385; IEWT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto...; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF01094; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00248; GPCRNGR.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS02659; G_PROTEIN_RECP_F3_4; 1.
KW Receptor.
SQ SEQUENCE. 940 AA; 105813 MW; 06DAB7803B6878B3 CRC64;

Query Match 67.4%; Score 3644.5; DB 2; Length 940;
Best Local Similarity 71.6%; Pred. No. 2.9e-247;
Matches 687; Conservative 114; Mismatches 124; Indels 35; Gaps 9;

QY 4 LHCOLLFLGFTLLQSYNVSGYGNQAKKGGDIILGGLPFIHFGVAAKDDKLSREATK 63
DB 6 LH-YLIDLG-----SGVISTYGNQRAQMTGDIILGGLPFIHFGISSKDNLAARESTK 60
QY 64 CIRYNGRFRWLQAMIFAEIEINNSMTFLNITLGYRIEDTNTVSKALEATLSFVAQNK 123
DB 61 CVRFNFRGFWLQAMVFAIEEINNSMTFLNITLGYRIEDTNTVSKALEATLSFVAQNK 120
QY 124 IDSINLDFCNCSDHPSTIAVVGATSGISITAVANLLGLFYIPOVSYASSRLLSNKE 183
DB 121 IDSINLDFCNCSDHPSTIAVVGATSGISITAVANLLGLFYIPOVSYASSRLLSNKE 180
QY 184 YKAFRTIPDEHQATAMADVIEYFQWNVYASVADDDYGRPGVEXFEKEMEERDICIHL 240
DB 181 YKAFRTIPDEHQATAMADVIEYFQWNVYASVADDDYGRPGVEXFEKEMEERDICIHL 240
QY 244 SEMISQYTKQLEFADVTNONSAAKVIIVFNGPDLPLQIIVERNITDRIWLASEAW 303
DB 241 NELISQYFDECEIKALVDRIENSTAKVIIVFASGPDIEFLIKEMVRNITDRIWLASEAW 300
QY 304 ASSSLIAKPYFHVVGTTIGFALRAGRIIPGNKFLKEVHPSSSDNGFVKEFEWETFCY 363
DB 301 ASSSLIAKPYFHVVGTTIGFALRAGRIIPGNKFLKEVHPSSSDNGFVKEFEWETFCY 360
QY 364 FTBKTTLTKNSKVPBGPAQOGSGKAGNSRRTALRHCTGEENITSVETPYLDYTHLR 423
DB 361 LEDS--PRQES-----NGS-----DSRPLCTGEEDITSVETPYLDYTHLR 401
QY 424 ISYVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLHLKFTNSMGE 483
DB 402 ISYVAVYSIAHALQDIHSCKPGTIGFANGSCADIKKVEAWQVNLHLHLKFTNSMGE 461
QY 484 QVDFDQGLDKGNYTINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILMSGFSK 543
DB 462 KVHFDENADMEANYTINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILMSGFSK 521
QY 544 VVFPNCSRDVCGTRKGIIEGPTCCFECMACAEFSDENDASACTCPNDFWSNENHT 603
DB 522 EYVFPNCSRDVCGTRKGIIEGPTCCFECMACAEFSDENDASACTCPNDFWSNENHT 581
QY 604 TSICAKIEYLSWTEPFGIALTIFAVLGILITSVFVGVFKFRNTPIVKATNRELSYLL 663
DB 582 TFCFLKEIEFLSWTEPFGIALTIFAVLGILITSVFVGVFKFRNTPIVKATNRELSYLL 641
QY 664 FSLICFSSSLIFIGPRWTCRLRPAFGISFVLGICILVKTNRVLVFAKIPTSILHR 723
DB 642 LSLICFSSSLIFIGPRWTCRLRPAFGISFVLGICILVKTNRVLVFAKIPTSILHR 701
QY 724 RKWVGLNLOFLVFLCILVQIVTCIIWLTAPPSSYRNHELEDEVIFITCDGSLMALGF 783
```


Db 8 LVLGFSV-----ISTYGPQRAQKTDGILLGGLPFMHFGVTSKDQDLAARPESTECVRY 63
 QY 68 NFRGFWLQAMFAIEEINNSMTFNPITLGYRIFDTCTNTVSKALEATLSFVAQNKIDSL 127
 Db 64 NFRGFWLQAMFAIEEINNSMTFNPITLGYRIFDTCTNTVSKALEATLSFVAQNKIDSL 123
 QY 128 NLDFCNCSHDPSTTAVGATGSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF 187
 Db 124 NLDFCNCSHDPSTTAVGATGSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF 183
 QY 188 LRTIPNDEQATAMABIEBHFWNVTGLAADDVGRPGIDKFRPEAVKRDICIDFSEMI 247
 Db 184 MRTIPNDEQATAMABIEBHFWNVTGLAADDVGRPGIDKFRPEAVKRDICIDFSEMI 243
 QY 248 SQYTTQKLEFIADVTQNSAKVIVVFSNGPDLPLQIIEVNRNITDRIWLASEAWASS 307
 Db 244 SQYFEWQIQLVDRITENSASVIVVFSNGPDLPLQIIEVNRNITDRIWLASEAWASS 303
 QY 308 LIAKPEYFHVVGSTIGFALRAGRIQGNKFLXEVHPSRSSDNGFVKEPWEETFCYFTEK 367
 Db 304 LIAKPEYFHVVGSTIGFALRAGRIQGNKFLXEVHPSRSSDNGFVKEPWEETFCYFTEK 363
 QY 368 TITQLNKSVFSPGAPAAQDGGKAGNSRRRTALRHFTCTGSEENITSVETPYDYLRLISYN 427
 Db 364 --QRLRDSB-----NGS-----TSFRPLCTGEEDIMGAETPYDYLRLISYN 404
 QY 428 VYVAVYSIAHALQDHSCKPRTGIFANGSCADIKKVEAWQVNLHLHLKFTNSMGEQYDF 487
 Db 405 VYVAVHSIAQALQDILCTCPGRGFFSNNSCADIKKIEAWQVNLHLHLKFTNSMGEQYDF 464
 QY 488 DQDGLKGNVTIINWOLSADESVLPHEVGNVNAKPSDRININEKILMSGFSKVPWF 547
 Db 465 DENADPSGNYTIINWOLSADESVLPHEVGNVNAKPSDRININEKILMSGFSKVPWF 524
 QY 548 SNGSRDVCPTGRKGIIEGPTCCFCMCACAGEFSDENDASACTKPNDFNSNHNHTSCI 607
 Db 525 SNGSECEPTGRKGIIEGPTCCFCMCACAGEFSDENDASACTKPNDFNSNHNHTSCF 584
 QY 608 AKIEVLSWTEPGIALTITFAVLGILITFVLGVFKPNTPIVATNRRLSYLLLSLI 667
 Db 585 LKIEFELSWTEPGIALTITFAVLGILITFVLGVFKPNTPIVATNRRLSYLLLSLI 644
 QY 668 CCFSSSLIFIGPRDWTCLRQPAFGISFVLCSICILVKNRVLVFAKPISTLSHRXWV 727
 Db 645 CCFSSSLIFIGPRDWTCLRQPAFGISFVLCSICILVKNRVLVFAKPISTLSHRXWV 704
 QY 728 GLNLQFLVFLCIVLQVITCITWLTAPSSVYRNEHEDEVIFITCDGSLMALGFLICY 787
 Db 705 GLNLQFLVFLCIVLQVITCITWLTAPSSVYRNEHEDEVIFITCDGSLMALGFLICY 763
 QY 788 TCLLAACFFFAFKSKPLNFENAKFIITFSMLIPIFVIMISIPAYSTYKGFVSAVEVI 847
 Db 764 TCLLAACFFFAFKSKPLNFENAKFIITFSMLIPIFVIMISIPAYSTYKGFVSAVEVI 823
 QY 848 AILASSFGLLGIYFNKCVII 868
 Db 824 AILASSFGLLGIYFNKCVII 844
 RESULT 15
 Q8CDP3 PRELIMINARY; PRT; 783 AA.
 AC Q8CDP3
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:4930542I18 product:calcium-sensing receptor, full
 DE insert sequence. (fragment).
 GN Name=Gprc2a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The PANTOM Consortium;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hatada A.,
 RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK029770; BAC26608.1; -;
 DR MGD; MGII135151; Gprc2a.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto...; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR001828; ANF receptor.
 DR InterPro; IPR000068; Ca sens receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR011500; NCD3G_GPCR.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF receptor; 1.
 DR Pfam; PF07562; NCD3G; 1.

DR PRINTS; PRO0592; CASENSINGR.
DR PRINTS; PRO0248; GPCRMRG.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 783 AA; 87795 MW; 64BAE914566E19D5 CRC64;

Query Match 50.0%; Score 2707.5; DB 2; Length 783;
Best Local Similarity 70.8%; Pred. No. 1.9e-181;
Matches 533; Conservative 56; Mismatches 109; Indels 55; Gaps 7;

QY 301 EAWASSLIAPKPEYHVVGGTIGTIPALRAGRIPGPNKFLKEVHPSSSDNGFVKFEWETP 360
DB 1 EAWASSLIAPKPEYHVVGGTIGTIPALRAGRIPGPNKFLKEVHPSSSDNGFVKFEWETP 60

QY 361 NCYFTEKTLTQLK-NSKYPSHGPAQGDGSKAGNSRRTALRHPCTGGEENITSVETPYLDY 419
DB 61 NCYFTEKTLTQLK-NSKYPSHGPAQGDGSKAGNSRRTALRHPCTGGEENITSVETPYLDY 115

QY 420 TRLRISYNYVAVYSIAHALQDIHSCPGTGFANGSCADIKKVEAWQVLNHLHLKFTN 479
DB 116 EHLRISYNYVAVYSIAHALQDIHSCPGTGFANGSCADIKKVEAWQVLNHLHLKFTN 175

QY 480 SMGEQVDFDDQDLKGNVTIINWQISAEDESVLFEVGNVYAYAKPSDRNLNINEKKILWS 539
DB 176 NMGEQVDFDDQDLKGNVTIINWQISAEDESVLFEVGNVYAYAKPSDRNLNINEKKILWS 235

QY 540 GFSKVVPFNSCSDVCPGTRKGIIEGEPTCCFECMACAEGFSDENDASACTKCPNDFWS 599
DB 236 GFSKVVPFNSCSDVCPGTRKGIIEGEPTCCFECMACAEGFSDENDASACTKCPNDFWS 295

QY 600 NENHTSCIATKEIYVSWTEPPGIALTIFAVLGILITSVLGVFIKFRNTPIVKATNRELS 659
DB 296 NENHTSCIATKEIYVSWTEPPGIALTIFAVLGILITSVLGVFIKFRNTPIVKATNRELS 355

QY 660 YLLFSLICCFSSLIFFIGEPDWTCLRQAPAGISFVLICILVKTNRVLLVFEAKIP 719
DB 356 YLLFSLICCFSSLIFFIGEPDWTCLRQAPAGISFVLICILVKTNRVLLVFEAKIP 415

QY 720 TSLHRKWGLNLQFLVFLCIIIVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDGSLM 779
DB 416 TSLHRKWGLNLQFLVFLCIIIVQIVTCIIWLYTAPPSSYRNHELEDEVIFITCDGSLM 475

QY 780 ALGFLIGYTCILAAICFFPAFKSKLPENFNEAKITPSMLIFFIWIWISFIPAYVSTYK 839
DB 476 ALGFLIGYTCILAAICFFPAFKSKLPENFNEAKITPSMLIFFIWIWISFIPAYVSTYK 535

QY 840 FVSAYEVIALASSFGLLCIYFNKCYIILPFCRNTIEEVRCSAAHAFKVAARATLRR 899
DB 536 FVSAYEVIALASSFGLLCIYFNKCYIILPFCRNTIEEVRCSAAHAFKVAARATLRR 595

QY 900 SAASRRSSSLCGSTISSPASSTCGPG-----LTME 930
DB 596 SAASRRSSSLCGSTISSPASSTCGPG-----LTME 655

QY 931 MQ-----RGSTOKVSGGTIVLSLSEETGRVATLSRTARSRNADGRSGDDLPSSR 982
DB 656 MQ-----RGSTOKVSGGTIVLSLSEETGRVATLSRTARSRNADGRSGDDLPSSR 714

QY 983 HHQDGPQKCEFPQANDARYKAAPTKGTLESFG 1015
DB 715 HHQDGPQKCEFPQANDARYKAAPTKGTLESFG 736

Search completed: November 17, 2004, 11:57:23
Job time : 435 secs

This Page Blank (uspto)